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### INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7:
 C07H 21/04, C07K 1/00, 14/00, C12N 1/21, 15/00, 15/09, 15/63, 15/70, C12P 19/34

(11) International Publication Number:

WO 00/52027

(43) International Publication Date:

8 September 2000 (08.09.00)

(21) International Application Number:

PCT/US00/05432

A1

(22) International Filing Date:

2 March 2000 (02.03.00)

(30) Priority Data:

60/122,389 2 March 1999 (02.03.99) US 60/126,049 23 March 1999 (23.03.99) US 60/136,744 28 May 1999 (28.05.99) US

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(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

#### Published

With international search report.

With an indication in relation to deposited biological material furnished under Rule 13bis separately from the description.

(54) Title: COMPOSITIONS AND METHODS FOR USE IN RECOMBINATIONAL CLONING OF NUCLEIC ACIDS

#### (57) Abstract

The present invention relates generally to compositions and methods for use in recombinational cloning of nucleic acid molecules. In particular, the invention relates to nucleic acid molecules encoding one or more recombination sites or portions thereof, to nucleic acid molecules comprising one or more of these recombination site nucleotide sequences and optionally comprising one or more additional physical or functional nucleotide sequences. The invention also relates to vectors comprising the nucleic acid molecules of the invention, to host cells comprising the vectors or nucleic acid molecules of the invention, to methods of producing polypeptides using the nucleic acid molecules of the invention, and to polypeptides encoded by these nucleic acid molecules or produced by the methods of the invention. The invention also relates to antibodies that bind to one or more polypeptides of the invention or epitopes thereof. The invention also relates to the use of these compositions in methods for recombinational cloning of nucleic acids, in vitro and in vivo, to provide chimeric DNA molecules that have particular characteristics and/or DNA segments.

Document AP20 Appl. No. 09/732,914

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# Compositions and Methods for Use in Recombinational Cloning of Nucleic Acids

#### BACKGROUND OF THE INVENTION

#### Field of the Invention

The present invention relates generally to recombinant DNA technology. More particularly, the present invention relates to compositions and methods for use in recombinational cloning of nucleic acid molecules. The invention relates specifically to nucleic acid molecules encoding one or more recombination sites or one or more partial recombination sites, particularly attB, attP, attL, and attR, and fragments, mutants, variants and derivatives thereof. The invention also relates to such nucleic acid molecules wherein the one or more recombination site nucleotide sequences is operably linked to the one or more additional physical or functional nucleotide sequences. The invention also relates to vectors comprising the nucleic acid molecules of the invention, to host cells comprising the vectors or nucleic acid molecules of the invention, to methods of producing polypeptides and RNAs encoded by the nucleic acid molecules of the invention, and to polypeptides encoded by these nucleic acid molecules or produced by the methods of the invention, which may be fusion proteins. The invention also relates to antibodies that bind to one or more polypeptides of the invention or epitopes thereof, which may be monoclonal or polyclonal antibodies. The invention also relates to the use of these nucleic acid molecules, vectors, polypeptides and antibodies in methods for recombinational cloning of nucleic acids, in vitro and in vivo, to provide chimeric DNA molecules that have particular characteristics and/or DNA segments. More particularly, the antibodies of the invention may be used to identify and/or purify proteins or fusion proteins encoded by the nucleic acid molecules or vectors of the invention, or to identify and/or purify the nucleic acid molecules of the invention.

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#### Related Art

Site-specific recombinases. Site-specific recombinases are proteins that are present in many organisms (e.g. viruses and bacteria) and have been characterized to have both endonuclease and ligase properties. These recombinases (along with associated proteins in some cases) recognize specific sequences of bases in DNA and exchange the DNA segments flanking those segments. The recombinases and associated proteins are collectively referred to as "recombination proteins" (see, e.g., Landy, A., Current Opinion in Biotechnology 3:699-707 (1993)).

Numerous recombination systems from various organisms have been described. See, e.g., Hoess et al., Nucleic Acids Research 14(6):2287 (1986); Abremski et al., J. Biol. Chem. 261(1):391 (1986); Campbell, J. Bacteriol. 174(23):7495 (1992); Qian et al., J. Biol. Chem. 267(11):7794 (1992); Araki et al., J. Mol. Biol. 225(1):25 (1992); Maeser and Kahnmann Mol. Gen. Genet. 230:170-176) (1991); Esposito et al., Nucl. Acids Res. 25(18):3605 (1997).

Many of these belong to the integrase family of recombinases (Argos et al. EMBO J. 5:433-440 (1986); Voziyanov et al., Nucl. Acids Res. 27:930 (1999)). Perhaps the best studied of these are the Integrase/att system from bacteriophage  $\lambda$  (Landy, A. Current Opinions in Genetics and Devel. 3:699-707 (1993)), the Cre/loxP system from bacteriophage P1 (Hoess and Abremski (1990) In Nucleic Acids and Molecular Biology, vol. 4. Eds.: Eckstein and Lilley, Berlin-Heidelberg: Springer-Verlag; pp. 90-109), and the FLP/FRT system from the Saccharomyces cerevisiae 2  $\mu$  circle plasmid (Broach et al. Cell 29:227-234 (1982)).

Backman (U.S. Patent No. 4,673,640) discloses the *in vivo* use of  $\lambda$  recombinase to recombine a protein producing DNA segment by enzymatic site-specific recombination using wild-type recombination sites attB and attP.

Hasan and Szybalski (Gene 56:145-151 (1987)) discloses the use of  $\lambda$  Int recombinase in vivo for intramolecular recombination between wild type attP and attB sites which flank a promoter. Because the orientations of these sites are

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inverted relative to each other, this causes an irreversible flipping of the promoter region relative to the gene of interest.

Palazzolo et al. Gene 88:25-36 (1990), discloses phage lambda vectors having bacteriophage  $\lambda$  arms that contain restriction sites positioned outside a cloned DNA sequence and between wild-type loxP sites. Infection of E. coli cells that express the Cre recombinase with these phage vectors results in recombination between the loxP sites and the *in vivo* excision of the plasmid replicon, including the cloned cDNA.

Pósfai et al. (Nucl. Acids Res. 22:2392-2398 (1994)) discloses a method for inserting into genomic DNA partial expression vectors having a selectable marker, flanked by two wild-type FRT recognition sequences. FLP site-specific recombinase as present in the cells is used to integrate the vectors into the genome at predetermined sites. Under conditions where the replicon is functional, this cloned genomic DNA can be amplified.

Bebee *et al.* (U.S. Patent No. 5,434,066) discloses the use of site-specific recombinases such as Cre for DNA containing two *loxP* sites for *in vivo* recombination between the sites.

Boyd (*Nucl. Acids Res. 21*:817-821 (1993)) discloses a method to facilitate the cloning of blunt-ended DNA using conditions that encourage intermolecular ligation to a dephosphorylated vector that contains a wild-type loxP site acted upon by a Cre site-specific recombinase present in *E. coli* host cells.

Waterhouse et al. (WO 93/19172 and Nucleic Acids Res. 21 (9):2265 (1993)) disclose an in vivo method where light and heavy chains of a particular antibody were cloned in different phage vectors between loxP and loxP 511 sites and used to transfect new E. coli cells. Cre, acting in the host cells on the two parental molecules (one plasmid, one phage), produced four products in equilibrium: two different cointegrates (produced by recombination at either loxP or loxP 511 sites), and two daughter molecules, one of which was the desired product.

Schlake & Bode (*Biochemistry 33*:12746-12751 (1994)) discloses an *in vivo* method to exchange expression cassettes at defined chromosomal locations, each flanked by a wild type and a spacer-mutated FRT recombination site. A

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double-reciprocal crossover was mediated in cultured mammalian cells by using this FLP/FRT system for site-specific recombination.

Hartley et al. (U.S. Patent No. 5,888,732) disclose compositions and methods for recombinational exchange of nucleic acid segments and molecules, including for use in recombinational cloning of a variety of nucleic acid molecules in vitro and in vivo, using a combination of wildtype and mutated recombination sites and recombination proteins.

*Transposases.* The family of enzymes, the transposases, has also been used to transfer genetic information between replicons. Transposons are structurally variable, being described as simple or compound, but typically encode the recombinase gene flanked by DNA sequences organized in inverted orientations. Integration of transposons can be random or highly specific. Representatives such as Tn7, which are highly site-specific, have been applied to the *in vivo* movement of DNA segments between replicons (Lucklow *et al.*, *J. Virol.* 67:4566-4579 (1993)).

Devine and Boeke *Nucl. Acids Res.* 22:3765-3772 (1994), discloses the construction of artificial transposons for the insertion of DNA segments, *in vitro*, into recipient DNA molecules. The system makes use of the integrase of yeast TY1 virus-like particles. The DNA segment of interest is cloned, using standard methods, between the ends of the transposon-like element TY1. In the presence of the TY1 integrase, the resulting element integrates randomly into a second target DNA molecule.

Recombination Sites. Also key to the integration/recombination reactions mediated by the above-noted recombination proteins and/or transposases are recognition sequences, often termed "recombination sites," on the DNA molecules participating in the integration/recombination reactions. These recombination sites are discrete sections or segments of DNA on the participating nucleic acid molecules that are recognized and bound by the recombination proteins during the initial stages of integration or recombination. For example, the recombination site for Cre recombinase is loxP which is a 34 base pair sequence comprised of two 13 base pair inverted repeats (serving as the recombinase binding sites) flanking an 8 base pair core sequence. See Figure 1 of Sauer, B., Curr. Opin. Biotech.

5:521-527 (1994). Other examples of recognition sequences include the *attB*, *attP*, *attL*, and *attR* sequences which are recognized by the recombination protein λ Int. *attB* is an approximately 25 base pair sequence containing two 9 base pair core-type Int binding sites and a 7 base pair overlap region, while *attP* is an approximately 240 base pair sequence containing core-type Int binding sites and arm-type Int binding sites as well as sites for auxiliary proteins integration host factor (IHF), FIS and excisionase (Xis). *See* Landy, *Curr. Opin. Biotech.* 3:699-707 (1993); *see also* U.S. Patent No. 5,888,732, which is incorporated by reference herein.

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DNA cloning. The cloning of DNA segments currently occurs as a daily routine in many research labs and as a prerequisite step in many genetic analyses. The purpose of these clonings is various, however, two general purposes can be considered: (1) the initial cloning of DNA from large DNA or RNA segments (chromosomes, YACs, PCR fragments, mRNA, etc.), done in a relative handful of known vectors such as pUC, pGem, pBlueScript, and (2) the subcloning of these DNA segments into specialized vectors for functional analysis. A great deal of time and effort is expended both in the transfer of DNA segments from the initial cloning vectors to the more specialized vectors. This transfer is called subcloning.

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The basic methods for cloning have been known for many years and have changed little during that time. A typical cloning protocol is as follows:

- (1) digest the DNA of interest with one or two restriction enzymes:
- (2) gel purify the DNA segment of interest when known;
- (3) prepare the vector by cutting with appropriate restriction enzymes, treating with alkaline phosphatase, gel purify etc., as appropriate;
- (4) ligate the DNA segment to the vector, with appropriate controls to eliminate background of uncut and self-ligated vector;
  - (5) introduce the resulting vector into an E. coli host cell;
  - (6) pick selected colonies and grow small cultures overnight:
  - (7) make DNA minipreps; and

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(8) analyze the isolated plasmid on agarose gels (often after diagnostic restriction enzyme digestions) or by PCR.

The specialized vectors used for subcloning DNA segments are functionally diverse. These include but are not limited to: vectors for expressing nucleic acid molecules in various organisms; for regulating nucleic acid molecule expression; for providing tags to aid in protein purification or to allow tracking of proteins in cells; for modifying the cloned DNA segment (e.g., generating deletions); for the synthesis of probes (e.g., riboprobes); for the preparation of templates for DNA sequencing; for the identification of protein coding regions; for the fusion of various protein-coding regions; to provide large amounts of the DNA of interest, etc. It is common that a particular investigation will involve subcloning the DNA segment of interest into several different specialized vectors.

As known in the art, simple subclonings can be done in one day (e.g., the DNA segment is not large and the restriction sites are compatible with those of the subcloning vector). However, many other subclonings can take several weeks, especially those involving unknown sequences, long fragments, toxic genes, unsuitable placement of restriction sites, high backgrounds, impure enzymes, etc. Subcloning DNA fragments is thus often viewed as a chore to be done as few times as possible.

Several methods for facilitating the cloning of DNA segments have been described, e.g., as in the following references.

Ferguson, J., et al. Gene 16:191 (1981), discloses a family of vectors for subcloning fragments of yeast DNA. The vectors encode kanamycin resistance. Clones of longer yeast DNA segments can be partially digested and ligated into the subcloning vectors. If the original cloning vector conveys resistance to ampicillin, no purification is necessary prior to transformation, since the selection will be for kanamycin.

Hashimoto-Gotoh, T., et al. Gene 41:125 (1986), discloses a subcloning vector with unique cloning sites within a streptomycin sensitivity gene; in a streptomycin-resistant host, only plasmids with inserts or deletions in the dominant sensitivity gene will survive streptomycin selection.

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Accordingly, traditional subcloning methods, using restriction enzymes and ligase, are time consuming and relatively unreliable. Considerable labor is expended, and if two or more days later the desired subclone can not be found among the candidate plasmids, the entire process must then be repeated with alternative conditions attempted. Although site specific recombinases have been used to recombine DNA in vivo, the successful use of such enzymes in vitro was expected to suffer from several problems. For example, the site specificities and efficiencies were expected to differ in vitro; topologically linked products were expected, and the topology of the DNA substrates and recombination proteins was expected to differ significantly in vitro (see, e.g., Adams et al, J. Mol. Biol. 226:661-73 (1992)). Reactions that could go on for many hours in vivo were expected to occur in significantly less time in vitro before the enzymes became inactive. In addition, the stabilities of the recombination enzymes after incubation for extended periods of time in in vitro reactions was unknown, as were the effects of the topologies (i.e., linear, coiled, supercoiled, etc.) of the nucleic acid molecules involved in the reaction. Multiple DNA recombination products were expected in the biological host used, resulting in unsatisfactory reliability, specificity or efficiency of subcloning. Thus, in vitro recombination reactions were not expected to be sufficiently efficient to yield the desired levels of product.

Accordingly, there is a long felt need to provide an alternative subcloning system that provides advantages over the known use of restriction enzymes and ligases.

# SUMMARY OF THE INVENTION

The present invention relates to nucleic acid molecules encoding one or more recombination sites or one or more partial recombination sites, particularly attB, attP, attL, and attR, and fragments, mutants, variants and derivatives thereof. The invention also relates to such nucleic acid molecules comprising one or more of the recombination site nucleotide sequences or portions thereof and one or more additional physical or functional nucleotide sequences, such as those

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encoding one or more multiple cloning sites, one or more transcription termination sites, one or more transcriptional regulatory sequences (e.g., one or more promoters, enhancers, or repressors), one or more translational signal sequences, one or more nucleotide sequences encoding a fusion partner protein or peptide (e.g., GST, His<sub>6</sub> or thioredoxin), one or more selection markers or modules, one or more nucleotide sequences encoding localization signals such as nuclear localization signals or secretion signals, one or more origins of replication, one or more protease cleavage sites, one or more desired proteins or peptides encoded by a gene or a portion of a gene, and one or more 5' or 3' polynucleotide tails (particularly a poly-G tail). The invention also relates to such nucleic acid molecules wherein the one or more recombination site nucleotide sequences is operably linked to the one or more additional physical or functional nucleotide sequences.

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The invention also relates to primer nucleic acid molecules comprising the recombination site nucleotide sequences of the invention (or portions thereof), and to such primer nucleic acid molecules linked to one or more target-specific (e.g., one or more gene-specific) primer nucleic acid sequences. Such primers may also comprise sequences complementary or homologous to DNA or RNA sequences to be amplified, e.g., by PCR, RT-PCR, etc. Such primers may also comprise sequences or portions of sequences useful in the expression of protein genes (ribosome binding sites, localization signals, protease cleavage sites, repressor binding sites, promoters, transcription stops, stop codons, etc.). Said primers may also comprise sequences or portions of sequences useful in the manipulation of DNA molecules (restriction sites, transposition sites, sequencing primers, etc.). The primers of the invention may be used in nucleic acid synthesis and preferably are used for amplification (e.g., PCR) of nucleic acid molecules. When the primers of the invention include target- or gene-specific sequences (any sequence contained within the target to be synthesized or amplified including translation signals, gene sequences, stop codons, transcriptional signals (e.g., promoters) and the like), amplification or synthesis of target sequences or genes may be accomplished. Thus, the invention relates to synthesis of a nucleic acid molecules comprising mixing one or more primers of the invention with a nucleic acid

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template, and incubating said mixture under conditions sufficient to make a first nucleic acid molecule complementary to all or a portion of said template. Thus, the invention relates specifically to a method of synthesizing a nucleic acid molecule comprising:

(a) mixing a nucleic acid template with a polypeptide having polymerase activity and one or more primers comprising one or more recombination sites or portions thereof; and

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule complementary to all or a portion of said template and which preferably comprises one or more recombination sites or portions thereof.

Such method of the invention may further comprise incubating said first synthesized nucleic acid molecule under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule. Such synthesis may provide for a first nucleic acid molecule having a recombination site or portion thereof at one or both of its termini.

In a preferred aspect, for the synthesis of the nucleic acid molecules, at least two primers are used wherein each primer comprises a homologous sequence at its terminus and/or within internal sequences of each primer (which may have a homology length of about 2 to about 500 bases, preferably about 3 to about 100 bases, about 4 to about 50 bases, about 5 to about 25 bases and most preferably about 6 to about 18 base overlap). In a preferred aspect, the first such primer comprises at least one target-specific sequence and at least one recombination site or portion thereof while the second primer comprises at least one recombination site or portion thereof. Preferably, the homologous regions between the first and second primers comprise at least a portion of the recombination site. In another aspect, the homologous regions between the first and second primers may comprise one or more additional sequences, e.g., expression signals, translational start motifs, or other sequences adding functionality to the desired nucleic acid sequence upon amplification. In practice, two pairs of primers prime synthesis or amplification of a nucleic acid molecule. In a preferred aspect, all or at least a portion of the synthesized or amplified nucleic acid molecule will be homologous

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to all or a portion of the template and further comprises a recombination site or a portion thereof at at least one terminus and preferably both termini of the synthesized or amplified molecule. Such synthesized or amplified nucleic acid molecule may be double stranded or single stranded and may be used in the recombinational cloning methods of the invention. The homologous primers of the invention provide a substantial advantage in that one set of the primers may be standardized for any synthesis or amplification reaction. That is, the primers providing the recombination site sequences (without the target specific sequences) can be pre-made and readily available for use. This in practice allows the use of shorter custom made primers that contain the target specific sequence needed to synthesize or amplify the desired nucleic acid molecule. Thus, this provides reduced time and cost in preparing target specific primers (e.g., shorter primers containing the target specific sequences can be prepared and used in synthesis reactions). The standardized primers, on the other hand, may be produced in mass to reduce cost and can be readily provided (e.g., in kits or as a product) to facilitate synthesis of the desired nucleic acid molecules.

Thus, in one preferred aspect, the invention relates to a method of synthesizing or amplifying one or more nucleic acid molecules comprising:

- (a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity and at least a first primer comprising a template specific sequence (complementary to or capable of hybridizing to said templates) and at least a second primer comprising all or a portion of a recombination site wherein said at least a portion of said second primer is homologous to or complementary to at least a portion of said first primer; and
- (b) incubating said mixture under conditions sufficient to synthesize or amplify one or more nucleic acid molecules complementary to all or a portion of said templates and comprising one or more recombination sites or portions thereof at one and preferably both termini of said molecules.

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More specifically, the invention relates to a method of synthesizing or amplifying one or more nucleic acid molecules comprising:

- (a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity and at least a first primer comprising a template specific sequence (complementary to or capable of hybridizing to said templates) and at least a portion of a recombination site, and at least a second primer comprising all or a portion of a recombination site wherein said at least a portion of said recombination site on said second primer is complementary to or homologous to at least a portion of said recombination site on said first primer; and
- (b) incubating said mixture under conditions sufficient to synthesize or amplify one or more nucleic acid molecules complementary to all or a portion of said templates and comprising one or more recombination sites or portions thereof at one and preferably both termini of said molecules.

In a more preferred aspect, the invention relates to a method of amplifying or synthesizing one or more nucleic acid molecules comprising:

- (a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity and one or more first primers comprising at least a portion of a recombination site and a template specific sequence (complementary to or capable of hybridizing to said template);
- (b) incubating said mixture under conditions sufficient to synthesize or amplify one or more first nucleic acid molecules complementary to all or a portion of said templates wherein said molecules comprise at least a portion of a recombination site at one and preferably both termini of said molecules;
- (c) mixing said molecules with one or more second primers comprising one or more recombination sites, wherein said recombination sites of said second primers are homologous to or

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complementary to at least a portion of said recombination sites on said first nucleic acid molecules; and

(d) incubating said mixture under conditions sufficient to synthesize or amplify one or more second nucleic acid molecules complementary to all or a portion of said first nucleic acid molecules and which comprise one or more recombination sites at one and preferably both termini of said molecules.

The invention also relates to vectors comprising the nucleic acid molecules of the invention, to host cells comprising the vectors or nucleic acid molecules of the invention, to methods of producing polypeptides encoded by the nucleic acid molecules of the invention, and to polypeptides encoded by these nucleic acid molecules or produced by the methods of the invention, which may be fusion proteins. The invention also relates to antibodies that bind to one or more polypeptides of the invention or epitopes thereof, which may be monoclonal or polyclonal antibodies. The invention also relates to the use of these nucleic acid molecules, primers, vectors, polypeptides and antibodies in methods for recombinational cloning of nucleic acids, *in vitro* and *in vivo*, to provide chimeric DNA molecules that have particular characteristics and/or DNA segments.

The antibodies of the invention may have particular use to identify and/or purify peptides or proteins (including fusion proteins produced by the invention), and to identify and/or purify the nucleic acid molecules of the invention or portions thereof.

The methods for *in vitro* or *in vivo* recombinational cloning of nucleic acid molecule generally relate to recombination between at least a first nucleic acid molecule having at least one recombination site and a second nucleic acid molecule having at least one recombination site to provide a chimeric nucleic acid molecule. In one aspect, the methods relate to recombination between and first vector having at least one recombination site and a second vector having at least one recombination site to provide a chimeric vector. In another aspect, a nucleic acid molecule having at least one recombination site is combined with a vector having at least one recombination site to provide a chimeric vector. In a most preferred aspect, the nucleic acid molecules or vectors used in recombination

comprise two or more recombination sites. In a more specific embodiment of the invention, the recombination methods relate to a Destination Reaction (also referred to herein as an "LR reaction") in which recombination occurs between an Entry clone and a Destination Vector. Such a reaction transfers the nucleic acid molecule of interest from the Entry Clone into the Destination Vector to create an Expression Clone. The methods of the invention also specifically relate to an Entry or Gateward reaction (also referred to herein as a "BP reaction") in which an Expression Clone is recombined with a Donor vector to produce an Entry clone. In other aspects, the invention relates to methods to prepare Entry clones by combining an Entry vector with at least one nucleic acid molecule (e.g., gene or portion of a gene). The invention also relates to conversion of a desired vector into a Destination Vector by including one or more (preferably at least two) recombination sites in the vector of interest. In a more preferred aspect, a nucleic acid molecule (e.g., a cassette) having at least two recombination sites flanking a selectable marker (e.g., a toxic gene or a genetic element preventing the survival of a host cell containing that gene or element, and/or preventing replication, partition or heritability of a nucleic acid molecule (e.g., a vector or plasmid) comprising that gene or element) is added to the vector to make a Destination Vector of the invention.

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Preferred vectors for use in the invention include prokaryotic vectors, eukaryotic vectors, or vectors which may shuttle between various prokaryotic and/or eukaryotic systems (e.g. shuttle vectors). Preferred prokaryotic vectors for use in the invention include but are not limited to vectors which may propagate and/or replicate in gram negative and/or gram positive bacteria, including bacteria of the genera Escherichia, Salmonella, Proteus, Clostridium, Klebsiella, Bacillus, Streptomyces, and Pseudomonas and preferably in the species E. coli. Eukaryotic vectors for use in the invention include vectors which propagate and/or replicate and yeast cells, plant cells, mammalian cells, (particularly human and mouse), fungal cells, insect cells, nematode cells, fish cells and the like. Particular vectors of interest include but are not limited to cloning vectors, sequencing vectors, expression vectors, fusion vectors, two-hybrid vectors, gene therapy vectors, phage display vectors, gene-targeting vectors, PACs, BACs, YACs, MACs, and

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reverse two-hybrid vectors. Such vectors may be used in prokaryotic and/or eukaryotic systems depending on the particular vector.

In another aspect, the invention relates to kits which may be used in carrying out the methods of the invention, and more specifically relates to cloning or subcloning kits and kits for carrying out the LR Reaction (e.g., making an Expression Clone), for carrying out the BP Reaction (e.g., making an Entry Clone), and for making Entry Clone and Destination Vector molecules of the invention. Such kits may comprise a carrier or receptacle being compartmentalized to receive and hold therein any number of containers. Such containers may contain any number of components for carrying out the methods of the invention or combinations of such components. In particular, a kit of the invention may comprise one or more components (or combinations thereof) selected from the group consisting of one or more recombination proteins or auxiliary factors or combinations thereof, one or more compositions comprising one or more recombination proteins or auxiliary factors or combinations thereof (for example, GATEWAY™ LR Clonase™ Enzyme Mix or GATEWAY™ BP Clonase™ Enzyme Mix), one or more reaction buffers, one or more nucleotides, one or more primers of the invention, one or more restriction enzymes, one or more ligases, one or more polypeptides having polymerase activity (e.g., one or more reverse transcriptases or DNA polymerases), one or more proteinases (e.g., proteinase K or other proteinases), one or more Destination Vector molecules, one or more Entry Clone molecules, one or more host cells (e.g. competent cells, such as E. coli cells, yeast cells, animal cells (including mammalian cells, insect cells, nematode cells, avian cells, fish cells, etc.), plant cells, and most particularly E. coli DB3.1 host cells, such as E. coli LIBRARY EFFICIENCY® DB3.1™ Competent Cells), instructions for using the kits of the invention (e.g., to carry out the methods of the invention), and the like. In related aspects, the kits of the invention may comprise one or more nucleic acid molecules encoding one or more recombination sites or portions thereof, particularly one or more nucleic acid molecules comprising a nucleotide sequence encoding the one or more recombination sites or portions thereof of the invention. Preferably, such nucleic acid molecules comprise at least two recombination sites which flank a selectable

marker (e.g., a toxic gene and/or antibiotic resistance gene). In a preferred aspect, such nucleic acid molecules are in the form of a cassette (e.g., a linear nucleic acid molecule comprising one or more and preferably two or more recombination sites or portions thereof).

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Kits for inserting or adding recombination sites to nucleic acid molecules of interest may comprise one or more nucleases (preferably restriction endonucleases), one or more ligases, one or more topoisomerases, one or more polymerases, and one or more nucleic acid molecules or adapters comprising one or more recombination sites. Kits for integrating recombination sites into one or more nucleic acid molecules of interest may comprise one or more components (or combinations thereof) selected from the group consisting of one or more integration sequences comprising one or more recombination sites. Such integration sequences may comprise one or more transposons, integrating viruses, homologous recombination sequences, RNA molecules, one or more host cells and the like.

Kits for making the Entry Clone molecules of the invention may comprise any or a number of components and the composition of such kits may vary depending on the specific method involved. Such methods may involve inserting the nucleic acid molecules of interest into an Entry or Donor Vector by the recombinational cloning methods of the invention, or using conventional molecular biology techniques (e.g., restriction enzyme digestion and ligation). In a preferred aspect, the Entry Clone is made using nucleic acid amplification or synthesis products. Kits for synthesizing Entry Clone molecules from amplification or synthesis products may comprise one or more components (or combinations thereof) selected from the group consisting of one or more Donor Vectors (e.g., one or more attP vectors including, but not limited to, pDONR201 (Figure 49), pDONR202 (Figure 50), pDONR203 (Figure 51), pDONR204 (Figure 52), pDONR205 (Figure 53), pDONR206 (Figure 53), and the like), one or more polypeptides having polymerase activity (preferably DNA polymerases and most preferably thermostable DNA polymerases), one or more proteinases, one or more reaction buffers, one or more nucleotides, one or more primers comprising one or

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more recombination sites or portions thereof, and instructions for making one or more Entry Clones.

Kits for making the Destination vectors of the invention may comprise any number of components and the compositions of such kits may vary depending on the specific method involved. Such methods may include the recombination methods of the invention or conventional molecular biology techniques (e.g., restriction endonuclease digestion and ligation). In a preferred aspect, the Destination vector is made by inserting a nucleic acid molecule comprising at least one recombination site (or portion thereof) of the invention (preferably a nucleic acid molecule comprising at least two recombination sites or portions thereof flanking a selectable marker) into a desired vector to convert the desired vector into a Destination vector of the invention. Such kits may comprise at least one component (or combinations thereof) selected from the group consisting of one or more restriction endonucleases, one or more ligases, one or more polymerases, one or more nucleotides, reaction buffers, one or more nucleic acid molecules comprising at least one recombination site or portion thereof (preferably at least one nucleic acid molecule comprising at least two recombination sites flanking at least one selectable marker, such as a cassette comprising at least one selectable marker such as antibiotic resistance genes and/or toxic genes), and instructions for making such Destination vectors.

The invention also relates to kits for using the antibodies of the invention in identification and/or isolation of peptides and proteins (which may be fusion proteins) produced by the nucleic acid molecules of the invention, and for identification and/or isolation of the nucleic acid molecules of the invention or portions thereof. Such kits may comprise one or more components (or combination thereof) selected from the group consisting of one or more antibodies of the invention, one or more detectable labels, one or more solid supports and the like.

Other preferred embodiments of the present invention will be apparent to one of ordinary skill in light of what is known in the art, in light of the following drawings and description of the invention, and in light of the claims.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts one general method of the present invention, wherein the starting (parent) DNA molecules can be circular or linear. The goal is to exchange the new subcloning vector D for the original cloning vector B. It is desirable in one embodiment to select for AD and against all the other molecules, including the Cointegrate. The square and circle are sites of recombination: e.g., lox (such as loxP) sites, att sites, etc. For example, segment D can contain expression signals, protein fusion domains, new drug markers, new origins of replication, or specialized functions for mapping or sequencing DNA. It should be noted that the cointegrate molecule contains Segment D (Destination vector) adjacent to segment A (Insert), thereby juxtaposing functional elements in D with the insert in A. Such molecules can be used directly in vitro (e.g., if a promoter is positioned adjacent to a gene-for in vitro transcription/translation) or in vivo (following isolation in a cell capable of propagating ccdB-containing vectors) by selecting for the selection markers in Segments B+D. As one skilled in the art will recognize, this single step method has utility in certain envisioned applications of the invention.

Figure 2 is a more detailed depiction of the recombinational cloning system of the invention, referred to herein as the "GATEWAY™ Cloning System." This figure depicts the production of Expression Clones via a "Destination Reaction," which may also be referred to herein as an "LR Reaction." A kan' vector (referred to herein as an "Entry clone") containing a DNA molecule of interest (e.g., a gene) localized between an attL1 site and an attL2 site is reacted with an amp' vector (referred to herein as a "Destination Vector") containing a toxic or "death" gene localized between an attR1 site and an attR2 site, in the presence of GATEWAY™ LR Clonase™ Enzyme Mix (a mixture of Int, IHF and Xis). After incubation at 25°C for about 60 minutes, the reaction yields an amp' Expression Clone containing the DNA molecule of interest localized between an attB1 site and an attB2 site, and a kan' byproduct molecule, as well as intermediates. The reaction mixture may then be transformed into host cells (e.g., E. coli) and clones containing the nucleic acid molecule of interest may

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be selected by plating the cells onto ampicillin-containing media and picking amp<sup>r</sup> colonies.

Figure 3 is a schematic depiction of the cloning of a nucleic acid molecule from an Entry clone into multiple types of Destination vectors, to produce a variety of Expression Clones. Recombination between a given Entry clone and different types of Destination vectors (not shown), via the LR Reaction depicted in Figure 2, produces multiple different Expression Clones for use in a variety of applications and host cell types.

Figure 4 is a detailed depiction of the production of Entry Clones via a "BP reaction," also referred to herein as an "Entry Reaction" or a "Gateward Reaction." In the example shown in this figure, an ampr expression vector containing a DNA molecule of interest (e.g., a gene) localized between an attB1 site and an attB2 site is reacted with a kan Donor vector (e.g., an attP vector, here, GATEWAYTM pDONR201 (see Figure 49A-C)) containing a toxic or "death" gene localized between an attP1 site and an attP2 site, in the presence of GATEWAY™ BP Clonase™ Enzyme Mix (a mixture of Int and IHF). After incubation at 25°C for about 60 minutes, the reaction yields a kan' Entry clone containing the DNA molecule of interest localized between an attL1 site and an attL2 site, and an ampr by-product molecule. The Entry clone may then be transformed into host cells (e.g., E. coli) and clones containing the Entry clone (and therefore the nucleic acid molecule of interest) may be selected by plating the cells onto kanamycin-containing media and picking kan' colonies. Although this figure shows an example of use of a kan' Donor vector, it is also possible to use Donor vectors containing other selection markers, such as the gentamycin resistance or tetracycline resistance markers, as discussed herein.

Figure 5 is a more detailed schematic depiction of the LR ("Destination") reaction (Figure 5A) and the BP ("Entry" or "Gateward") reaction (Figure 5B) of the GATEWAY<sup>TM</sup> Cloning System, showing the reactants, products and byproducts of each reaction.

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Figure 6 shows the sequences of the attB1 and attB2 sites flanking a gene of interest after subcloning into a Destination Vector to create an Expression Clone.

Figure 7 is a schematic depiction of four ways to make Entry Clones using the compositions and methods of the invention: 1. using restriction enzymes and ligase; 2. starting with a cDNA library prepared in an attL Entry Vector; 3. using an Expression Clone from a library prepared in an attB Expression Vector via the BxP reaction; and 4. recombinational cloning of PCR fragments with terminal attB sites, via the BxP reaction. Approaches 3 and 4 rely on recombination with a Donor vector (here, an attP vector such as pDONR201 (see Figure 49A-C), pDONR202 (see Figure 50A-C), pDONR203 (see Figure 51A-C), pDONR204 (see Figure 52A-C), pDONR205 (see Figure 53A-C), or pDONR206 (see Figure 54A-C), for example) that provides an Entry Clone carrying a selection marker such as kan<sup>r</sup>, gen<sup>r</sup>, tet<sup>r</sup>, or the like.

Figure 8 is a schematic depiction of cloning of a PCR product by a BxP (Entry or Gateward) reaction. A PCR product with 25 bp terminal attB sites (plus four Gs) is shown as a substrate for the BxP reaction. Recombination between the attB-PCR product of a gene and a Donor vector (which donates an Entry Vector that carries kan) results in an Entry Clone of the PCR product.

Figure 9 is a listing of the nucleotide sequences of the recombination sites designated herein as attB1, attB2, attP1, attP2, attL1, attL2, attR1 and attR2. Sequences are written conventionally, from 5' to 3'.

Figures 10-20: The plasmid backbone for all the Entry Vectors depicted herein is the same, and is shown in Figure 10A for the Entry Vector pENTR1A. For other Entry Vectors shown in Figures 11-20, only the sequences shown in Figure "A" for each figure set (i.e., Figure 11A, Figure 12A, etc.) are different (within the attL1-attL2 cassettes) from those shown in Figure 10 -- the plasmid backbone is identical.

Figure 10 is a schematic depiction of the physical map and cloning sites (Figure 10A), and the nucleotide sequence (Figure 10B), of the Entry Vector pENTR1A.

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Figure 11 is a schematic depiction of the cloning sites (Figure 11A) and the nucleotide sequence (Figure 11B) of the Entry Vector pENTR2B.

Figure 12 is a schematic depiction of the cloning sites (Figure 12A) and the nucleotide sequence (Figure 12B) of the Entry Vector pENTR3C.

Figure 13 is a schematic depiction of the cloning sites (Figure 13A) and the nucleotide sequence (Figure 13B) of the Entry Vector pENTR4.

Figure 14 is a schematic depiction of the cloning sites (Figure 14A) and the nucleotide sequence (Figure 14B) of the Entry Vector pENTR5.

Figure 15 is a schematic depiction of the cloning sites (Figure 15A) and the nucleotide sequence (Figure 15B) of the Entry Vector pENTR6.

Figure 16 is a schematic depiction of the cloning sites (Figure 16A) and the nucleotide sequence (Figure 16B) of the Entry Vector pENTR7.

Figure 17 is a schematic depiction of the cloning sites (Figure 17A) and the nucleotide sequence (Figure 17B) of the Entry Vector pENTR8.

Figure 18 is a schematic depiction of the cloning sites (Figure 18A) and the nucleotide sequence (Figure 18B) of the Entry Vector pENTR9.

Figure 19 is a schematic depiction of the cloning sites (Figure 19A) and the nucleotide sequence (Figure 19B) of the Entry Vector pENTR10.

Figure 20 is a schematic depiction of the cloning sites (Figure 20A) and the nucleotide sequence (Figure 20B) of the Entry Vector pENTR11.

Figure 21 is a schematic depiction of the physical map and the Trc expression cassette (Figure 21A) showing the promoter sequences at -35 and at -10 from the initiation codon, and the nucleotide sequence (Figure 21B-D), of Destination Vector pDEST1. This vector may also be referred to as pTrc-DEST1.

Figure 22 is a schematic depiction of the physical map and the His6 expression cassette (Figure 22A) showing the promoter sequences at -35 and at -10 from the initiation codon, and the nucleotide sequence (Figure 22B-D), of Destination Vector pDEST2. This vector may also be referred to as pHis6-DEST2.

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Figure 23 is a schematic depiction of the physical map and the GST expression cassette (Figure 23A) showing the promoter sequences at -35 and at -10 from the initiation codon, and the nucleotide sequence (Figure 23B-D), of Destination Vector pDEST3. This vector may also be referred to as pGST-DEST3.

Figure 24 is a schematic depiction of the physical map and the His6-Trx expression cassette (Figure 24A) showing the promoter sequences at -35 and at -10 from the initiation codon and a TEV protease cleavage site, and the nucleotide sequence (Figure 24B-D), of Destination Vector pDEST4. This vector may also be referred to as pTrx-DEST4.

Figure 25 is a schematic depiction of the attR1 and attR2 sites (Figure 25A), the physical map (Figure 25B), and the nucleotide sequence (Figure 25C-D), of Destination Vector pDEST5. This vector may also be referred to as pSPORT(+)-DEST5.

Figure 26 is a schematic depiction of the attR1 and attR2 sites (Figure 26A), the physical map (Figure 26B), and the nucleotide sequence (Figure 26C-D), of Destination Vector pDEST6. This vector may also be referred to as pSPORT(-)-DEST6.

Figure 27 is a schematic depiction of the attR1 site, CMV promoter, and the physical map (Figure 27A), and the nucleotide sequence (Figure 27B-C), of Destination Vector pDEST7. This vector may also be referred to as pCMV-DEST7.

Figure 28 is a schematic depiction of the attR1 site, baculovirus polyhedrin promoter, and the physical map (Figure 28A), and the nucleotide sequence (Figure 28B-D), of Destination Vector pDEST8. This vector may also be referred to as pFastBac-DEST8.

Figure 29 is a schematic depiction of the attR1 site, Semliki Forest Virus promoter, and the physical map (Figure 29A), and the nucleotide sequence (Figure 29B-E), of Destination Vector pDEST9. This vector may also be referred to as pSFV-DEST9.

Figure 30 is a schematic depiction of the attR1 site, baculovirus polyhedrin promoter, His6 fusion domain, and the physical map (Figure 30A), and the nucleotide sequence (Figure 30B-D), of Destination Vector pDEST10. This vector may also be referred to as pFastBacHT-DEST10.

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Figure 31 is a schematic depiction of the attR1 cassette containing a tetracycline-regulated CMV promoter and the physical map (Figure 31A), and the nucleotide sequence (Figure 31B-D), of Destination Vector pDEST11. This vector may also be referred to as pTet-DEST11.

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Figure 32 is a schematic depiction of the attR1 site, the start of the mRNA of the CMV promoter, and the physical map (Figure 32A), and the nucleotide sequence (Figure 32B-D), of Destination Vector pDEST12.2. This vector may also be referred to as pCMVneo-DEST12, as pCMV-DEST12, or as pDEST12.

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Figure 33 is a schematic depiction of the attR1 site, the  $\lambda P_L$  promoter, and the physical map (Figure 33A), and the nucleotide sequence (Figure 33B-C), of Destination Vector pDEST13. This vector may also be referred to as  $p\lambda P_L$ -DEST13.

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Figure 34 is a schematic depiction of the attR1 site, the T7 promoter, and the physical map (Figure 34A), and the nucleotide sequence (Figure 34B-D), of Destination Vector pDEST14. This vector may also be referred to as pPT7-DEST14.

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Figure 35 is a schematic depiction of the attR1 site, the T7 promoter, and the N-terminal GST fusion sequence, and the physical map (Figure 35A), and the nucleotide sequence (Figure 35B-D), of Destination Vector pDEST15. This vector may also be referred to as pT7 GST-DEST15.

Figure 36 is a schematic depiction of the attR1 site, the T7 promoter, and the N-terminal thioredoxin fusion sequence, and the physical map (Figure 36A), and the nucleotide sequence (Figure 36B-D), of Destination Vector pDEST16. This vector may also be referred to as pT7 Trx-DEST16.

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Figure 37 is a schematic depiction of the attR1 site, the T7 promoter, and the N-terminal His6 fusion sequence, and the physical map (Figure 37A), and the

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nucleotide sequence (Figure 37B-D), of Destination Vector pDEST17. This vector may also be referred to as pT7 His-DEST17.

Figure 38 is a schematic depiction of the attR1 site and the p10 baculovirus promoter, and the physical map (Figure 38A), and the nucleotide sequence (Figure 38B-D), of Destination Vector pDEST18. This vector may also be referred to as pFBp10-DEST18.

Figure 39 is a schematic depiction of the attR1 site, and the 39k baculovirus promoter, and the physical map (Figure 39A), and the nucleotide sequence (Figure 39B-D), of Destination Vector pDEST19. This vector may also be referred to as pFB39k-DEST19.

Figure 40 is a schematic depiction of the attR1 site, the *polh* baculovirus promoter, and the N-terminal GST fusion sequence, and the physical map (Figure 40A), and the nucleotide sequence (Figure 40B-D), of Destination Vector pDEST20. This vector may also be referred to as pFB GST-DEST20.

Figure 41 is a schematic depiction of a 2-hybrid vector with a DNA-binding domain, the attR1 site, and the ADH promoter, and the physical map (Figure 41A), and the nucleotide sequence (Figure 41B-E), of Destination Vector pDEST21. This vector may also be referred to as pDB Leu-DEST21.

Figure 42 is a schematic depiction of a 2-hybrid vector with an activation domain, the attR1 site, and the ADH promoter, and the physical map (Figure 42A), and the nucleotide sequence (Figure 42B-D), of Destination Vector pDEST22. This vector may also be referred to as pPC86-DEST22.

Figure 43 is a schematic depiction of the attR1 and attR2 sites, the T7 promoter, and the C-terminal His6 fusion sequence, and the physical map (Figure 43A), and the nucleotide sequence (Figure 43B-D), of Destination Vector pDEST23. This vector may also be referred to as pC-term-His6-DEST23.

Figure 44 is a schematic depiction of the attR1 and attR2 sites, the T7 promoter, and the C-terminal GST fusion sequence, and the physical map (Figure 44A), and the nucleotide sequence (Figure 44B-D), of Destination Vector pDEST24. This vector may also be referred to as pC-term-GST-DEST24.

Figure 45 is a schematic depiction of the attR1 and attR2 sites, the T7 promoter, and the C-terminal thioredoxin fusion sequence, and the physical map (Figure 45A), and the nucleotide sequence (Figure 45B-D), of Destination Vector pDEST25. This vector may also be referred to as pC-term-Trx-DEST25.

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Figure 46 is a schematic depiction of the attR1 site, the CMV promoter. and an N-terminal His6 fusion sequence, and the physical map (Figure 46A), and the nucleotide sequence (Figure 46B-D), of Destination Vector pDEST26. This vector may also be referred to as pCMV-SPneo-His-DEST26.

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Figure 47 is a schematic depiction of the attR1 site, the CMV promoter, and an N-terminal GST fusion sequence, and the physical map (Figure 47A), and the nucleotide sequence (Figure 47B-D), of Destination Vector pDEST27. This vector may also be referred to as pCMV-Spneo-GST-DEST27.

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Figure 48 is a depiction of the physical map (Figure 48A), the cloning sites (Figure 48B), and the nucleotide sequence (Figure 48C-D), for the attB cloning vector plasmid pEXP501. This vector may also be referred to equivalently herein as pCMV•SPORT6, pCMVSPORT6, and pCMVSport6.

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Figure 49 is a depiction of the physical map (Figure 49A), and the nucleotide sequence (Figure 49B-C), for the Donor plasmid pDONR201 which donates a kanamycin-resistant vector in the BP Reaction. This vector may also be referred to as pAttPkanr Donor Plasmid, or as pAttPkan Donor Plasmid

Figure 50 is a depiction of the physical map (Figure 50A), and the nucleotide sequence (Figure 50B-C), for the Donor plasmid pDONR202 which donates a kanamycin-resistant vector in the BP Reaction.

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Figure 51 is a depiction of the physical map (Figure 51A), and the nucleotide sequence (Figure 51B-C), for the Donor plasmid pDONR203 which donates a kanamycin-resistant vector in the BP Reaction.

Figure 52 is a depiction of the physical map (Figure 52A), and the nucleotide sequence (Figure 52B-C), for the Donor plasmid pDONR204 which donates a kanamycin-resistant vector in the BP Reaction.

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Figure 53 is a depiction of the physical map (Figure 53A), and the nucleotide sequence (Figure 53B-C), for the Donor plasmid pDONR205 which donates a tetracycline-resistant vector in the BP Reaction.

Figure 54 is a depiction of the physical map (Figure 54A), and the nucleotide sequence (Figure 54B-C), for the Donor plasmid pDONR206 which donates a gentamycin-resistant vector in the BP Reaction. This vector may also be referred to as pENTR22 attP Donor Plasmid, pAttPGenr Donor Plasmid, or pAttPgent Donor Plasmid.

Figure 55 depicts the attB1 site, and the physical map, of an Entry Clone (pENTR7) of CAT subcloned into the Destination Vector pDEST2 (Figure 22).

Figure 56 depicts the DNA components of Reaction B of the one-tube BxP reaction described in Example 16, pEZC7102 and attB-tet-PCR

Figure 57 is a physical map of the desired product of Reaction B of the one-tube BxP reaction described in Example 16, tetx7102.

Figure 58 is a physical map of the Destination Vector pEZC8402.

Figure 59 is a physical map of the expected tet<sup>r</sup> subclone product, tetx8402, resulting from the LxR Reaction with tetx7102 (Figure 57) plus pEZC8402 (Figure 58).

Figure 60 is a schematic depiction of the bacteriophage lambda recombination pathways in *E. coli*.

Figure 61 is a schematic depiction of the DNA molecules participating in the LR Reaction. Two different co-integrates form during the LR Reaction (only one of which is shown here), depending on whether attL1 and attR1 or attL2 and attR2 are first to recombine. In one aspect, the invention provides directional cloning of a nucleic acid molecule of interest, since the recombination sites react with specificity (attL1 reacts with attR1; attL2 with attR2; attB1 with attP1; and attB2 with attP2). Thus, positioning of the sites allows construction of desired vectors having recombined fragments in the desired orientation.

Figure 62 is a depiction of native and fusion protein expression using the recombinational cloning methods and compositions of the invention. In the upper figure depicting native protein expression, all of the translational start signals are

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included between the attB1 and attB2 sites; therefore, these signals must be present in the starting Entry Clone. The lower figure depicts fusion protein expression (here showing expression with both N-terminal and C-terminal fusion tags so that ribosomes read through attB1 and attB2 to create the fusion protein). Unlike native protein expression vectors, N-terminal fusion vectors have their translational start signals upstream of the attB1 site.

Figure 63 is a schematic depiction of three GATEWAY<sup>TM</sup> Cloning System cassettes. Three blunt-ended cassettes are depicted which convert standard expression vectors to Destination Vectors. Each of the depicted cassettes provides amino-terminal fusions in one of three possible reading frames, and each has a distinctive restriction cleavage site as shown.

Figure 64 shows the physical maps of plasmids containing three attR reading frame cassettes, pEZC15101 (reading frame A; Figure 64A), pEZC15102 (reading frame B; Figure 64B), and pEZC15103 (reading frame C; Figure 64C).

Figure 65 depicts the attB primers used for amplifying the tet and amp genes from pBR322 by the cloning methods of the invention.

Figure 66 is a table listing the results of recombinational cloning of the tet and amp PCR products made using the primers shown in Figure 65.

Figure 67 is a graph showing the effect of the number of guanines (G's) contained on the 5' end of the PCR primers on the cloning efficiency of PCR products. It is noted, however, that other nucleotides besides guanine (including A, T, C, U or combinations thereof) may be used as 5' extensions on the PCR primers to enhance cloning efficiency of PCR products.

Figure 68 is a graph showing a titration of various amounts of attP and attB reactants in the BxP reaction, and the effects on cloning efficiency of PCR products.

Figure 69 is a series of graphs showing the effects of various weights (Figure 69A) or moles (Figure 69B) of a 256 bp PCR product on formation of colonies, and on efficiency of cloning of the 256 bp PCR product into a Donor Vector (Figure 69C).

Figure 70 is a series of graphs showing the effects of various weights (Figure 70A) or moles (Figure 70B) of a 1 kb PCR product on formation of colonies, and on efficiency of cloning of the 1 kb PCR product into a Donor Vector (Figure 70C).

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Figure 71 is a series of graphs showing the effects of various weights (Figure 71A) or moles (Figure 71B) of a 1.4 kb PCR product on formation of colonies, and on efficiency of cloning of the 1.4 kb PCR product into a Donor Vector (Figure 71C).

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Figure 72 is a series of graphs showing the effects of various weights (Figure 72A) or moles (Figure 72B) of a 3.4 kb PCR product on formation of colonies, and on efficiency of cloning of the 3.4 kb PCR product into a Donor Vector (Figure 72C).

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Figure 73 is a series of graphs showing the effects of various weights (Figure 73A) or moles (Figure 73B) of a 4.6 kb PCR product on formation of colonies, and on efficiency of cloning of the 4.6 kb PCR product into a Donor Vector (Figure 73C).

Figure 74 is photograph of an ethidium bromide-stained gel of a titration of a 6.9 kb PCR product in a BxP reaction.

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Figure 75 is a graph showing the effects of various amounts of a 10.1 kb PCR product on formation of colonies upon cloning of the 10.1 kb PCR product into a Donor Vector.

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Figure 76 is photograph of an ethidium bromide-stained gel of a titration of a 10.1 kb PCR product in a BxP reaction.

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Figure 77 is a table summarizing the results of the PCR product cloning efficiency experiments depicted in Figures 69-74, for PCR fragments ranging in size from 0.256 kb to 6.9 kb.

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Figure 78 is a depiction of the sequences at the ends of attR Cassettes. Sequences contributed by the Cm<sup>r</sup>-ccdB cassette are shown, including the outer ends of the flanking attR sites (boxed). The staggered cleavage sites for Int are indicated in the boxed regions. Following recombination with an Entry Clone, only the outer sequences in attR sites contribute to the resulting attB sites in the

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Expression Clone. The underlined sequences at both ends dictate the different reading frames (reading frames A, B, or C, with two alternative reading frame C cassettes depicted) for fusion proteins.

Figure 79 is a depiction of several different attR cassettes (in reading frames A, B, or C) which may provide fusion codons at the amino-terminus of the encoded protein.

Figure 80 illustrates the single-cutting restriction sites in an attR reading frame A cassette of the invention.

Figure 81 illustrates the single-cutting restriction sites in an attR reading frame B cassette of the invention.

Figure 82 illustrates the single-cutting restriction sites in two alternative attR reading frame C cassettes of the invention (Figures 82A and 82B) depicted in Figure 78.

Figure 83 shows the physical map (Figure 83A), and the nucleotide sequence (Figure 83B-C), for an attR reading frame C parent plasmid prfC Parent III, which contains an attR reading frame C cassette of the invention (alternative A in Figures 78 and 82).

Figure 84 is a physical map of plasmid pEZC1301.

Figure 85 is a physical map of plasmid pEZC1313.

Figure 86 is a physical map of plasmid pEZ14032.

Figure 87 is a physical map of plasmid pMAB58.

Figure 88 is a physical map of plasmid pMAB62.

Figure 89 is a depiction of a synthesis reaction using two pairs of homologous primers of the invention.

Figure 90 is a schematic depiction of the physical map (Figure 90A), and the nucleotide sequence (Figure 90B-D), of Destination Vector pDEST28.

Figure 91 is a schematic depiction of the physical map (Figure 91A), and the nucleotide sequence (Figure 91B-D), of Destination Vector pDEST29.

Figure 92 is a schematic depiction of the physical map (Figure 92A), and the nucleotide sequence (Figure 92B-D), of Destination Vector pDEST30.

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Figure 93 is a schematic depiction of the physical map (Figure 93A), and the nucleotide sequence (Figure 93B-D), of Destination Vector pDEST31.

Figure 94 is a schematic depiction of the physical map (Figure 94A), and the nucleotide sequence (Figure 94B-E), of Destination Vector pDEST32

Figure 95 is a schematic depiction of the physical map (Figure 95A), and the nucleotide sequence (Figure 95B-D), of Destination Vector pDEST33.

Figure 96 is a schematic depiction of the physical map (Figure 96A), and the nucleotide sequence (Figure 96B-D), of Destination Vector pDEST34.

Figure 97 is a depiction of the physical map (Figure 97A), and the nucleotide sequence (Figure 97B-C), for the Donor plasmid pDONR207 which donates a gentamycin-resistant vector in the BP Reaction.

Figure 98 is a schematic depiction of the physical map (Figure 98A), and the nucleotide sequence (Figure 98B-D), of the 2-hybrid vector pMAB85.

Figure 99 is a schematic depiction of the physical map (Figure 99A), and the nucleotide sequence (Figure 99B-D), of the 2-hybrid vector pMAB86.

#### DETAILED DESCRIPTION OF THE INVENTION

#### Definitions

In the description that follows, a number of terms used in recombinant DNA technology are utilized extensively. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided.

**Byproduct**: is a daughter molecule (a new clone produced after the second recombination event during the recombinational cloning process) lacking the segment which is desired to be cloned or subcloned.

Cointegrate: is at least one recombination intermediate nucleic acid molecule of the present invention that contains both parental (starting) molecules. It will usually be linear. In some embodiments it can be circular. RNA and polypeptides may be expressed from cointegrates using an appropriate host cell strain, for example *E. coli* DB3.1 (particularly *E. coli* LIBRARY EFFICIENCY®

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DB3.1<sup>TM</sup> Competent Cells), and selecting for both selection markers found on the cointegrate molecule.

Host: is any prokaryotic or eukaryotic organism that can be a recipient of the recombinational cloning Product, vector, or nucleic acid molecule of the invention. A "host," as the term is used herein, includes prokaryotic or eukaryotic organisms that can be genetically engineered. For examples of such hosts, see Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1982).

Insert or Inserts: include the desired nucleic acid segment or a population of nucleic acid segments (segment A of Figure 1) which may be manipulated by the methods of the present invention. Thus, the terms Insert(s) are meant to include a particular nucleic acid (preferably DNA) segment or a population of segments. Such Insert(s) can comprise one or more nucleic acid molecules.

Insert Donor: is one of the two parental nucleic acid molecules (e.g. RNA or DNA) of the present invention which carries the Insert. The Insert Donor molecule comprises the Insert flanked on both sides with recombination sites. The Insert Donor can be linear or circular. In one embodiment of the invention, the Insert Donor is a circular DNA molecule and further comprises a cloning vector sequence outside of the recombination signals (see Figure 1). When a population of Inserts or population of nucleic acid segments are used to make the Insert Donor, a population of Insert Donors results and may be used in accordance with the invention. Examples of such Insert Donor molecules are GATEWAY<sup>TM</sup> Entry Vectors, which include but are not limited to those Entry Vectors depicted in Figures 10-20, as well as other vectors comprising a gene of interest flanked by one or more attL sites (e.g., attL1, attL2, etc.), or by one or more attB sites (e.g., attB1, attB2, etc.) for the production of library clones.

**Product**: is one of the desired daughter molecules comprising the A and D sequences which is produced after the second recombination event during the recombinational cloning process (see Figure 1). The Product contains the nucleic acid which was to be cloned or subcloned. In accordance with the invention, when a population of Insert Donors are used, the resulting population of Product

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molecules will contain all or a portion of the population of Inserts of the Insert Donors and preferably will contain a representative population of the original molecules of the Insert Donors.

**Promoter**: is a DNA sequence generally described as the 5'-region of a gene, located proximal to the start codon. The transcription of an adjacent DNA segment is initiated at the promoter region. A repressible promoter's rate of transcription decreases in response to a repressing agent. An inducible promoter's rate of transcription increases in response to an inducing agent. A constitutive promoter's rate of transcription is not specifically regulated, though it can vary under the influence of general metabolic conditions.

Recognition sequence: Recognition sequences are particular sequences which a protein, chemical compound, DNA, or RNA molecule (e.g., restriction endonuclease, a modification methylase, or a recombinase) recognizes and binds. In the present invention, a recognition sequence will usually refer to a recombination site. For example, the recognition sequence for Cre recombinase is loxP which is a 34 base pair sequence comprised of two 13 base pair inverted repeats (serving as the recombinase binding sites) flanking an 8 base pair core See Figure 1 of Sauer, B., Current Opinion in Biotechnology 5:521-527 (1994). Other examples of recognition sequences are the attB, attP, attL, and attR sequences which are recognized by the recombinase enzyme  $\lambda$  Integrase. attB is an approximately 25 base pair sequence containing two 9 base pair core-type Int binding sites and a 7 base pair overlap region. attP is an approximately 240 base pair sequence containing core-type Int binding sites and arm-type Int binding sites as well as sites for auxiliary proteins integration host factor (IHF), FIS and excisionase (Xis). See Landy, Current Opinion in Biotechnology 3:699-707 (1993). Such sites may also be engineered according to the present invention to enhance production of products in the methods of the invention. When such engineered sites lack the P1 or H1 domains to make the recombination reactions irreversible (e.g., attR or attP), such sites may be designated attR' or attP' to show that the domains of these sites have been modified in some way.

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Recombination proteins: include excisive or integrative proteins, enzymes, co-factors or associated proteins that are involved in recombination reactions involving one or more recombination sites, which may be wild-type proteins (See Landy, Current Opinion in Biotechnology 3:699-707 (1993)), or mutants, derivatives (e.g., fusion proteins containing the recombination protein sequences or fragments thereof), fragments, and variants thereof.

Recombination site: is a recognition sequence on a DNA molecule participating in an integration/recombination reaction by the recombinational cloning methods of the invention. Recombination sites are discrete sections or segments of DNA on the participating nucleic acid molecules that are recognized and bound by a site-specific recombination protein during the initial stages of integration or recombination. For example, the recombination site for Cre recombinase is *loxP* which is a 34 base pair sequence comprised of two 13 base pair inverted repeats (serving as the recombinase binding sites) flanking an 8 base pair core sequence. *See* Figure 1 of Sauer, B., *Curr. Opin. Biotech.* 5:521-527 (1994). Other examples of recognition sequences include the *attB*, *attP*, *attL*, and *attR* sequences described herein, and mutants, fragments, variants and derivatives thereof, which are recognized by the recombination protein λ Int and by the auxiliary proteins integration host factor (IHF), FIS and excisionase (Xis). *See* Landy, *Curr. Opin. Biotech.* 3:699-707 (1993).

Recombinational Cloning: is a method described herein, whereby segments of nucleic acid molecules or populations of such molecules are exchanged, inserted, replaced, substituted or modified, in vitro or in vivo. By "in vitro" and "in vivo" herein is meant recombinational cloning that is carried out outside of host cells (e.g., in cell-free systems) or inside of host cells (e.g., using recombination proteins expressed by host cells), respectively.

Repression cassette: is a nucleic acid segment that contains a repressor or a Selectable marker present in the subcloning vector.

Selectable marker: is a DNA segment that allows one to select for or against a molecule (e.g., a replicon) or a cell that contains it, often under particular conditions. These markers can encode an activity, such as, but not limited to,

production of RNA, peptide, or protein, or can provide a binding site for RNA, peptides, proteins, inorganic and organic compounds or compositions and the like. Examples of Selectable markers include but are not limited to: (1) DNA segments that encode products which provide resistance against otherwise toxic compounds (e.g., antibiotics); (2) DNA segments that encode products which are otherwise lacking in the recipient cell (e.g., tRNA genes, auxotrophic markers); (3) DNA segments that encode products which suppress the activity of a gene product; (4) DNA segments that encode products which can be readily identified (e.g., phenotypic markers such as β-galactosidase, green fluorescent protein (GFP), and cell surface proteins); (5) DNA segments that bind products which are otherwise detrimental to cell survival and/or function; (6) DNA segments that otherwise inhibit the activity of any of the DNA segments described in Nos. 1-5 above (e.g., antisense oligonucleotides); (7) DNA segments that bind products that modify a substrate (e.g. restriction endonucleases); (8) DNA segments that can be used to isolate or identify a desired molecule (e.g. specific protein binding sites); (9) DNA segments that encode a specific nucleotide sequence which can be otherwise nonfunctional (e.g., for PCR amplification of subpopulations of molecules); (10) DNA segments, which when absent, directly or indirectly confer resistance or sensitivity to particular compounds; (11) DNA segments that encode products which are toxic in recipient cells; (12) DNA segments that inhibit replication, partition or heritability of nucleic acid molecules that contain them; and/or (13) DNA segments that encode conditional replication functions, e.g., replication in certain hosts or host cell strains or under certain environmental conditions (e.g., temperature, nutritional conditions, etc.).

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Selection scheme: is any method which allows selection, enrichment, or identification of a desired Product or Product(s) from a mixture containing an Entry Clone or Vector, a Destination Vector, a Donor Vector, an Expression Clone or Vector, any intermediates (e.g. a Cointegrate or a replicon), and/or Byproducts. The selection schemes of one preferred embodiment have at least two components that are either linked or unlinked during recombinational cloning. One component is a Selectable marker. The other component controls the expression in vitro or in vivo of the Selectable marker, or survival of the cell (or

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the nucleic acid molecule, e.g., a replicon) harboring the plasmid carrying the Selectable marker. Generally, this controlling element will be a repressor or inducer of the Selectable marker, but other means for controlling expression or activity of the Selectable marker can be used. Whether a repressor or activator is used will depend on whether the marker is for a positive or negative selection, and the exact arrangement of the various DNA segments, as will be readily apparent to those skilled in the art. A preferred requirement is that the selection scheme results in selection of or enrichment for only one or more desired Products. As defined herein, selecting for a DNA molecule includes (a) selecting or enriching for the presence of the desired DNA molecule, and (b) selecting or enriching against the presence of DNA molecules that are not the desired DNA molecule.

In one embodiment, the selection schemes (which can be carried out in reverse) will take one of three forms, which will be discussed in terms of Figure 1. The first, exemplified herein with a Selectable marker and a repressor therefore, selects for molecules having segment D and lacking segment C. The second selects against molecules having segment C and for molecules having segment D. Possible embodiments of the second form would have a DNA segment carrying a gene toxic to cells into which the *in vitro* reaction products are to be introduced. A toxic gene can be a DNA that is expressed as a toxic gene product (a toxic protein or RNA), or can be toxic in and of itself. (In the latter case, the toxic gene is understood to carry its classical definition of "heritable trait".)

Examples of such toxic gene products are well known in the art, and include, but are not limited to, restriction endonucleases (e.g., DpnI), apoptosis-related genes (e.g. ASK1 or members of the bcl-2/ced-9 family), retroviral genes including those of the human immunodeficiency virus (HIV), defensins such as NP-1, inverted repeats or paired palindromic DNA sequences, bacteriophage lytic genes such as those from ΦX174 or bacteriophage T4; antibiotic sensitivity genes such as rpsL, antimicrobial sensitivity genes such as pheS, plasmid killer genes, eukaryotic transcriptional vector genes that produce a gene product toxic to bacteria, such as GATA-1, and genes that kill hosts in the absence of a suppressing function, e.g., kicB, ccdB, ΦX174 E (Liu, Q. et al., Curr. Biol.

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8:1300-1309 (1998)), and other genes that negatively affect replicon stability and/or replication. A toxic gene can alternatively be selectable *in vitro*, e.g., a restriction site.

Many genes coding for restriction endonucleases operably linked to inducible promoters are known, and may be used in the present invention. See, e.g. U.S. Patent Nos. 4,960,707 (DpnI and DpnII); 5,000,333, 5,082,784 and 5,192,675 (KpnI); 5,147,800 (NgoAIII and NgoAI); 5,179,015 (FspI and HaeIII): 5,200,333 (HaeII and TaqI); 5,248,605 (HpaII); 5,312,746 (ClaI); 5,231,021 and 5,304,480 (XhoI and XhoII); 5,334,526 (AluI); 5,470,740 (NsiI); 5,534,428 (SstI/SacI); 5,202,248 (NcoI); 5,139,942 (NdeI); and 5,098,839 (PacI). See also Wilson, G.G., Nucl. Acids Res. 19:2539-2566 (1991); and Lunnen, K.D., et al., Gene 74:25-32 (1988).

In the second form, segment *D* carries a Selectable marker. The toxic gene would eliminate transformants harboring the Vector Donor, Cointegrate, and Byproduct molecules, while the Selectable marker can be used to select for cells containing the Product and against cells harboring only the Insert Donor.

The third form selects for cells that have both segments A and D in cis on the same molecule, but not for cells that have both segments in trans on different molecules. This could be embodied by a Selectable marker that is split into two inactive fragments, one each on segments A and D.

The fragments are so arranged relative to the recombination sites that when the segments are brought together by the recombination event, they reconstitute a functional Selectable marker. For example, the recombinational event can link a promoter with a structural nucleic acid molecule (e.g., a gene), can link two fragments of a structural nucleic acid molecule, or can link nucleic acid molecules that encode a heterodimeric gene product needed for survival, or can link portions of a replicon

Site-specific recombinase: is a type of recombinase which typically has at least the following four activities (or combinations thereof): (1) recognition of one or two specific nucleic acid sequences; (2) cleavage of said sequence or sequences; (3) topoisomerase activity involved in strand exchange; and (4) ligase

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activity to reseal the cleaved strands of nucleic acid. See Sauer, B., Current Opinions in Biotechnology 5:521-527 (1994). Conservative site-specific recombination is distinguished from homologous recombination and transposition by a high degree of sequence specificity for both partners. The strand exchange mechanism involves the cleavage and rejoining of specific DNA sequences in the absence of DNA synthesis (Landy, A. (1989) Ann. Rev. Biochem. 58:913-949).

**Subcloning vector**: is a cloning vector comprising a circular or linear nucleic acid molecule which includes preferably an appropriate replicon. In the present invention, the subcloning vector (segment D in Figure 1) can also contain functional and/or regulatory elements that are desired to be incorporated into the final product to act upon or with the cloned DNA Insert (segment A in Figure 1). The subcloning vector can also contain a Selectable marker (preferably DNA).

Vector: is a nucleic acid molecule (preferably DNA) that provides a useful biological or biochemical property to an Insert. Examples include plasmids. phages, autonomously replicating sequences (ARS), centromeres, and other sequences which are able to replicate or be replicated in vitro or in a host cell, or to convey a desired nucleic acid segment to a desired location within a host cell. A Vector can have one or more restriction endonuclease recognition sites at which the sequences can be cut in a determinable fashion without loss of an essential biological function of the vector, and into which a nucleic acid fragment can be spliced in order to bring about its replication and cloning. Vectors can further provide primer sites, e.g., for PCR, transcriptional and/or translational initiation and/or regulation sites, recombinational signals, replicons, Selectable markers, etc. Clearly, methods of inserting a desired nucleic acid fragment which do not require the use of homologous recombination, transpositions or restriction enzymes (such as, but not limited to, UDG cloning of PCR fragments (U.S. Patent No. 5,334,575, entirely incorporated herein by reference), T:A cloning, and the like) can also be applied to clone a fragment into a cloning vector to be used according to the present invention. The cloning vector can further contain one or more selectable markers suitable for use in the identification of cells transformed with the cloning vector.

**Vector Donor**: is one of the two parental nucleic acid molecules (e.g. RNA or DNA) of the present invention which carries the DNA segments comprising the DNA vector which is to become part of the desired Product. The Vector Donor comprises a subcloning vector D (or it can be called the cloning vector if the Insert Donor does not already contain a cloning vector (e.g., for PCR fragments containing attB sites, see below)) and a segment C flanked by recombination sites (see Figure 1). Segments C and/or D can contain elements that contribute to selection for the desired Product daughter molecule, as described above for selection schemes. The recombination signals can be the same or different, and can be acted upon by the same or different recombinases. In addition, the Vector Donor can be linear or circular. Examples of such Vector Donor molecules include GATEWAY<sup>TM</sup> Destination Vectors, which include but are not limited to those Destination Vectors depicted in Figures 21-47 and 90-96.

Primer: refers to a single stranded or double stranded oligonucleotide that is extended by covalent bonding of nucleotide monomers during amplification or polymerization of a nucleic acid molecule (e.g. a DNA molecule). In a preferred aspect, a primer comprises one or more recombination sites or portions of such recombination sites. Portions of recombination sites comprise at least 2 bases (or basepairs, abbreviated herein as "bp"), at least 5-200 bases, at least 10-100 bases, at least 15-75 bases, at least 15-50 bases, at least 15-25 bases, or at least 16-25 bases, of the recombination sites of interest, as described in further detail below and in the Examples. When using portions of recombination sites, the missing portion of the recombination site may be provided as a template by the newly synthesized nucleic acid molecule. Such recombination sites may be located within and/or at one or both termini of the primer. Preferably, additional sequences are added to the primer adjacent to the recombination site(s) to enhance or improve recombination and/or to stabilize the recombination site during recombination. Such stabilization sequences may be any sequences (preferably G/C rich sequences) of any length. Preferably, such sequences range in size from 1 to about 1000 bases, 1 to about 500 bases, and 1 to about 100 bases, 1 to about 60 bases, 1 to about 25, 1 to about 10, 2 to about 10 and preferably about 4 bases.

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Preferably, such sequences are greater than 1 base in length and preferably greater than 2 bases in length.

Template: refers to double stranded or single stranded nucleic acid molecules which are to be amplified, synthesized or sequenced. In the case of double stranded molecules, denaturation of its strands to form a first and a second strand is preferably performed before these molecules will be amplified. synthesized or sequenced, or the double stranded molecule may be used directly as a template. For single stranded templates, a primer complementary to a portion of the template is hybridized under appropriate conditions and one or more polypeptides having polymerase activity (e.g. DNA polymerases and/or reverse transcriptases) may then synthesize a nucleic acid molecule complementary to all or a portion of said template. Alternatively, for double stranded templates, one or more promoters may be used in combination with one or more polymerases to make nucleic acid molecules complementary to all or a portion of the template. The newly synthesized molecules, according to the invention, may be equal or shorter in length than the original template. Additionally, a population of nucleic acid templates may be used during synthesis or amplification to produce a population of nucleic acid molecules typically representative of the original template population.

Adapter: is an oligonucleotide or nucleic acid fragment or segment (preferably DNA) which comprises one or more recombination sites (or portions of such recombination sites) which in accordance with the invention can be added to a circular or linear Insert Donor molecule as well as other nucleic acid molecules described herein. When using portions of recombination sites, the missing portion may be provided by the Insert Donor molecule. Such adapters may be added at any location within a circular or linear molecule, although the adapters are preferably added at or near one or both termini of a linear molecule. Preferably, adapters are positioned to be located on both sides (flanking) a particular nucleic acid molecule of interest. In accordance with the invention, adapters may be added to nucleic acid molecules of interest by standard recombinant techniques (e.g. restriction digest and ligation). For example, adapters may be added to a circular molecule by first digesting the molecule with

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an appropriate restriction enzyme, adding the adapter at the cleavage site and reforming the circular molecule which contains the adapter(s) at the site of cleavage. In other aspects, adapters may be added by homologous recombination, by integration of RNA molecules, and the like. Alternatively, adapters may be ligated directly to one or more and preferably both termini of a linear molecule thereby resulting in linear molecule(s) having adapters at one or both termini. In one aspect of the invention, adapters may be added to a population of linear molecules, (e.g. a cDNA library or genomic DNA which has been cleaved or digested) to form a population of linear molecules containing adapters at one and preferably both termini of all or substantial portion of said population.

Adapter-Primer: is primer molecule which comprises one or more recombination sites (or portions of such recombination sites) which in accordance with the invention can be added to a circular or linear nucleic acid molecule described herein. When using portions of recombination sites, the missing portion may be provided by a nucleic acid molecule (e.g., an adapter) of the invention. Such adapter-primers may be added at any location within a circular or linear molecule, although the adapter-primers are preferably added at or near one or both termini of a linear molecule. Examples of such adapter-primers and the use thereof in accordance with the methods of the invention are shown in Example 25 herein. Such adapter-primers may be used to add one or more recombination sites or portions thereof to circular or linear nucleic acid molecules in a variety of contexts and by a variety of techniques, including but not limited to amplification (e.g., PCR), ligation (e.g., enzymatic or chemical/synthetic ligation), recombination (e.g., homologous or non-homologous (illegitimate) recombination) and the like.

**Library**: refers to a collection of nucleic acid molecules (circular or linear). In one embodiment, a library may comprise a plurality (*i.e.*, two or more) of DNA molecules, which may or may not be from a common source organism, organ, tissue, or cell. In another embodiment, a library is representative of all or a portion or a significant portion of the DNA content of an organism (a "genomic" library), or a set of nucleic acid molecules representative of all or a portion or a significant portion of the expressed nucleic acid molecules (a cDNA library) in a

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cell, tissue, organ or organism. A library may also comprise random sequences made by *de novo* synthesis, mutagenesis of one or more sequences and the like. Such libraries may or may not be contained in one or more vectors.

Amplification: refers to any *in vitro* method for increasing a number of copies of a nucleotide sequence with the use of a polymerase. Nucleic acid amplification results in the incorporation of nucleotides into a DNA and/or RNA molecule or primer thereby forming a new molecule complementary to a template. The formed nucleic acid molecule and its template can be used as templates to synthesize additional nucleic acid molecules. As used herein, one amplification reaction may consist of many rounds of replication. DNA amplification reactions include, for example, polymerase chain reaction (PCR). One PCR reaction may consist of 5-100 "cycles" of denaturation and synthesis of a DNA molecule.

Oligonucleotide: refers to a synthetic or natural molecule comprising a covalently linked sequence of nucleotides which are joined by a phosphodiester bond between the 3' position of the deoxyribose or ribose of one nucleotide and the 5' position of the deoxyribose or ribose of the adjacent nucleotide. This term may be used interchangeably herein with the terms "nucleic acid molecule" and "polynucleotide," without any of these terms necessarily indicating any particular length of the nucleic acid molecule to which the term specifically refers.

Nucleotide: refers to a base-sugar-phosphate combination. Nucleotides are monomeric units of a nucleic acid molecule (DNA and RNA). The term nucleotide includes ribonucleoside triphosphates ATP, UTP, CTG, GTP and deoxyribonucleoside triphosphates such as dATP, dCTP, dITP, dUTP, dGTP, dTTP, or derivatives thereof. Such derivatives include, for example, [αS]dATP, 7-deaza-dGTP and 7-deaza-dATP. The term nucleotide as used herein also refers to dideoxyribonucleoside triphosphates (ddNTPs) and their derivatives. Illustrated examples of dideoxyribonucleoside triphosphates include, but are not limited to, ddATP, ddCTP, ddGTP, ddITP, and ddTTP. According to the present invention, a "nucleotide" may be unlabeled or detectably labeled by well known techniques. Detectable labels include, for example, radioactive isotopes, fluorescent labels, chemiluminescent labels, bioluminescent labels and enzyme labels.

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Hybridization: The terms "hybridization" and "hybridizing" refers to base pairing of two complementary single-stranded nucleic acid molecules (RNA and/or DNA) to give a double stranded molecule. As used herein, two nucleic acid molecules may be hybridized, although the base pairing is not completely complementary. Accordingly, mismatched bases do not prevent hybridization of two nucleic acid molecules provided that appropriate conditions, well known in the art, are used. In some aspects, hybridization is said to be under "stringent conditions." By "stringent conditions" as used herein is meant overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Other terms used in the fields of recombinant DNA technology and molecular and cell biology as used herein will be generally understood by one of ordinary skill in the applicable arts.

## Overview

Two reactions constitute the recombinational cloning system of the present invention, referred to herein as the "GATEWAYTM Cloning System," as depicted generally in Figure 1. The first of these reactions, the LR Reaction (Figure 2), which may also be referred to interchangeably herein as the Destination Reaction, is the main pathway of this system. The LR Reaction is a recombination reaction between an Entry vector or clone and a Destination Vector, mediated by a cocktail of recombination proteins such as the GATEWAYTM LR Clonase<sup>TM</sup> Enzyme Mix described herein. This reaction transfers nucleic acid molecules of interest (which may be genes, cDNAs, cDNA libraries, or fragments thereof) from the Entry Clone to an Expression Vector, to create an Expression Clone.

The sites labeled L, R, B, and P are respectively the attL, attR, attB, and attP recombination sites for the bacteriophage  $\lambda$  recombination proteins that constitute the Clonase cocktail (referred to herein variously as "Clonase" or

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"GATEWAY™ LR Clonase™ Enzyme Mix" (for recombination protein mixtures mediating attL x attR recombination reactions, as described herein) or "GATEWAY™ BP Clonase™ Enzyme Mix" (for recombination protein mixtures mediating attB x attP recombination reactions, as described herein)). The Recombinational Cloning reactions are equivalent to concerted, highly specific, cutting and ligation reactions. Viewed in this way, the recombination proteins cut to the left and right of the nucleic acid molecule of interest in the Entry Clone and ligate it into the Destination vector, creating a new Expression Clone.

The nucleic acid molecule of interest in an Expression Clone is flanked by the small attB1 and attB2 sites. The orientation and reading frame of the nucleic acid molecule of interest are maintained throughout the subcloning, because attL1 reacts only with attR1, and attL2 reacts only with attR2. Likewise, attB1 reacts only with attP1, and attB2 reacts only with attP2. Thus, the invention also relates to methods of controlled or directional cloning using the recombination sites of the invention (or portions thereof), including variants, fragments, mutants and derivatives thereof which may have altered or enhanced specificity. The invention also relates more generally to any number of recombination site partners or pairs (where each recombination site is specific for and interacts with its corresponding recombination site). Such recombination sites are preferably made by mutating or modifying the recombination site to provide any number of necessary specificities (e.g., attB1-10, attP1-10, attL1-10, attR1-10, etc.), non-limiting examples of which are described in detail in the Examples herein.

When an aliquot from the recombination reaction is transformed into host cells (e.g., E. coli) and spread on plates containing an appropriate selection agent, e.g., an antibiotic such as ampicillin with or without methicillin, cells that take up the desired clone form colonies. The unreacted Destination Vector does not give ampicillin-resistant colonies, even though it carries the ampicillin-resistance gene, because it contains a toxic gene, e.g., ccdB. Thus selection for ampicillin resistance selects for E. coli cells that carry the desired product, which usually comprise >90% of the colonies on the ampicillin plate.

To participate in the Recombinational (or "GATEWAYTM") Cloning Reaction, a nucleic acid molecule of interest first may be cloned into an Entry

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Vector, creating an Entry Clone. Multiple options are available for creating Entry Clones, including: cloning of PCR sequences with terminal attB recombination sites into Entry Vectors; using the GATEWAY<sup>TM</sup> Cloning System recombination reaction; transfer of genes from libraries prepared in GATEWAY<sup>TM</sup> Cloning System vectors by recombination into Entry Vectors; and cloning of restriction enzymegenerated fragments and PCR fragments into Entry Vectors by standard recombinant DNA methods. These approaches are discussed in further detail herein.

A key advantage of the GATEWAYTM Cloning System is that a nucleic acid molecule of interest (or even a population of nucleic acid molecules of interest) present as an Entry Clone can be subcloned in parallel into one or more Destination Vectors in a simple reactions for anywhere from about 30 seconds to about 60 minutes (preferably about 1-60 minutes, about 1-45 minutes, about 1-30 minutes, about 2-60 minutes, about 2-45 minutes, about 2-30 minutes, about 1-2 minutes, about 30-60 minutes, about 45-60 minutes, or about 30-45 minutes). Longer reaction times (e.g., 2-24 hours, or overnight) may increase recombination efficiency, particularly where larger nucleic acid molecules are used, as described in the Examples herein. Moreover, a high percentage of the colonies obtained carry the desired Expression Clone. This process is illustrated schematically in Figure 3, which shows an advantage of the invention in which the molecule of interest can be moved simultaneously or separately into multiple Destination Vectors. In the LR Reaction, one or both of the nucleic acid molecules to be recombined may have any topology (e.g., linear, relaxed circular, nicked circular, supercoiled, etc.), although one or both are preferably linear.

The second major pathway of the GATEWAY<sup>TM</sup> Cloning System is the BP Reaction (Figure 4), which may also be referred to interchangeably herein as the Entry Reaction or the Gateward Reaction. The BP Reaction may recombine an Expression Clone with a Donor Plasmid (the counterpart of the byproduct in Figure 2). This reaction transfers the nucleic acid molecule of interest (which may have any of a variety of topologies, including linear, coiled, supercoiled, etc.) in the Expression Clone into an Entry Vector, to produce a new Entry Clone. Once this nucleic acid molecule of interest is cloned into an Entry

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Vector, it can be transferred into new Expression Vectors, through the LR Reaction as described above. In the BP Reaction, one or both of the nucleic acid molecules to be recombined may have any topology (e.g., linear, relaxed circular, nicked circular, supercoiled, etc.), although one or both are preferably linear.

A useful variation of the BP Reaction permits rapid cloning and expression of products of amplification (e.g., PCR) or nucleic acid synthesis. Amplification (e.g., PCR) products synthesized with primers containing terminal 25 bp attB sites serve as efficient substrates for the Gateward Cloning reaction. Such amplification products may be recombined with a Donor Vector to produce an Entry Clone (see Figure 7). The result is an Entry Clone containing the amplification fragment. Such Entry Clones can then be recombined with Destination Vectors -- through the LR Reaction -- to yield Expression Clones of the PCR product.

Additional details of the LR Reaction are shown in Figure 5A. The GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix that mediates this reaction contains lambda recombination proteins Int (Integrase), Xis (Excisionase), and IHF (Integration Host Factor). In contrast, the GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix, which mediates the BP Reaction (Figure 5B), comprises Int and IHF alone.

The recombination (att) sites of each vector comprise two distinct segments, donated by the parental vectors. The staggered lines dividing the two portions of each att site, depicted in Figures 5A and 5B, represent the seven-base staggered cut produced by Int during the recombination reactions. This structure is seen in greater detail in Figure 6, which displays the attB recombination sequences of an Expression Clone, generated by recombination between the attL1 and attL2 sites of an Entry Clone and the attR1 and attR2 sites of a Destination Vector.

The nucleic acid molecule of interest in the Expression Clone is flanked by attB sites: attB1 to the left (amino terminus) and attB2 to the right (carboxy terminus). The bases in attB1 to the left of the seven-base staggered cut produced by Int are derived from the Destination vector, and the bases to the right of the staggered cut are derived from the Entry Vector (see Figure 6). Note that the sequence is displayed in triplets corresponding to an open reading frame. If the reading frame of the nucleic acid molecule of interest cloned in the Entry Vector

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is in phase with the reading frame shown for attB1, amino-terminal protein fusions can be made between the nucleic acid molecule of interest and any GATEWAY<sup>TM</sup> Cloning System Destination Vector encoding an amino-terminal fusion domain. Entry Vectors and Destination Vectors that enable cloning in all three reading frames are described in more detail herein, particularly in the Examples.

The LR Reaction allows the transfer of a desired nucleic acid molecule of interest into new Expression Vectors by recombining a Entry Clone with various Destination Vectors. To participate in the LR or Destination Reaction, however, a nucleic acid molecule of interest preferably is first converted to a Entry Clone. Entry Clones can be made in a number of ways, as shown in Figure 7.

One approach is to clone the nucleic acid molecule of interest into one or more of the Entry Vectors, using standard recombinant DNA methods, with restriction enzymes and ligase. The starting DNA fragment can be generated by restriction enzyme digestion or as a PCR product. The fragment is cloned between the attL1 and attL2 recombination sites in the Entry Vector. Note that a toxic or "death" gene (e.g., ccdB), provided to minimize background colonies from incompletely digested Entry Vector, must be excised and replaced by the nucleic acid molecule of interest.

A second approach to making an Entry Clone (Figure 7) is to make a library (genomic or cDNA) in an Entry Vector, as described in detail herein. Such libraries may then be transferred into Destination Vectors for expression screening, for example in appropriate host cells such as yeast cells or mammalian cells.

A third approach to making Entry Clones (Figure 7) is to use Expression Clones obtained from cDNA molecules or libraries prepared in Expression Vectors. Such cDNAs or libraries, flanked by attB sites, can be introduced into a Entry Vector by recombination with a Donor Vector via the BP Reaction. If desired, an entire Expression Clone library can be transferred into the Entry Vector through the BP Reaction. Expression Clone cDNA libraries may also be constructed in a variety of prokaryotic and eukaryotic GATEWAY<sup>TM</sup>-modified vectors (e.g., the pEXP501 Expression Vector (see Figure 48), and 2-hybrid and

attB library vectors), as described in detail herein, particularly in the Examples below.

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A fourth, and potentially most versatile, approach to making an Entry Clone (Figure 7) is to introduce a sequence for a nucleic acid molecule of interest into an Entry Vector by amplification (e.g., PCR) fragment cloning. This method is diagramed in Figure 8. The DNA sequence first is amplified (for example, with PCR) as outlined in detail below and in the Examples herein, using primers containing one or more bp, two or more bp, three or more bp, four or more bp, five or more bp, preferably six or more bp, more preferably 6-25 bp (particularly 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25) bp of the attB nucleotide sequences (such as, but not limited to, those depicted in Figure 9), and optionally one or more, two or more, three or more, four or more, and most preferably four or five or more additional terminal nucleotide bases which preferably are guanines. The PCR product then may be converted to a Entry Clone by performing a BP Reaction, in which the attB-PCR product recombines with a Donor Vector containing one or more attP sites. Details of this approach and protocols for PCR fragment subcloning are provided in Examples 8 and 21-25.

A variety of Entry Clones may be produced by these methods, providing a wide array of cloning options; a number of specific Entry Vectors are also available commercially from Life Technologies, Inc. (Rockville, MD). The Examples herein provide a more in-depth description of selected Entry Vectors and details of their cloning sites. Choosing the optimal Entry Vector for a particular application is discussed in Example 4.

Entry Vectors and Destination Vectors should be constructed so that the amino-terminal region of a nucleic acid molecule of interest (e.g., a gene, cDNA library or insert, or fragment thereof) will be positioned next to the attL1 site. Entry Vectors preferably contain the rrnB transcriptional terminator upstream of the attL1 site. This sequence ensures that expression of cloned nucleic acid molecules of interest is reliably "off" in E. coli, so that even toxic genes can be successfully cloned. Thus, Entry Clones may be designed to be transcriptionally silent. Note also that Entry Vectors, and hence Entry Clones, may contain the kanamycin antibiotic resistance (kan') gene to facilitate selection of host cells

containing Entry Clones after transformation. In certain applications, however, Entry Clones may contain other selection markers, including but not limited to a gentamycin resistance (gen') or tetracycline resistance (tet') gene, to facilitate selection of host cells containing Entry Clones after transformation.

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Once a nucleic acid molecule of interest has been cloned into an Entry Vector, it may be moved into a Destination Vector. The upper right portion of Figure 5A shows a schematic of a Destination Vector. The thick arrow represents some function (often transcription or translation) that will act on the nucleic acid molecule of interest in the clone. During the recombination reaction, the region between the attR1 and attR2 sites, including a toxic or "death" gene (e.g., ccdB), is replaced by the DNA segment from the Entry Clone. Selection for recombinants that have acquired the ampicillin resistance (amp<sup>r</sup>) gene (carried on the Destination Vector) and that have also lost the death gene ensures that a high percentage (usually >90%) of the resulting colonies will contain the correct insert.

To move a nucleic acid molecule of interest into a Destination Vector, the Destination Vector is mixed with the Entry Clone comprising the desired nucleic acid molecule of interest, a cocktail of recombination proteins (e.g., GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix) is added, the mixture is incubated (preferably at about 25°C for about 60 minutes, or longer under certain circumstances, e.g. for transfer of large nucleic acid molecules, as described below) and any standard host cell (including bacterial cells such as E. coli; animal cells such as insect cells, mammalian cells, nematode cells and the like; plant cells; and yeast cells) strain is transformed with the reaction mixture. The host cell used will be determined by the desired selection (e.g., E. coli DB3.1, available commercially from Life Technologies, Inc., allows survival of clones containing the ccdB death gene, and thus can be used to select for cointegrate molecules -i.e., molecules that are hybrids between the Entry Clone and Destination Vector). The Examples below provide further details and protocols for use of Entry and Destination Vectors in transferring nucleic acid molecules of interest and expressing RNAs or polypeptides encoded by these nucleic acid molecules in a variety of host cells.

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- The cloning system of the invention therefore offers multiple advantages:
- Once a nucleic acid molecule of interest is cloned into the GATEWAYTM Cloning System, it can be moved into and out of other vectors with complete fidelity of reading frame and orientation. That is, since the reactions proceed whereby attL1 on the Entry Clone recombines with attR1 on the Destination Vector, the directionality of the nucleic acid molecule of interest is maintained or may be controlled upon transfer from the Entry Clone into the Destination Vector. Hence, the GATEWAYTM Cloning System provides a powerful and easy method of directional cloning of nucleic acid molecule of interest.
- One-step cloning or subcloning: Mix the Entry Clone and the Destination
   Vector with Clonase, incubate, and transform.
- Clone PCR products readily by in vitro recombination, by adding attB sites to PCR primers. Then directly transfer these Entry Clones into Destination Vectors. This process may also be carried out in one step (see Examples below).
- Powerful selections give high reliability: >90% (and often >99%) of the colonies contain the desired DNA in its new vector.
- One-step conversion of existing standard vectors into GATEWAY<sup>TM</sup>
   Cloning System vectors.
- Ideal for large vectors or those with few cloning sites.
- Recombination sites are short (25 bp), and may be engineered to contain no stop codons or secondary structures.
- Reactions may be automated, for high-throughput applications (e.g., for diagnostic purposes or for therapeutic candidate screening).
- The reactions are economical: 0.3 μg of each DNA; no restriction enzymes, phosphatase, ligase, or gel purification. Reactions work well with miniprep DNA.
- Transfer multiple clones, and even libraries, into one or more Destination Vectors, in a single experiment.
- A variety of Destination Vectors may be produced, for applications including, but not limited to:

- •Protein expression in E. coli: native proteins; fusion proteins with GST, His6, thioredoxin, etc., for purification, or one or more epitope tags; any promoter useful in expressing proteins in E. coli may be used, such as ptrc, λP<sub>L</sub>, and T7 promoters.
- Protein expression in eukaryotic cells: CMV promoter, baculovirus (with or without His6 tag), Semliki Forest virus, Tet regulation.
- •DNA sequencing (all *lac* primers), RNA probes, phagemids (both strands)
- A variety of Entry Vectors (for recombinational cloning entry by standard recombinant DNA methods) may be produced:
  - •Strong transcription stop just upstream, for genes toxic to E. coli.
  - •Three reading frames.
  - •With or without TEV protease cleavage site.
  - •Motifs for prokaryotic and / or eukaryotic translation.
  - Compatible with commercial cDNA libraries.
- Expression Clone cDNA (attB) libraries, for expression screening, including
   2-hybrid libraries and phage display libraries, may also be constructed.

## Recombination Site Sequences

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In one aspect, the invention relates to nucleic acid molecules, which may or may not be isolated nucleic acid molecules, comprising one or more nucleotide sequences encoding one or more recombination sites or portions thereof. In particular, this aspect of the invention relates to such nucleic acid molecules comprising one or more nucleotide sequences encoding attB, attP, attL, or attR, or portions of these recombination site sequences. The invention also relates to mutants, derivatives, and fragments of such nucleic acid molecules. Unless otherwise indicated, all nucleotide sequences that may have been determined by sequencing a DNA molecule herein were determined using manual or automated DNA sequencing, such as dideoxy sequencing, according to methods that are routine to one of ordinary skill in the art (Sanger, F., and Coulson, A.R., J. Mol. Biol. 94:444-448 (1975); Sanger, F., et al., Proc. Natl. Acad. Sci. USA 74:5463-5467 (1977)). All amino acid sequences of polypeptides encoded by DNA

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molecules determined herein were predicted by conceptual translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by these approaches, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by such methods are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

Unless otherwise indicated, each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U). Thus, the invention relates to sequences of the invention in the form of DNA or RNA molecules, or hybrid DNA/RNA molecules, and their corresponding complementary DNA, RNA, or DNA/RNA strands.

In a first such aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attB1, or mutants, fragments, variants or derivatives thereof. Such nucleic acid molecules may comprise an attB1 nucleotide sequence having the sequence set forth in Figure 9, such as: ACAAGTTTGTACAAAAAAGCAGGCT, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attB1, or mutants, fragments, variants or derivatives thereof. As one of ordinary skill will appreciate, however, certain mutations, insertions, or deletions of one or more bases in the attB1 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional

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integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the *attB1* sequence are encompassed within the scope of the invention.

In a related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attB2, or mutants, fragments, variants or derivatives thereof. Such nucleic acid molecules may comprise an attB2 nucleotide sequence having the sequence set forth in Figure 9, such as: ACCCAGCTTTCTTGTACAAAGTGGT, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attB2, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attB2 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules, hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attB2 sequence are encompassed within the scope of the invention.

A recombinant host cell comprising a nucleic acid molecule containing attB1 and attB2 sites (the vector pEXP501, also known as pCMVSport6; see Figure 48), *E. coli* DB3.1(pCMVSport6), was deposited on February 27, 1999, with the Collection, Agricultural Research Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604 USA, as Deposit No. NRRL B-30108. The attB1 and attB2 sites within the deposited nucleic acid molecule are contained in nucleic acid cassettes in association with one or more additional functional sequences as described in more detail below.

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AATCATTATTG, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attP1, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attP1 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attP1 sequence are encompassed within the scope of the invention.

In another related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attP2, or mutants, fragments, variants or derivatives thereof. Such nucleic acid molecules may comprise an attP2 nucleotide sequence having the sequence set forth in Figure 9. such as: CAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTG-CAACAAATTGATAAGCAATGCTTTCTTATAATGCCAACTTT-GTACAAGAAAGCTGAACGAGAAACGTAAAATGATA-TAAATATCAATATTAAATTAGATTTTGCATAAAAAACAG-ACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAA-CTACTTAGATGGTATTAGTGACCTGTA, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attP2, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attP2 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attP2 sequence are encompassed within the scope of the invention.

A recombinant host cell comprising a nucleic acid molecule (the attP vector pDONR201, also known as pENTR21-attPkan or pAttPkan; see Figure 49) containing attP1 and attP2 sites, *E. coli* DB3.1(pAttPkan) (also called *E. coli* DB3.1(pAHKan)), was deposited on February 27, 1999, with the Collection, Agricultural Research Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604 USA, as Deposit No. NRRL B-30099. The attP1 and attP2 sites within the deposited nucleic acid molecule are contained in nucleic acid

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cassettes in association with one or more additional functional sequences as described in more detail below.

In another related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attR1, or mutants, fragments, variants or derivatives thereof. Such nucleic acid molecules may comprise an attR1 nucleotide sequence having the sequence set forth in Figure 9. ACAAGTTTGTACAAAAAAGCTGAACGAGsuch AAACGTAAAATGATATAAATATCAATATATTAAATTAGATTTTGCAT-AAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCA-CTATG, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attR1, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attR1 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attR1 sequence are encompassed within the scope of the invention.

In another related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attR2, or mutants, fragments, variants or derivatives thereof. Such nucleic acid molecules may comprise an attR2 nucleotide sequence having the sequence set forth in Figure 9. GCAGGTCGACCATAGTGACTGGATATsuch GTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTA-ATTTAATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTT-TCTTGTACAAAGTGGT, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attR2, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attR2 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attR2 sequence are encompassed within the scope of the invention.

Recombinant host cell strains containing attR1 sites apposed to cloning sites in reading frame A, reading frame B, and reading frame C, *E. coli* DB3.1(pEZC15101) (reading frame A; see Figure 64A), *E. coli* DB3.1(pEZC15102) (reading frame B; see Figure 64B), and *E. coli* DB3.1(pEZC15103) (reading frame C; see Figure 64C), and containing corresponding attR2 sites, were deposited on February 27, 1999, with the Collection, Agricultural Research Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604 USA, as Deposit Nos. NRRL B-30103, NRRL B-30104, and NRRL B-30105, respectively. The attR1 and attR2 sites within the deposited nucleic acid molecules are contained in nucleic acid cassettes in association with one or more additional functional sequences as described in more detail below.

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In another related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attL1, or mutants, fragments, variants and derivatives thereof. Such nucleic acid molecules may comprise an attL1 nucleotide sequence having the sequence set forth in Figure 9, such as: CAA ATA ATG ATT TTA TTT TGA CTG ATA GTG ACC TGT TCG TTG CAA CAA ATT GAT AAG CAA TGC TTT TTT ATA ATG CCA ACT TTG TAC AAA AAA GCA GGC T, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attL1, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attL1 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attL1 sequence are encompassed within the scope of the invention.

In another related aspect, the invention provides nucleic acid molecules comprising one or more nucleotide sequences encoding attL2, or mutants, fragments, variants and derivatives thereof. Such nucleic acid molecules may comprise an attL2 nucleotide sequence having the sequence set forth in Figure 9, such as: C AAA TAA TGA TTT TAT TTT GAC TGA TAG TGA CCT GTT CGT TGC AAC AAA TTG ATA AGC AAT GCT TTC TTA TAA TGC CAA

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CTT TGT ACA AGA AAG CTG GGT, or a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 9 for attL2, or mutants, fragments, variants or derivatives thereof. As noted above for attB1, certain mutations, insertions, or deletions of one or more bases in the attL2 sequence contained in the nucleic acid molecules of the invention may be made without compromising the structural and functional integrity of these molecules; hence, nucleic acid molecules comprising such mutations, insertions, or deletions in the attL2 sequence are encompassed within the scope of the invention.

Recombinant host cell strains containing attL1 sites apposed to cloning sites in reading frame A, reading frame B, and reading frame C, E. coli DB3.1(pENTR1A) (reading frame A; see Figure 10), E. coli DB3.1(pENTR2B) (reading frame B; see Figure 11), and E. coli DB3.1(pENTR3C) (reading frame C; see Figure 12), and containing corresponding attL2 sites, were deposited on February 27, 1999, with the Collection, Agricultural Research Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604 USA, as Deposit Nos. NRRL B-30100, NRRL B-30101, and NRRL B-30102, respectively. The attL1 and attL2 sites within the deposited nucleic acid molecules are contained in nucleic acid cassettes in association with one or more additional functional sequences as described in more detail below.

Each of the recombination site sequences described herein or portions thereof, or the nucleotide sequence cassettes contained in the deposited clones, may be cloned or inserted into a vector of interest (for example, using the recombinational cloning methods described herein and/or standard restriction cloning techniques that are routine in the art) to generate, for example, Entry Vectors or Destination Vectors which may be used to transfer a desired segment of a nucleic acid molecule of interest (e.g., a gene, cDNA molecule, or cDNA library) into a desired vector or into a host cell.

Using the information provided herein, such as the nucleotide sequences for the recombination site sequences described herein, an isolated nucleic acid molecule of the present invention encoding one or more recombination sites or portions thereof may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Preferred such

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methods include PCR-based cloning methods, such as reverse transcriptase-PCR (RT-PCR) using primers such as those described herein and in the Examples below. Alternatively, vectors comprising the cassettes containing the recombination site sequences described herein are available commercially from Life Technologies, Inc. (Rockville, MD).

The invention is also directed to nucleic acid molecules comprising one or more of the recombination site sequences or portions thereof and one or more additional nucleotide sequences, which may encode functional or structural sites such as one or more multiple cloning sites, one or more transcription termination sites, one or more transcriptional regulatory sequences (which may be promoters, enhancers, repressors, and the like), one or more translational signals (e.g., secretion signal sequences), one or more origins of replication, one or more fusion partner peptides (particularly glutathione S-transferase (GST), hexahistidine (His,), and thioredoxin (Trx)), one or more selection markers or modules, one or more nucleotide sequences encoding localization signals such as nuclear localization signals or secretion signals, one or more origins of replication, one or more protease cleavage sites, one or more genes or portions of genes encoding a protein or polypeptide of interest, and one or more 5' polynucleotide extensions (particularly an extension of guanine residues ranging in length from about 1 to about 20, from about 2 to about 15, from about 3 to about 10, from about 4 to about 10, and most preferably an extension of 4 or 5 guanine residues at the 5' end of the recombination site nucleotide sequence. The one or more additional functional or structural sequences may or may not flank one or more of the recombination site sequences contained on the nucleic acid molecules of the invention.

In some nucleic acid molecules of the invention, the one or more nucleotide sequences encoding one or more additional functional or structural sites may be operably linked to the nucleotide sequence encoding the recombination site. For example, certain nucleic acid molecules of the invention may have a promoter sequence operably linked to a nucleotide sequence encoding a recombination site or portion thereof of the invention, such as a T7 promoter, a phage lambda PL

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promoter, an *E. coli lac*; *trp* or *tac* promoter, and other suitable promoters which will be familiar to the skilled artisan.

Nucleic acid molecules of the present invention, which may be isolated nucleic acid molecules, may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically, or in the form of DNA-RNA hybrids. The nucleic acid molecules of the invention may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand. The nucleic acid molecules of the invention may also have a number of topologies, including linear, circular, coiled, or supercoiled.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells, and those DNA molecules purified (partially or substantially) from a solution whether produced by recombinant DNA or synthetic chemistry techniques. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention.

The present invention further relates to mutants, fragments, variants and derivatives of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of one or more recombination sites. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism (see Lewin, B., ed., Genes II, , John Wiley & Sons, New York (1985)). Non-naturally occurring variants may be produced using art-known mutagenesis techniques, such as those described hereinbelow.

Such variants include those produced by nucleotide substitutions, deletions or additions or portions thereof, or combinations thereof. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding

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regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the encoded polypeptide(s) or portions thereof, and which also do not substantially alter the reactivities of the recombination site nucleic acid sequences in recombination reactions. Also especially preferred in this regard are conservative substitutions.

Particularly preferred mutants, fragments, variants, and derivatives of the nucleic acid molecules of the invention include, but are not limited to, insertions. deletions or substitutions of one or more nucleotide bases within the 15 bp core region (GCTTTTTTATACTAA) which is identical in all four wildtype lambda att sites, attB, attP, attL and attR (see U.S. Application Nos. 08/663,002, filed June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12. 1998, and 09/177,387, filed October 23, 1998, which describes the core region in further detail, and the disclosures of which are incorporated herein by reference in their entireties). Analogously, the core regions in attB1, attP1, attL1 and attR1 are identical to one another, as are the core regions in attB2, attP2, attL2 and attR2. Particularly preferred in this regard are nucleic acid molecules comprising insertions, deletions or substitutions of one or more nucleotides within the seven bp overlap region (TTTATAC, which is defined by the cut sites for the integrase protein and is the region where strand exchange takes place) that occurs within this 15 bp core region (GCTTTTTTATACTAA). Examples of such preferred mutants, fragments, variants and derivatives according to this aspect of the invention include, but are not limited to, nucleic acid molecules in which the thymine at position 1 of the seven by overlap region has been deleted or substituted with a guanine, cytosine, or adenine; in which the thymine at position 2 of the seven bp overlap region has been deleted or substituted with a guanine, cytosine, or adenine; in which the thymine at position 3 of the seven bp overlap region has been deleted or substituted with a guanine, cytosine, or adenine, in which the adenine at position 4 of the seven bp overlap region has been deleted or substituted with a guanine, cytosine, or thymine; in which the thymine at position 5 of the seven bp overlap region has been deleted or substituted with a

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guanine, cytosine, or adenine, in which the adenine at position 6 of the seven bp overlap region has been deleted or substituted with a guanine, cytosine, or thymine; and in which the cytosine at position 7 of the seven bp overlap region has been deleted or substituted with a guanine, thymine, or adenine, or any combination of one or more such deletions and/or substitutions within this seven bp overlap region. As described in detail in Example 21 herein, mutants of the nucleic acid molecules of the invention in which substitutions have been made within the first three positions of the seven bp overlap (TTTATAC) have been found in the present invention to strongly affect the specificity of recombination, mutant nucleic acid molecules in which substitutions have been made in the last four positions (TTTATAC) only partially alter recombination specificity, and mutant nucleic acid molecules comprising nucleotide substitutions outside of the seven bp overlap, but elsewhere within the 15 bp core region, do not affect specificity of recombination but do influence the efficiency of recombination.

Hence, in an additional aspect, the present invention is also directed to nucleic acid molecules comprising one or more recombination site nucleotide sequences that affect recombination specificity, particularly one or more nucleotide sequences that may correspond substantially to the seven base pair overlap within the 15 bp core region, having one or more mutations that affect recombination specificity. Particularly preferred such molecules may comprise a consensus sequence (described in detail in Example 21 herein) such as NNNATAC, wherein "N" refers to any nucleotide (i.e., may be A, G, T/U or C), with the proviso that if one of the first three nucleotides in the consensus sequence is a T/U, then at least one of the other two of the first three nucleotides is not a T/U.

In a related aspect, the present invention is also directed to nucleic acid molecules comprising one or more recombination site nucleotide sequences that enhance recombination efficiency, particularly one or more nucleotide sequences that may correspond substantially to the core region and having one or more mutations that enhance recombination efficiency. By sequences or mutations that "enhance recombination efficiency" is meant a sequence or mutation in a recombination site, preferably in the core region (e.g., the 15 bp core region of att recombination sites), that results in an increase in cloning efficiency (typically

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measured by determining successful cloning of a test sequence, e.g., by determining CFU/ml for a given cloning mixture) when recombining molecules comprising the mutated sequence or core region as compared to molecules that do not comprise the mutated sequence or core region (e.g., those comprising a wildtype recombination site core region sequence). More specifically, whether or not a given sequence or mutation enhances recombination efficiency may be determined using the sequence or mutation in recombinational cloning as described herein, and determining whether the sequence or mutation provides enhanced recombinational cloning efficiency when compared to a non-mutated (e.g., wildtype) sequence. Methods of determining preferred cloning efficiencyenhancing mutations for a number of recombination sites, particularly for att recombination sites, are described herein, for example in Examples 22-25. Examples of preferred such mutant recombination sites include but are not limited to the attL consensus core sequence of caacttnntnnnannaagttg (wherein "n" represents any nucleotide), for example the attL5 sequence agcctgctttattatactaagttggcatta and the attL6 sequence agcctgcttttttatattaagttggcatta; the attB1.6 sequence ggggacaactttgtacaaaaaagttggct; the attB2.2 sequence ggggacaactttgtacaagaaagctgggt; and the attB2.10 sequence ggggacaactttgtacaagaaagttgggt. Those of skill in the art will appreciate that, in addition to the core region, other portions of the att site may affect the efficiency of recombination. There are five so-called arm binding sites for the integrase protein in the bacteriophage lambda attP site, two in attR (P1 and P2), and three in attL (P'1, P'2 and P'3). Compared to the core binding sites, the integrase protein binds to arm sites with high affinity and interacts with core and arm sites through two different domains of the protein. As with the core binding site a consensus sequence for the arm binding site consisting of C/AAGTCACTAT has been inferred from sequence comparison of the five arm binding sites and seven non-att sites (Ross and Landy, Proc. Natl. Acad. Sci. USA 79:7724-7728 (1982)). Each arm site has been mutated and tested for its effect in the excision and integration reactions (Numrych et al., Nucl. Acids Res. 18:3953 (1990)). Hence, specific sites are utilized in each reaction in different ways, namely, the P1 and P'3

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sites are essential for the integration reaction whereas the other three sites are dispensable to the integration reaction to varying degrees. Similarly, the P2, P'1 and P'2 sites are most important for the excision reaction, whereas P1 and P'3 are completely dispensable. Interestingly, when P2 is mutated the integration reaction occurs more efficiently than with the wild type attP site. Similarly, when P1 and P'3 are mutated the excision reaction occurs more efficiently. The stimulatory effect of mutating integrase arm binding sites can be explained by removing sites that compete or inhibit a specific recombination pathway or that function in a reaction that converts products back to starting substrates. In fact there is evidence for an XIS-independent LR reaction (Abremski and Gottesman, J. Mol. Biol. 153:67-78 (1981)). Thus, in addition to modifications in the core region of the att site, the present invention contemplates the use of att sites containing one or more modifications in the integrase arm-type binding sites. In some preferred embodiments, one or more mutations may be introduced into one or more of the P1, P1, P2, P2 and P3 sites. In some preferred embodiments, multiple mutations may be introduced into one or more of these sites. Preferred such mutations include those which increase the recombination in vitro. For example, in some embodiments mutations may be introduced into the arm-type binding sites such that integrative recombination, corresponding to the BP reaction, is enhanced. In other embodiments, mutations may be introduced into the arm-type binding sites such that excisive recombination, corresponding to the LR reaction, is enhanced. Of course, based on the guidance contained herein, particularly in the construction and evaluation of effects of mutated recombination sites upon recombinational specificity and efficiency, analogous mutated or engineered sequences may be produced for other recombination sites described herein (including but not limited to lox, FRT, and the like) and used in accordance with the invention. For example, much like the mutagenesis strategy used to select core binding sites that enhance recombination efficiency, similar strategies can be employed to select changes in the arms of attP, attL and attR, and in analogous sequences in other recombination sites such as lox, FRT and the like, that enhance recombination efficiency. Hence, the construction and evaluation of such mutants is well within the abilities of those of ordinary skill in the art without undue experimentation.

One suitable methodology for preparing and evaluating such mutations is found in Numrych, et al., (1990) Nucleic Acids Research 18(13): 3953-3959.

Other mutant sequences and nucleic acid molecules that may be suitable to enhance recombination efficiency will be apparent from the description herein, or may be easily determined by one of ordinary skill using only routine experimentation in molecular biology in view of the description herein and information that is readily available in the art

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Since the genetic code is well known in the art, it is also routine for one of ordinary skill in the art to produce degenerate variants of the nucleic acid molecules described herein without undue experimentation. Hence, nucleic acid molecules comprising degenerate variants of nucleic acid sequences encoding the recombination sites described herein are also encompassed within the scope of the invention.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 50% identical, at least 60% identical, at least 70% identical, at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to the nucleotide sequences of the seven bp overlap region within the 15 bp core region of the recombination sites described herein, or the nucleotide sequences of attB1, attB2, attP1, attP2, attL1, attL2, attR1 or attR2 as set forth in Figure 9 (or portions thereof), or a nucleotide sequence complementary to any of these nucleotide sequences, or fragments, variants, mutants, and derivatives thereof.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence encoding a particular recombination site or portion thereof is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations (e.g., insertions, substitutions, or deletions) per each 100 nucleotides of the reference nucleotide sequence encoding the recombination site. For example, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference attB1 nucleotide sequence, up to 5% of the nucleotides in the attB1 reference sequence may be

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deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the attB1 reference sequence may be inserted into the attB1 reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, a given recombination site nucleotide sequence or portion thereof can be determined conventionally using known computer programs such as DNAsis software (Hitachi Software, San Bruno, California) for initial sequence alignment followed by ESEE version 3.0 DNA/protein sequence software (cabot@trog.mbb.sfu.ca) for multiple sequence alignments. Alternatively, such determinations may be accomplished using the BESTFIT program (Wisconsin Sequence Analysis Package, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711), which employs a local homology algorithm (Smith and Waterman, Advances in Applied Mathematics 2: 482-489 (1981)) to find the best segment of homology between two sequences. When using DNAsis, ESEE, BESTFIT or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

The present invention is directed to nucleic acid molecules at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the attB1, attB2, attP1, attP2, attL1, attL2, attR1 or attR2 nucleotide sequences as set forth in Figure 9, or to the nucleotide sequence of the deposited clones, irrespective of whether they encode particular functional polypeptides. This is because even where a particular nucleic acid molecule does not encode a particular functional polypeptide, one of skill in the art would still know how to use the nucleic acid

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molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer.

Mutations can also be introduced into the recombination site nucleotide sequences for enhancing site specific recombination or altering the specificities of the reactants, etc. Such mutations include, but are not limited to: recombination sites without translation stop codons that allow fusion proteins to be encoded; recombination sites recognized by the same proteins but differing in base sequence such that they react largely or exclusively with their homologous partners allowing multiple reactions to be contemplated; and mutations that prevent hairpin formation of recombination sites. Which particular reactions take place can be specified by which particular partners are present in the reaction mixture.

There are well known procedures for introducing specific mutations into nucleic acid sequences. A number of these are described in Ausubel, F.M. et al., Current Protocols in Molecular Biology, Wiley Interscience, New York (1989-1996). Mutations can be designed into oligonucleotides, which can be used to modify existing cloned sequences, or in amplification reactions. Random mutagenesis can also be employed if appropriate selection methods are available to isolate the desired mutant DNA or RNA. The presence of the desired mutations can be confirmed by sequencing the nucleic acid by well known methods.

The following non-limiting methods can be used to modify or mutate a given nucleic acid molecule encoding a particular recombination site to provide mutated sites that can be used in the present invention:

- 1. By recombination of two parental DNA sequences by site-specific (e.g. attL and attR to give attP) or other (e.g. homologous) recombination mechanisms where the parental DNA segments contain one or more base alterations resulting in the final mutated nucleic acid molecule;
- By mutation or mutagenesis (site-specific, PCR, random, spontaneous, etc)
   directly of the desired nucleic acid molecule;
- 3. By mutagenesis (site-specific, PCR, random, spontaneous, etc) of parental DNA sequences, which are recombined to generate a desired nucleic acid molecule;

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- By reverse transcription of an RNA encoding the desired core sequence;
   and
- 5. By *de novo* synthesis (chemical synthesis) of a sequence having the desired base changes, or random base changes followed by sequencing or functional analysis according to methods that are routine in the art.

The functionality of the mutant recombination sites can be demonstrated in ways that depend on the particular characteristic that is desired. For example, the lack of translation stop codons in a recombination site can be demonstrated by expressing the appropriate fusion proteins. Specificity of recombination between homologous partners can be demonstrated by introducing the appropriate molecules into in vitro reactions, and assaying for recombination products as described herein or known in the art. Other desired mutations in recombination sites might include the presence or absence of restriction sites, translation or transcription start signals, protein binding sites, particular coding sequences, and other known functionalities of nucleic acid base sequences. Genetic selection schemes for particular functional attributes in the recombination sites can be used according to known method steps. For example, the modification of sites to provide (from a pair of sites that do not interact) partners that do interact could be achieved by requiring deletion, via recombination between the sites, of a DNA sequence encoding a toxic substance. Similarly, selection for sites that remove translation stop sequences, the presence or absence of protein binding sites, etc., can be easily devised by those skilled in the art.

Accordingly, the present invention also provides a nucleic acid molecule, comprising at least one DNA segment having at least one, and preferably at least two, engineered recombination site nucleotide sequences of the invention flanking a selectable marker and/or a desired DNA segment, wherein at least one of said recombination site nucleotide sequences has at least one engineered mutation that enhances recombination *in vitro* in the formation of a Cointegrate DNA or a Product DNA. Such engineered mutations may be in the core sequence of the recombination site nucleotide sequence of the invention; *see* U.S. Application Nos. 08/486,139, filed June 7, 1995, 08/663,002, filed June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12, 1998, and 09/177,387, filed

October 23, 1998, the disclosures of which are all incorporated herein by reference in their entireties.

While in the preferred embodiment the recombination sites differ in sequence and do not interact with each other, it is recognized that sites comprising the same sequence, which may interact with each other, can be manipulated or engineered to inhibit recombination with each other. Such conceptions are considered and incorporated herein. For example, a protein binding site (e.g., an antibody-binding site, a histone-binding site, an enzyme-binding site, or a binding site for any nucleic acid molecule-binding protein) can be engineered adjacent to one of the sites. In the presence of the protein that recognizes the engineered site, the recombinase fails to access the site and another recombination site in the nucleic acid molecule is therefore used preferentially. In the cointegrate this site can no longer react since it has been changed, e.g., from attB to attL. During or upon resolution of the cointegrate, the protein can be inactivated (e.g., by antibody, heat or a change of buffer) and the second site can undergo recombination.

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The nucleic acid molecules of the invention can have at least one mutation that confers at least one enhancement of said recombination, said enhancement selected from the group consisting of substantially (i) favoring integration; (ii) favoring recombination; (ii) relieving the requirement for host factors; (iii) increasing the efficiency of said Cointegrate DNA or Product DNA formation; (iv) increasing the specificity of said Cointegrate DNA or Product DNA formation; and (v) adding or deleting protein binding sites.

In other embodiments, the nucleic acid molecules of the invention may be PCR primer molecules, which comprise one or more of the recombination site sequences described herein or portions thereof, particularly those shown in Figure 9 (or sequences complementary to those shown in Figure 9), or mutants, fragments, variants or derivatives thereof, attached at the 3' end to a target-specific template sequence which specifically interacts with a target nucleic acid molecule which is to be amplified. Primer molecules according to this aspect of the invention may further comprise one or more, (e.g., 1, 2, 3, 4, 5, 10, 20, 25, 50, 100, 500, 1000, or more) additional bases at their 5' ends, and preferably comprise one or more (particularly four or five) additional bases, which are preferably

guanines, at their 5' ends, to increase the efficiency of the amplification products incorporating the primer molecules in the recombinational cloning system of the invention. Such nucleic acid molecules and primers are described in detail in the examples herein, particularly in Examples 22-25.

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Certain primers of the invention may comprise one or more nucleotide deletions in the attB1, attB2, attP1, attP2, attL1, attL2, attR1 or attR2 sequences as set forth in Figure 9. In one such aspect, for example, attB2 primers may be constructed in which one or more of the first four nucleotides at the 5' end of the attB2 sequence shown in Figure 9 have been deleted. Primers according to this aspect of the invention may therefore have the sequence:

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The primer nucleic acid molecules according to this aspect of the invention may be produced synthetically by attaching the recombination site sequences depicted in Figure 9, or portions thereof, to the 5' end of a standard PCR target-specific primer according to methods that are well-known in the art. Alternatively, additional primer nucleic acid molecules of the invention may be produced synthetically by adding one or more nucleotide bases, which preferably correspond to one or more, preferably five or more, and more preferably six or more, contiguous nucleotides of the *att* nucleotide sequences described herein (*see*, *e.g.*, Example 20 herein; *see also* U.S. Application Nos. 08/663,002, filed June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12, 1998, and 09/177,387, filed October 23, 1998, the disclosures of which are all incorporated herein by reference in their entireties), to the 5' end of a standard PCR target-specific primer according to methods that are well-known in the art, to provide

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primers having the specific nucleotide sequences described herein. As noted above, primer nucleic acid molecules according to this aspect of the invention may also optionally comprise one, two, three, four, five, or more additional nucleotide bases at their 5' ends, and preferably will comprise four or five guanines at their 5' ends. In one particularly preferred such aspect, the primer nucleic acid molecules of the invention may comprise one or more, preferably five or more, more preferably six or more, still more preferably 6-18 or 6-25, and most preferably 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25, contiguous nucleotides or bp of the *att*B1 or *att*B2 nucleotide sequences depicted in Figure 9 (or nucleotides complementary thereto), linked to the 5' end of a target-specific (*e.g.*, a gene-specific) primer molecule. Primer nucleic acid molecules according to this aspect of the invention include, but are not limited to, *att*B1- and *att*B2-derived primer nucleic acid molecules having the following nucleotide sequences:

15	ACAAGTTTGTACAAAAAAGCAGGCT-nnnnnnnnnnnn n
	$ACCACTTTGTACAAGAAAGCTGGGT-nnnnnnnnnnnn \dots n\\$
	TGTACAAAAAGCAGGCT-nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
	TGTACAAGAAAGCTGGGT-nnnnnnnnnnnnnn n
	ACAAAAAGCAGGCT-nnnnnnnnnnnn n
20	ACAAGAAAGCTGGGT-nnnnnnnnnnnn n
	AAAAAGCAGGCT-nnnnnnnnnnnn n
	AGAAAGCTGGGT-nnnnnnnnnnnnn n
	AAAAGCAGGCT-nnnnnnnnnnnn n
	GAAAGCTGGGT-nnnnnnnnnnn n
25	AAAGCAGGCT-nnnnnnnnnnnn n
	AAAGCTGGGT-nnnnnnnnnnnn n
	AAGCAGGCT-nnnnnnnnnnn n
	AAGCTGGGT-nnnnnnnnnnn n
	AGCAGGCT-nnnnnnnnnnnn n
30	AGCTGGGT-nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
	GCAGGCT-nnnnnnnnnnnn n

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CTGGGT-nnnnnnnnnnnnn...n,

Of course, it will be apparent to one of ordinary skill from the teachings contained herein that additional primer nucleic acid molecules analogous to those specifically described herein may be produced using one or more, preferably five or more, more preferably six or more, still more preferably ten or more, 15 or more, 20 or more, 25 or more, 30 or more, etc. (through to and including all) of the contiguous nucleotides or bp of the attP1, attP2, attL1, attL2, attR1 or attR2 nucleotide sequences depicted in Figure 9 (or nucleotides complementary thereto), linked to the 5' end of a target-specific (e.g., a gene-specific) primer molecule. As noted above, such primer nucleic acid molecules may optionally further comprise one, two, three, four, five, or more additional nucleotide bases at their 5' ends, and preferably will comprise four guanines at their 5' ends. Other primer molecules comprising the attB1, attB2, attP1, attP2, attL1, attL2, attR1 and attR2 sequences depicted in Figure 9, or portions thereof, may be made by one of ordinary skill without resorting to undue experimentation in accordance with the guidance provided herein.

The primers of the invention described herein are useful in producing PCR fragments having a nucleic acid molecule of interest flanked at each end by a recombination site sequence (as described in detail below in Example 9), for use in cloning of PCR-amplified DNA fragments using the recombination system of the invention (as described in detail below in Examples 8, 19 and 21-25).

## Vectors

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The invention also relates to vectors comprising one or more of the nucleic acid molecules of the invention, as described herein. In accordance with the invention, any vector may be used to construct the vectors of the invention. In

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particular, vectors known in the art and those commercially available (and variants or derivatives thereof) may in accordance with the invention be engineered to include one or more nucleic acid molecules encoding one or more recombination sites (or portions thereof), or mutants, fragments, or derivatives thereof, for use in the methods of the invention. Such vectors may be obtained from, for example, Vector Laboratories Inc., InVitrogen, Promega, Novagen, New England Biolabs, Clontech, Roche, Pharmacia, EpiCenter, OriGenes Technologies Inc., Stratagene, Perkin Elmer, Pharmingen, Life Technologies, Inc., and Research Genetics. Such vectors may then for example be used for cloning or subcloning nucleic acid molecules of interest. General classes of vectors of particular interest include prokaryotic and/or eukaryotic cloning vectors, Expression Vectors, fusion vectors, two-hybrid or reverse two-hybrid vectors, shuttle vectors for use in different hosts, mutagenesis vectors, transcription vectors, vectors for receiving large inserts and the like.

Other vectors of interest include viral origin vectors (M13 vectors, bacterial phage  $\lambda$  vectors, bacteriophage P1 vectors, adenovirus vectors, herpesvirus vectors, retrovirus vectors, phage display vectors, combinatorial library vectors), high, low, and adjustable copy number vectors, vectors which have compatible replicons for use in combination in a single host (pACYC184 and pBR322) and eukaryotic episomal replication vectors (pCDM8).

Particular vectors of interest include prokaryotic Expression Vectors such as pcDNA II, pSL301, pSE280, pSE380, pSE420, pTrcHisA, B, and C, pRSET A, B, and C (Invitrogen, Inc.), pGEMEX-1, and pGEMEX-2 (Promega, Inc.), the pET vectors (Novagen, Inc.), pTrc99A, pKK223-3, the pGEX vectors, pEZZ18, pRIT2T, and pMC1871 (Pharmacia, Inc.), pKK233-2 and pKK388-1 (Clontech, Inc.), and pProEx-HT (Life Technologies, Inc.) and variants and derivatives thereof. Destination Vectors can also be made from eukaryotic Expression Vectors such as pFastBac, pFastBac HT, pFastBac DUAL, pSFV, and pTet-Splice (Life Technologies, Inc.), pEUK-C1, pPUR, pMAM, pMAMneo, pBI101, pBI121, pDR2, pCMVEBNA, and pYACneo (Clontech), pSVK3, pSVL, pMSG, pCH110, and pKK232-8 (Pharmacia, Inc.), p3'SS, pXT1, pSG5, pPbac, pMbac, pMC1neo, and pOG44 (Stratagene, Inc.), and pYES2, pAC360, pBlueBacHis A,

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B, and C, pVL1392, pBsueBacIII, pCDM8, pcDNA1, pZeoSV, pcDNA3 pREP4, pCEP4, and pEBVHis (Invitrogen, Inc.) and variants or derivatives thereof.

Other vectors of particular interest include pUC18, pUC19, pBlueScript, pSPORT, cosmids, phagemids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes), MACs (mammalian artificial chromosomes), pQE70, pQE60, pQE9 (Quiagen), pBS vectors, PhageScript vectors, BlueScript vectors, pNH8A, pNH16A, pNH18A, pNH46A (Stratagene), pcDNA3 (InVitrogen), pGEX, pTrsfus, pTrc99A, pET-5, pET-9, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), pSPORT1, pSPORT2, pCMVSPORT2.0 and pSV-SPORT1 (Life Technologies, Inc.) and variants or derivatives thereof.

Additional vectors of interest include pTrxFus, pThioHis, pLEX, pTrcHis, pTrcHis2, pRSET, pBlueBacHis2, pcDNA3.1/His, pcDNA3.1(-)/Myc-His. pSecTag, pEBVHis, pPIC9K, pPIC3.5K, pAO815, pPICZ, pPICZa, pGAPZ. pGAPZa, pBlueBac4.5, pBlueBacHis2, pMelBac, pSinRep5, pSinHis, pIND, pIND(SP1), pVgRXR, pcDNA2.1. pYES2, pZErO1.1, pZErO-2.1, pCR-Blunt. pSE280, pSE380, pSE420, pVL1392, pVL1393, pCDM8, pcDNA1.1, pcDNA1.1/Amp, pcDNA3.1, pcDNA3.1/Zeo, pSe,SV2, pRc/CMV2, pRc/RSV. pREP4, pREP7, pREP8, pREP9, pREP10, pCEP4, pEBVHis, pCR3.1, pCR2.1, pCR3.1-Uni, and pCRBac from Invitrogen; λExCell, λgt11, pTrc99A, pKK223-3. pGEX-1\lambdaT, pGEX-2T, pGEX-2TK, pGEX-4T-1, pGEX-4T-2, pGEX-4T-3. pGEX-3X, pGEX-5X-1, pGEX-5X-2, pGEX-5X-3, pEZZ18, pRIT2T, pMC1871, pSVK3, pSVL, pMSG, pCH110, pKK232-8, pSL1180, pNEO, and pUC4K from Pharmacia; pSCREEN-1b(+), pT7Blue(R), pT7Blue-2, pCITE-4abc(+), pOCUS-2, pTAg, pET-32 LIC, pET-30 LIC, pBAC-2cp LIC, pBACgus-2cp LIC, pT7Blue-2 LIC, pT7Blue-2, λSCREEN-1, λBlueSTAR, pET-3abcd, pET-7abc, pET9abcd, pET11abcd, pET12abc, pET-14b, pET-15b, pET-16b, pET-17b-pET-17xb, pET-19b, pET-20b(+), pET-21abcd(+), pET-22b(+), pET-23abcd(+), pET-24abcd(+), pET-25b(+), pET-26b(+), pET-27b(+), pET-28abc(+), pET-29abc(+), pET-30abc(+), pET-31b(+), pET-32abc(+), pET-33b(+), pBAC-1, pBACgus-1, pBAC4x-1, pBACgus4x-1, pBAC-3cp, pBACgus-2cp, pBACsurf-1, plg, Signal plg, pYX, Selecta Vecta-Neo, Selecta Vecta - Hyg, and Selecta Vecta - Gpt from Novagen; pLexA, pB42AD, pGBT9, pAS2-1,

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pGAD424, pACT2, pGAD GL, pGAD GH, pGAD10, pGilda, pEZM3, pEGFP, pEGFP-1, pEGFP-N, pEGFP-C, pEBFP, pGFPuv, pGFP, p6xHis-GFP, pSEAP2-Basic, pSEAP2-Contral, pSEAP2-Promoter, pSEAP2-Enhancer, pßgal-Basic, pβgal-Control, pβgal-Promoter, pβgal-Enhancer, pCMVβ, pTet-Off, pTet-On, pTK-Hyg, pRetro-Off, pRetro-On, pIRES1neo, pIRES1hyg, pLXSN, pLNCX, pLAPSN, pMAMneo, pMAMneo-CAT, pMAMneo-LUC, pPUR, pSV2neo, pYEX4T-1/2/3, pYEX-S1, pBacPAK-His, pBacPAK8/9, pAcUW31, BacPAK6, pTriplEx,  $\lambda gt10$ ,  $\lambda gt11$ , pWE15, and  $\lambda TriplEx$  from Clontech; Lambda ZAP II, pBK-CMV, pBK-RSV, pBluescript II KS +/-, pBluescript II SK +/-, pAD-GAL4, pBD-GAL4 Cam, pSurfscript, Lambda FIX II, Lambda DASH, Lambda EMBL3, Lambda EMBL4, SuperCos, pCR-Script Amp, pCR-Script Cam, pCR-Script Direct, pBS +/-, pBC KS +/-, pBC SK +/-, Phagescript, pCAL-n-EK, pCAL-n, pCAL-c, pCAL-kc, pET-3abcd, pET-11abcd, pSPUTK, pESP-1, pCMVLacI, pOPRSVI/MCS, pOPI3 CAT, pXT1, pSG5, pPbac, pMbac, pMC1neo, pMC1neo Poly A, pOG44, pOG45, pFRTβGAL, pNEOβGAL, pRS403, pRS404, pRS405, pRS406, pRS413, pRS414, pRS415, and pRS416 from Stratagene.

Two-hybrid and reverse two-hybrid vectors of particular interest include pPC86, pDBLeu, pDBTrp, pPC97, p2.5, pGAD1-3, pGAD10, pACt, pACT2, pGADGL, pGADGH, pAS2-1, pGAD424, pGBT8, pGBT9, pGAD-GAL4, pLexA, pBD-GAL4, pHISi, pHISi-1, placZi, pB42AD, pDG202, pJK202, pJG4-5, pNLexA, pYESTrp and variants or derivatives thereof.

Yeast Expression Vectors of particular interest include pESP-1, pESP-2, pESC-His, pESC-Trp, pESC-URA, pESC-Leu (Stratagene), pRS401, pRS402, pRS411, pRS412, pRS421, pRS422, and variants or derivatives thereof.

According to the invention, the vectors comprising one or more nucleic acid molecules encoding one or more recombination sites, or mutants, variants, fragments, or derivatives thereof, may be produced by one of ordinary skill in the art without resorting to undue experimentation using standard molecular biology methods. For example, the vectors of the invention may be produced by introducing one or more of the nucleic acid molecules encoding one or more recombination sites (or mutants, fragments, variants or derivatives thereof) into one or more of the vectors described herein, according to the methods described,

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for example, in Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1982). In a related aspect of the invention, the vectors may be engineered to contain, in addition to one or more nucleic acid molecules encoding one or more recombination sites (or portions thereof), one or more additional physical or functional nucleotide sequences, such as those encoding one or more multiple cloning sites, one or more transcription termination sites, one or more transcriptional regulatory sequences (e.g., one or more promoters, enhancers, or repressors), one or more selection markers or modules, one or more genes or portions of genes encoding a protein or polypeptide of interest, one or more translational signal sequences, one or more nucleotide sequences encoding a fusion partner protein or peptide (e.g., GST, Hise or thioredoxin), one or more origins of replication, and one or more 5' or 3' polynucleotide tails (particularly a poly-G tail). According to this aspect of the invention, the one or more recombination site nucleotide sequences (or portions thereof) may optionally be operably linked to the one or more additional physical or functional nucleotide sequences described herein.

Preferred vectors according to this aspect of the invention include, but are not limited to: pENTR1A (Figures 10A and 10B), pENTR2B (Figures 11A and 11B), pENTR3C (Figures 12A and 12B), pENTR4 (Figures 13A and 13B), pENTR5 (Figures 14A and 14B), pENTR6 (Figures 15A and 15B), pENTR7 (Figures 16A and 16B), pENTR8 (Figures 17A and 17B), pENTR9 (Figures 18A and 18B). pENTR10 (Figures 19A and 19B), pENTR11 (Figures 20A and 20B), pDEST1 (Figures 21A-D), pDEST2 (Figure 22A-D), pDEST3 (Figure 23A-D), pDEST4 (Figure 24A-D), pDEST5 (Figure 25A-D), pDEST6 (Figure 26A-D), pDEST7 (Figure 27A-C), pDEST8 (Figure 28A-D), pDEST9 (Figure 29A-E), pDEST10 (Figure 30A-D), pDEST11 (Figure 31A-D), pDEST12.2 (also known as pDEST12) (Figure 32A-D), pDEST13 (Figure 33A-C), pDEST14 (Figure 34A-D), pDEST15 (Figure 35A-D), pDEST16 (Figure 36A-D), pDEST17 (Figure 37A-D), pDEST18 (Figure 38A-D), pDEST19 (Figure 39A-D), pDEST20 (Figure 40A-D), pDEST21 (Figure 41A-E), pDEST22 (Figure 42A-D), pDEST23 (Figure 43A-D), pDEST24 (Figure 44A-D), pDEST25 (Figure 45A-D), pDEST26 (Figure 46A-D), pDEST27 (Figure 47A-D), pEXP501 (also known

as pCMVSPORT6) (Figure 48A-B), pDONR201 (also known as pENTR21 attP vector or pAttPkan Donor Vector) (Figure 49), pDONR202 (Figure 50), pDONR203 (also known as pEZ15812) (Figure 51), pDONR204 (Figure 52). pDONR205 (Figure 53), pDONR206 (also known as pENTR22 attP vector or pAttPgen Donor Vector) (Figure 54), pMAB58 (Figure 87), pMAB62 (Figure 88), pDEST28 (Figure 90), pDEST29 (Figure 91), pDEST30 (Figure 92), pDEST31 (Figure 93), pDEST32 (Figure 94), pDEST33 (Figure 95), pDEST34 (Figure 96), pDONR207 (Figure 97), pMAB85 (Figure 98), pMAB86 (Figure 99), and fragments, mutants, variants, and derivatives thereof. However, it will be understood by one of ordinary skill that the present invention also encompasses other vectors not specifically designated herein, which comprise one or more of the isolated nucleic acid molecules of the invention encoding one or more recombination sites or portions thereof (or mutants, fragments, variants or derivatives thereof), and which may further comprise one or more additional physical or functional nucleotide sequences described herein which may optionally be operably linked to the one or more nucleic acid molecules encoding one or more recombination sites or portions thereof. Such additional vectors may be produced by one of ordinary skill according to the guidance provided in the present specification.

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#### **Polymerases**

Preferred polypeptides having reverse transcriptase activity (*i.e.*, those polypeptides able to catalyze the synthesis of a DNA molecule from an RNA template) for use in accordance with the present invention include, but are not limited to Moloney Murine Leukemia Virus (M-MLV) reverse transcriptase, Rous Sarcoma Virus (RSV) reverse transcriptase, Avian Myeloblastosis Virus (AMV) reverse transcriptase, Rous Associated Virus (RAV) reverse transcriptase, Myeloblastosis Associated Virus (MAV) reverse transcriptase, Human Immunodeficiency Virus (HIV) reverse transcriptase, retroviral reverse transcriptase, retrotransposon reverse transcriptase, hepatitis B reverse transcriptase, cauliflower mosaic virus reverse transcriptase and bacterial reverse transcriptase. Particularly preferred are those polypeptides having reverse

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transcriptase activity that are also substantially reduced in RNAse H activity (i.e., "RNAse H" polypeptides). By a polypeptide that is "substantially reduced in RNase H activity" is meant that the polypeptide has less than about 20%, more preferably less than about 15%, 10% or 5%, and most preferably less than about 2%, of the RNase H activity of a wildtype or RNase H<sup>+</sup> enzyme such as wildtype M-MLV reverse transcriptase. The RNase H activity may be determined by a variety of assays, such as those described, for example, in U.S. Patent No. 5,244,797, in Kotewicz, M.L. et al., Nucl. Acids Res. 16:265 (1988) and in Gerard, G.F., et al., FOCUS 14(5):91 (1992), the disclosures of all of which are fully incorporated herein by reference. Suitable RNAse H polypeptides for use in the present invention include, but are not limited to, M-MLV H reverse transcriptase, RSV H reverse transcriptase, AMV H reverse transcriptase, RAV H' reverse transcriptase, MAV H' reverse transcriptase, HIV H' reverse transcriptase, THERMOSCRIPTTM reverse transcriptase and THERMOSCRIPTTM II reverse transcriptase, and SUPERSCRIPTTM I reverse transcriptase and SUPERSCRIPT™ II reverse transcriptase, which are obtainable, for example, from Life Technologies, Inc. (Rockville, Maryland). See generally published PCT application WO 98/47912.

Other polypeptides having nucleic acid polymerase activity suitable for use in the present methods include thermophilic DNA polymerases such as DNA polymerase I, DNA polymerase III, Klenow fragment, T7 polymerase, and T5 polymerase, and thermostable DNA polymerases including, but not limited to, Thermus thermophilus (Tth) DNA polymerase, Thermus aquaticus (Taq) DNA polymerase, Thermotoga neopolitana (Tne) DNA polymerase, Thermotoga maritima (Tma) DNA polymerase, Thermococcus litoralis (Tli or VENT®) DNA polymerase, Pyrococcus furiosus (Pfu) DNA polymerase, Pyrococcus species GB-D (or DEEPVENT®) DNA polymerase, Pyrococcus woosii (Pwo) DNA polymerase, Bacillus sterothermophilus (Bst) DNA polymerase, Sulfolobus acidocaldarius (Sac) DNA polymerase, Thermus flavus (Tfl/Tub) DNA polymerase, Thermus ruber (Tru) DNA polymerase, Thermus flavus (Tfl/Tub) DNA polymerase, Thermus ruber (Tru) DNA polymerase, Thermus brockianus (DYNAZYME®) DNA polymerase, Methanobacterium thermoautotrophicum (Mth) DNA polymerase, and mutants,

variants and derivatives thereof. Such polypeptides are available commercially, for example from Life Technologies, Inc. (Rockville, MD), New Englan BioLabs (Beverly, MA), and Sigma/Aldrich (St. Louis, MO).

#### Host Cells

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The invention also relates to host cells comprising one or more of the nucleic acid molecules or vectors of the invention, particularly those nucleic acid molecules and vectors described in detail herein. Representative host cells that may be used according to this aspect of the invention include, but are not limited to, bacterial cells, yeast cells, plant cells and animal cells. Preferred bacterial host cells include Escherichia spp. cells (particularly E. coli cells and most particularly E. coli strains DH10B, Stbl2, DH5a, DB3, DB3.1 (preferably E. coli LIBRARY EFFICIENCY® DB3.1™ Competent Cells; Life Technologies, Inc., Rockville, MD), DB4 and DB5; see U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, the disclosure of which is incorporated by reference herein in its entirety), Bacillus spp. cells (particularly B. subtilis and B. megaterium cells), Streptomyces spp. cells, Erwinia spp. cells, Klebsiella spp. cells, Serratia spp. cells (particularly S. marcessans cells), Pseudomonas spp. cells (particularly P. aeruginosa cells), and Salmonella spp. cells (particularly S. typhimurium and S. typhi cells). Preferred animal host cells include insect cells (most particularly Drosophila melanogaster cells, Spodoptera frugiperda Sf9 and Sf21 cells and Trichoplusa High-Five cells), nematode cells (particularly C. elegans cells), avian cells, amphibian cells (particularly Xenopus laevis cells), reptilian cells, and mammalian cells (most particularly CHO, COS, VERO, BHK and human cells). Preferred yeast host cells include Saccharomyces cerevisiae cells and Pichia pastoris cells. These and other suitable host cells are available commercially, for example from Life Technologies, Inc. (Rockville, Maryland), American Type Culture Collection (Manassas, Virginia), and Agricultural Research Culture Collection (NRRL; Peoria, Illinois).

Methods for introducing the nucleic acid molecules and/or vectors of the invention into the host cells described herein, to produce host cells comprising one or more of the nucleic acid molecules and/or vectors of the invention, will be

familiar to those of ordinary skill in the art. For instance, the nucleic acid molecules and/or vectors of the invention may be introduced into host cells using well known techniques of infection, transduction, transfection, and transformation. The nucleic acid molecules and/or vectors of the invention may be introduced alone or in conjunction with other the nucleic acid molecules and/or vectors. Alternatively, the nucleic acid molecules and/or vectors of the invention may be introduced into host cells as a precipitate, such as a calcium phosphate precipitate. or in a complex with a lipid. Electroporation also may be used to introduce the nucleic acid molecules and/or vectors of the invention into a host. Likewise, such molecules may be introduced into chemically competent cells such as E. coli. If the vector is a virus, it may be packaged in vitro or introduced into a packaging cell and the packaged virus may be transduced into cells. Hence, a wide variety of techniques suitable for introducing the nucleic acid molecules and/or vectors of the invention into cells in accordance with this aspect of the invention are well known and routine to those of skill in the art. Such techniques are reviewed at length, for example, in Sambrook, J., et al., Molecular Cloning, a Laboratory Manual, 2nd Ed., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, pp. 16.30-16.55 (1989), Watson, J.D., et al., Recombinant DNA, 2nd Ed., New York: W.H. Freeman and Co., pp. 213-234 (1992), and Winnacker, E.-L. From Genes to Clones, New York: VCH Publishers (1987), which are illustrative of the many laboratory manuals that detail these techniques and which are incorporated by reference herein in their entireties for their relevant disclosures.

#### **Polypeptides**

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In another aspect, the invention relates to polypeptides encoded by the nucleic acid molecules of the invention (including polypeptides and amino acid sequences encoded by all possible reading frames of the nucleic acid molecules of the invention), and to methods of producing such polypeptides. Polypeptides of the present invention include purified or isolated natural products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, insect, mammalian, avian and higher plant cells.

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The polypeptides of the invention may be produced by synthetic organic chemistry, and are preferably produced by standard recombinant methods, employing one or more of the host cells of the invention comprising the vectors or isolated nucleic acid molecules of the invention. According to the invention, polypeptides are produced by cultivating the host cells of the invention (which comprise one or more of the nucleic acid molecules of the invention, preferably contained within an Expression Vector) under conditions favoring the expression of the nucleotide sequence contained on the nucleic acid molecule of the invention, such that the polypeptide encoded by the nucleic acid molecule of the invention is produced by the host cell. As used herein, "conditions favoring the expression of the nucleotide sequence" or "conditions favoring the production of a polypeptide" include optimal physical (e.g., temperature, humidity, etc.) and nutritional (e.g., culture medium, ionic) conditions required for production of a recombinant polypeptide by a given host cell. Such optimal conditions for a variety of host cells, including prokaryotic (bacterial), mammalian, insect, yeast, and plant cells will be familiar to one of ordinary skill in the art, and may be found, for example, in Sambrook, J., et al., Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, (1989), Watson, J.D., et al., Recombinant DNA, 2nd Ed., New York: W.H. Freeman and Co., and Winnacker, E.-L., From Genes to Clones, New York: VCH Publishers (1987).

In some aspects, it may be desirable to isolate or purify the polypeptides of the invention (e.g., for production of antibodies as described below), resulting in the production of the polypeptides of the invention in isolated form. The polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods of protein purification that are routine in the art, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. For example, His6 or GST fusion tags on polypeptides made by the methods of the invention may be isolated using appropriate affinity chromatography matrices which bind polypeptides bearing

His6 or GST tags, as will be familiar to one of ordinary skill in the art. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

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Isolated polypeptides of the invention include those comprising the amino acid sequences encoded by one or more of the reading frames of the polynucleotides comprising one or more of the recombination site-encoding nucleic acid molecules of the invention, including those encoding attB1, attB2, attP1, attP2, attL1, attL2, attR1 and attR2 having the nucleotide sequences set forth in Figure 9 (or nucleotide sequences complementary thereto), or fragments, variants, mutants and derivatives thereof, the complete amino acid sequences encoded by the polynucleotides contained in the deposited clones described herein; the amino acid sequences encoded by polynucleotides which hybridize under stringent hybridization conditions to polynucleotides having the nucleotide sequences encoding the recombination site sequences of the invention as set forth in Figure 9 (or a nucleotide sequence complementary thereto); or a peptide or polypeptide comprising a portion or a fragment of the above polypeptides. The invention also relates to additional polypeptides having one or more additional amino acids linked (typically by peptidyl bonds to form a nascent polypeptide) to the polypeptides encoded by the recombination site nucleotide sequences or the deposited clones. Such additional amino acid residues may comprise one or more functional peptide sequences, for example one or more fusion partner peptides (e.g., GST, His<sub>6</sub>, Trx, etc.) and the like.

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As used herein, the terms "protein," "peptide,""oligopeptide" and "polypeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of two or more amino acids, preferably five or more amino acids, or more preferably ten

or more amino acids, coupled by (a) peptidyl linkage(s), unless otherwise defined in the specific contexts below. As is commonly recognized in the art, all polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

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It will be recognized by those of ordinary skill in the art that some amino acid sequences of the polypeptides of the invention can be varied without significant effect on the structure or function of the polypeptides. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine structure and activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the polypeptide.

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Thus, the fragment, derivative or analog of the polypeptides of the invention, such as those comprising peptides encoded by the recombination site nucleotide sequences described herein, may be (i) one in which one or more of the amino acid residues are substituted with a conservative or non-conservative amino acid residue (preferably a conservative amino acid residue), and such substituted amino acid residue may be encoded by the genetic code or may be an amino acid (e.g.,

Thus, the invention further includes variants of the polypeptides of the invention, including allelic variants, which show substantial structural homology to the polypeptides described herein, or which include specific regions of these polypeptides such as the portions discussed below. Such mutants may include deletions, insertions, inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" or "conservative" amino acid substitutions will generally have little effect on activity.

Typical conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxylated residues Ser and Thr; exchange of the acidic residues Asp and Glu; substitution between the amidated residues Asn and Gln; exchange of the basic residues Lys and Arg; and replacements among the aromatic residues Phe and Tyr.

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desmosine, citrulline, ornithine, etc.) that is not encoded by the genetic code; (ii) one in which one or more of the amino acid residues includes a substituent group (e.g., a phosphate, hydroxyl, sulfate or other group) in addition to the normal "R" group of the amino acid; (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which additional amino acids are fused to the mature polypeptide, such as an immunoglobulin Fc region peptide, a leader or secretory sequence, a sequence which is employed for purification of the mature polypeptide (such as GST) or a proprotein sequence. Such fragments, derivatives and analogs are intended to be encompassed by the present invention, and are within the scope of those skilled in the art from the teachings herein and the state of the art at the time of invention.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. Recombinantly produced versions of the polypeptides of the invention can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). As used herein, the term "substantially purified" means a preparation of an individual polypeptide of the invention wherein at least 50%, preferably at least 60%, 70%, or 75% and more preferably at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% (by mass) of contaminating proteins (*i.e.*, those that are not the individual polypeptides described herein or fragments, variants, mutants or derivatives thereof) have been removed from the preparation.

The polypeptides of the present invention include those which are at least about 50% identical, at least 60% identical, at least 65% identical, more preferably at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98% or at least about 99% identical, to the polypeptides described herein. For example, preferred *att*B1-containing polypeptides of the invention include those that are at least about 50% identical, at least 60% identical, at least 65% identical, more preferably at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 99% identical,

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to the polypeptide(s) encoded by the three reading frames of a polynucleotide comprising a nucleotide sequence of attB1 having a nucleic acid sequence as set forth in Figure 9 (or a nucleic acid sequence complementary thereto), to a polypeptide encoded by a polynucleotide contained in the deposited cDNA clones described herein, or to a polypeptide encoded by a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising a nucleotide sequence of attB1 having a nucleic acid sequence as set forth in Figure 9 (or a nucleic acid sequence complementary thereto). Analogous polypeptides may be prepared that are at least about 65% identical, more preferably at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98% or at least about 99% identical, to the attB2, attP1, attP2, attL1, attL2, attR1 and attR2 polypeptides of the invention as depicted in Figure 9. The present polypeptides also include portions or fragments of the above-described polypeptides with at least 5, 10, 15, 20, or 25 amino acids.

By a polypeptide having an amino acid sequence at least, for example, 65% "identical" to a reference amino acid sequence of a given polypeptide of the invention is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to 35 amino acid alterations per each 100 amino acids of the reference amino acid sequence of a given polypeptide of the invention. In other words, to obtain a polypeptide having an amino acid sequence at least 65% identical to a reference amino acid sequence, up to 35% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 35% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino (N-) or carboxy (C-) terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence. As a practical matter, whether a given amino acid sequence is, for example, at least 65% identical to the amino acid sequence of a given polypeptide of the invention can be determined

conventionally using known computer programs such as those described above for nucleic acid sequence identity determinations, or more preferably using the CLUSTAL W program (Thompson, J.D., et al., Nucleic Acids Res. 22:4673-4680 (1994)).

The polypeptides of the present invention can be used as molecular weight

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markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. In addition, as described in detail below, the polypeptides of the present invention can be used to raise polyclonal and monoclonal antibodies which are useful in a variety of assays for detecting protein expression, localization, detection of interactions with other molecules, or

for the isolation of a polypeptide (including a fusion polypeptide) of the invention.

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In another aspect, the present invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention, which may be used to raise antibodies, particularly monoclonal antibodies, that bind specifically to a one or more of the polypeptides of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes (see, e.g., Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983)).

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As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well-known in the art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein (see, e.g., Sutcliffe, J.G., et al., Science 219:660-666 (1983)). Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are not confined to the immunodominant regions of intact proteins (i.e., immunogenic epitopes) or to the amino or carboxy

termini. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer peptides, especially those containing proline residues, usually are effective (Sutcliffe, J.G., et al., Science 219:660-666 (1983)).

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Epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least five, more preferably at least seven or more amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a given polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); sequences containing proline residues are particularly preferred.

Non-limiting examples of epitope-bearing polypeptides or peptides that can be used to generate antibodies specific for the polypeptides of the invention include certain epitope-bearing regions of the polypeptides comprising amino acid sequences encoded by polynucleotides comprising one or more of the recombination site-encoding nucleic acid molecules of the invention, including those encoding attB1, attB2, attP1, attP2, attL1, attL2, attR1 and attR2 having the nucleotide sequences set forth in Figure 9 (or a nucleotide sequence complementary thereto); the complete amino acid sequences encoded by the three reading frames of the polynucleotides contained in the deposited clones described herein; and the amino acid sequences encoded by all reading frames of polynucleotides which hybridize under stringent hybridization conditions to polynucleotides having the nucleotide sequences encoding the recombination site sequences (or portions thereof) of the invention as set forth in Figure 9 (or a nucleic acid sequence complementary thereto). Other epitope-bearing polypeptides or peptides that may be used to generate antibodies specific for the polypeptides

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of the invention will be apparent to one of ordinary skill in the art based on the primary amino acid sequences of the polypeptides of the invention described herein, via the construction of Kyte-Doolittle hydrophilicity and Jameson-Wolf antigenic index plots of the polypeptides of the invention using, for example, PROTEAN computer software (DNASTAR, Inc.; Madison, Wisconsin).

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis (see, e.g., U.S. Patent No. 4,631,211 and Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985), both of which are incorporated by reference herein in their entireties).

As one of skill in the art will appreciate, the polypeptides of the present invention and epitope-bearing fragments thereof may be immobilized onto a solid support, by techniques that are well-known and routine in the art. By "solid support" is intended any solid support to which a peptide can be immobilized. Such solid supports include, but are not limited to nitrocellulose, diazocellulose, glass, polystyrene, polyvinylchloride, polypropylene, polyethylene, dextran, Sepharose, agar, starch, nylon, beads and microtitre plates. Linkage of the peptide of the invention to a solid support can be accomplished by attaching one or both ends of the peptide to the support. Attachment may also be made at one or more internal sites in the peptide. Multiple attachments (both internal and at the ends of the peptide) may also be used according to the invention. Attachment can be via an amino acid linkage group such as a primary amino group, a carboxyl group, or a sulfhydryl (SH) group or by chemical linkage groups such as with cyanogen bromide (CNBr) linkage through a spacer. For non-covalent attachments to the support, addition of an affinity tag sequence to the peptide can be used such as GST (Smith, D.B., and Johnson, K.S., Gene 67:31 (1988)), polyhistidines (Hochuli, E., et al., J. Chromatog. 411:77 (1987)), or biotin. Such affinity tags WO 00/52027

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may be used for the reversible attachment of the peptide to the support. Such immobilized polypeptides or fragments may be useful, for example, in isolating antibodies directed against one or more of the polypeptides of the invention, or other proteins or peptides that recognize other proteins or peptides that bind to one or more of the polypeptides of the invention, as described below.

As one of skill in the art will also appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described herein can be combined with one or more fusion partner proteins or peptides, or portions thereof, including but not limited to GST, His<sub>6</sub>, Trx, and portions of the constant domain of immunoglobulins (Ig), resulting in chimeric or fusion polypeptides. These fusion polypeptides facilitate purification of the polypeptides of the invention (EP 0 394 827; Traunecker et al., Nature 331:84-86 (1988)) for use in analytical or diagnostic (including high-throughput) format.

#### Antibodies

In another aspect, the invention relates to antibodies that recognize and bind to the polypeptides (or epitope-bearing fragments thereof) or nucleic acid molecules (or portions thereof) of the invention. In a related aspect, the invention relates to antibodies that recognize and bind to one or more polypeptides encoded by all reading frames of one or more recombination site nucleic acid sequences or portions thereof, or to one or more nucleic acid molecules comprising one or more recombination site nucleic acid sequences or portions thereof, including but not limited to att sites (including attB1, attB2, attP1, attP2, attL1, attL2, attR1, attR2 and the like), lox sites (e.g., loxP, loxP511, and the like), FRT, and the like, or mutants, fragments, variants and derivatives thereof. See generally U.S. Patent No. 5,888,732, which is incorporated herein by reference in its entirety. The antibodies of the present invention may be polyclonal or monoclonal, and may be prepared by any of a variety of methods and in a variety of species according to methods that are well-known in the art. See, for instance, U.S. Patent No. 5,587,287; Sutcliffe, J.G., et al., Science 219:660-666 (1983); Wilson et al., Cell 37: 767 (1984); and Bittle, F.J., et al., J. Gen. Virol. 66:2347-2354 (1985). Antibodies specific for any of the polypeptides or nucleic acid molecules described

herein, such as antibodies specifically binding to one or more of the polypeptides encoded by the recombination site nucleotide sequences, or one or more nucleic acid molecules, described herein or contained in the deposited clones, antibodies against fusion polypeptides (e.g., binding to fusion polypeptides between one or more of the fusion partner proteins and one or more of the recombination site polypeptides of the invention, as described herein), and the like, can be raised against the intact polypeptides or polynucleotides of the invention or one or more antigenic polypeptide fragments thereof.

As used herein, the term "antibody" (Ab) may be used interchangeably with the terms "polyclonal antibody" or "monoclonal antibody" (mAb), except in specific contexts as described below. These terms, as used herein, are meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')<sub>2</sub> fragments) which are capable of specifically binding to a polypeptide or nucleic acid molecule of the invention or a portion thereof. It will therefore be appreciated that, in addition to the intact antibodies of the invention, Fab, F(ab')<sub>2</sub> and other fragments of the antibodies described herein, and other peptides and peptide fragments that bind one or more polypeptides or polynucleotides of the invention, are also encompassed within the scope of the invention. Such antibody fragments are typically produced by proteolytic cleavage of intact antibodies, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments). Antibody fragments, and peptides or peptide fragments, may also be produced through the application of recombinant DNA technology or through synthetic chemistry.

Epitope-bearing peptides and polypeptides, and nucleic acid molecules or portions thereof, of the invention may be used to induce antibodies according to methods well known in the art, as generally described herein (see, e.g., Sutcliffe, et al., supra; Wilson, et al., supra; and Bittle, F. J., et al., J. Gen. Virol. 66:2347-2354 (1985)).

Polyclonal antibodies according to this aspect of the invention may be made by immunizing an animal with one or more of the polypeptides or nucleic acid molecules of the invention described herein or portions thereof according to standard techniques (see, e.g., Harlow, E., and Lane, D., Antibodies: A

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Laboratory Manual, Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1988); Kaufman, P.B., et al., In: Handbook of Molecular and Cellular Methods in Biology and Medicine, Boca Raton, Florida: CRC Press, pp. 468-469 (1995)). For producing antibodies that recognize and bind to the polypeptides or nucleic acid molecules of the invention or portions thereof, animals may be immunized with free peptide or free nucleic acid molecules; however, antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as albumin, KLH, or tetanus toxoid (particularly for producing antibodies against the nucleic acid molecules of the invention or portions thereof; see Harlow and Lane, supra, at page 154), or to a solid phase carrier such as a latex or glass microbead. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N- hydroxysuccinimide ester (MBS). while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice may be immunized with either free (if the polypeptide immunogen is larger than about 25 amino acids in length) or carrier-coupled peptides or nucleic acid molecules, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide, polynucleotide, or carrier protein, and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of antibody which can be detected, for example, by ELISA assay using free peptide or nucleic acid molecule adsorbed to a solid surface. In another approach, cells expressing one or more of the polypeptides or polynucleotides of the invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies, according to routine immunological methods. In yet another method, a preparation of one or more of the polypeptides or polynucleotides of the invention is prepared and purified as described herein, to render it substantially free of natural contaminants. Such a preparation may then be introduced into an animal in order to produce polyclonal antisera of greater specific activity. The titer of antibodies in serum from an immunized animal, regardless of the method of immunization used, may be increased by selection of anti-peptide or anti-polynucleotide antibodies, for

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instance, by adsorption to the peptide or polynucleotide on a solid support and elution of the selected antibodies according to methods well known in the art.

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In an alternative method, the antibodies of the present invention are monoclonal antibodies (or fragments thereof which bind to one or more of the polypeptides of the invention). Such monoclonal antibodies can be prepared using hybridoma technology (Kohler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., In: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981)). In general, such procedures involve immunizing an animal (preferably a mouse) with a polypeptide or polynucleotide of the invention (or a fragment thereof), or with a cell expressing a polypeptide or polynucleotide of the invention (or a fragment thereof). The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the American Type Culture Collection, Rockville, Maryland. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterol. 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding one or more of the polypeptides or nucleic acid molecules of the invention, or fragments thereof. Hence, the present invention also provides hybridoma cells and cell lines producing monoclonal antibodies of the invention, particularly that recognize and bind to one or more of the polypeptides or nucleic acid molecules of the invention.

Alternatively, additional antibodies capable of binding to one or more of the polypeptides of the invention, or fragments thereof, may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, antibodies specific for one or more of the polypeptides or polynucleotides of the invention, prepared as described above, are used to immunize an animal, preferably a mouse. The splenocytes of such an

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animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to an antibody specific for one or more of the polypeptides or polynucleotides of the invention can be blocked by polypeptides of the invention themselves. Such antibodies comprise anti-idiotypic antibodies to the antibodies recognizing one or more of the polypeptides or polynucleotides of the invention, and can be used to immunize an animal to induce formation of further antibodies specific for one or more of the polypeptides or polynucleotides of the invention.

For use, the antibodies of the invention may optionally be detectably labeled by covalent or non-covalent attachment of one or more labels, including but not limited to chromogenic, enzymatic, radioisotopic, isotopic, fluorescent, toxic, chemiluminescent, or nuclear magnetic resonance contrast agents or other labels.

Examples of suitable enzyme labels include malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include <sup>3</sup>H, <sup>111</sup>In, <sup>125</sup>I, <sup>131</sup>I, <sup>32</sup>P, <sup>35</sup>S, <sup>14</sup>C, <sup>51</sup>Cr, <sup>57</sup>To, <sup>58</sup>Co, <sup>59</sup>Fe, <sup>75</sup>Se, <sup>152</sup>Eu, <sup>90</sup>Y, <sup>67</sup>Cu, <sup>217</sup>Ci, <sup>211</sup>At, <sup>212</sup>Pb, <sup>47</sup>Sc, <sup>109</sup>Pd, etc. <sup>111</sup>In is a preferred isotope where in vivo imaging is used since its avoids the problem of dehalogenation of the <sup>125</sup>I or <sup>131</sup>I-labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging (Perkins *et al.*, *Eur. J. Nucl. Med. 10*:296-301 (1985); Carasquillo *et al.*, *J. Nucl. Med. 28*:281-287 (1987)). For example, <sup>111</sup>In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumorous tissues, particularly the liver, and therefore enhances specificity of tumor localization (Esteban et al., J. Nucl. Med. 28:861-870 (1987)).

Examples of suitable non-radioactive isotopic labels include <sup>157</sup>Gd, <sup>55</sup>Mn, <sup>162</sup>Dy, <sup>52</sup>Tr, and <sup>56</sup>Fe.

Examples of suitable fluorescent labels include an <sup>152</sup>Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a

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phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, a green fluorescent protein (GFP) label, and a fluorescamine label.

Examples of suitable toxin labels include diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to the antibodies of the invention are provided by Kennedy et al., Clin. Chim. Acta 70:1-31 (1976), and Schurs et al., Clin. Chim. Acta 81:1-40 (1977). Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

It will be appreciated by one of ordinary skill that the antibodies of the present invention may alternatively be coupled to a solid support, to facilitate, for example, chromatographic and other immunological procedures using such solid phase-immobilized antibodies. Included among such procedures are the use of the antibodies of the invention to isolate or purify polypeptides comprising one or more epitopes encoded by the nucleic acid molecules of the invention (which may be fusion polypeptides or other polypeptides of the invention described herein), or to isolate or purify polynucleotides comprising one or more recombination site sequences of the invention or portions thereof. Methods for isolation and purification of polypeptides (and, by analogy, polynucleotides) by affinity chromatography, for example using the antibodies of the invention coupled to a solid phase support, are well-known in the art and will be familiar to one of ordinary skill. The antibodies of the invention may also be used in other applications, for example to cross-link or couple two or more proteins, polypeptides, polynucleotides, or portions thereof into a structural and/or functional complex. In one such use, an antibody of the invention may have two

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or more distinct epitope-binding regions that may bind, for example, a first polypeptide (which may be a polypeptide of the invention) at one epitope-binding region on the antibody and a second polypeptide (which may be a polypeptide of the invention) at a second epitope-binding region on the antibody, thereby bringing the first and second polypeptides into close proximity to each other such that the first and second polypeptides are able to interact structurally and/or functionally (as, for example, linking an enzyme and its substrate to carry out enzymatic catalysis, or linking an effector molecule and its receptor to carry out or induce a specific binding of the effector molecule to the receptor or a response to the effector molecule mediated by the receptor). Additional applications for the antibodies of the invention include, for example, the preparation of large-scale arrays of the antibodies, polypeptides, or nucleic acid molecules of the invention, or portions thereof, on a solid support, for example to facilitate high-throughput screening of protein or RNA expression by host cells containing nucleic acid molecules of the invention (known in the art as "chip array" protocols; see, e.g., U.S. Patent Nos. 5,856,101, 5,837,832, 5,770,456, 5,744,305, 5,631,734, and 5,593,839, which are directed to production and use of chip arrays of polypeptides (including antibodies) and polynucleotides, and the disclosures of which are incorporated herein by reference in their entireties). By "solid support" is intended any solid support to which an antibody can be immobilized. Such solid supports include, but are not limited to nitrocellulose, diazocellulose, glass, polystyrene, polyvinylchloride, polycarbonate, polypropylene, polyethylene, dextran, Sepharose, agar, starch, nylon, beads and microtitre plates. Preferred are beads made of glass, latex or a magnetic material. Linkage of an antibody of the invention to a solid support can be accomplished by attaching one or both ends of the antibody to the support. Attachment may also be made at one or more internal sites in the antibody. Multiple attachments (both internal and at the ends of the antibody) may also be used according to the invention. Attachment can be via an amino acid linkage group such as a primary amino group, a carboxyl group, or a sulfhydryl (SH) group or by chemical linkage groups such as with cyanogen bromide (CNBr) linkage through a spacer. For non-covalent attachments, addition of an affinity tag sequence to the peptide can be used such as GST

(Smith, D.B., and Johnson, K.S., Gene 67:31 (1988)), polyhistidines (Hochuli, E., et al., J. Chromatog. 411:77 (1987)), or biotin. Alternatively, attachment can be accomplished using a ligand which binds the Fc region of the antibodies of the invention, e.g., protein A or protein G. Such affinity tags may be used for the reversible attachment of the antibodies to the support. Peptides may also be recognized via specific ligand-receptor interactions or using phage display methodologies that will be familiar to the skilled artisan, for their ability to bind polypeptides of the invention or fragments thereof.

Kits

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In another aspect, the invention provides kits which may be used in producing the nucleic acid molecules, polypeptides, vectors, host cells, and antibodies, and in the recombinational cloning methods, of the invention. Kits according to this aspect of the invention may comprise one or more containers, which may contain one or more of the nucleic acid molecules, primers, polypeptides, vectors, host cells, or antibodies of the invention. In particular, a kit of the invention may comprise one or more components (or combinations thereof) selected from the group consisting of one or more recombination proteins (e.g., Int) or auxiliary factors (e.g. IHF and/or Xis) or combinations thereof, one or more compositions comprising one or more recombination proteins or auxiliary factors or combinations thereof (for example, GATEWAY™ LR Clonase™ Enzyme Mix or GATEWAY™ BP Clonase™ Enzyme Mix) one or more Destination Vector molecules (including those described herein), one or more Entry Clone or Entry Vector molecules (including those described herein), one or more primer nucleic acid molecules (particularly those described herein), one or more host cells (e.g. competent cells, such as E. coli cells, yeast cells, animal cells (including mammalian cells, insect cells, nematode cells, avian cells, fish cells, etc.), plant cells, and most particularly E. coli DB3, DB3.1 (preferably E. coli LIBRARY EFFICIENCY® DB3.1™ Competent Cells; Life Technologies, Inc., Rockville, MD), DB4 and DB5; see U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, and the corresponding U.S. Utility Application No. of Hartley et al., entitled "Cells Resistant to Toxic Genes and Uses Thereof," filed

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on even day herewith, the disclosures of which are incorporated by reference herein in its entirety), and the like. In related aspects, the kits of the invention may comprise one or more nucleic acid molecules encoding one or more recombination sites or portions thereof, such as one or more nucleic acid molecules comprising a nucleotide sequence encoding the one or more recombination sites (or portions thereof) of the invention, and particularly one or more of the nucleic acid molecules contained in the deposited clones described herein. Kits according to this aspect of the invention may also comprise one or more isolated nucleic acid molecules of the invention, one or more vectors of the invention, one or more primer nucleic acid molecules of the invention, and/or one or more antibodies of the invention. The kits of the invention may further comprise one or more additional containers containing one or more additional components useful in combination with the nucleic acid molecules, polypeptides, vectors, host cells, or antibodies of the invention, such as one or more buffers, one or more detergents. one or more polypeptides having nucleic acid polymerase activity, one or more polypeptides having reverse transcriptase activity, one or more transfection reagents, one or more nucleotides, and the like. Such kits may be used in any process advantageously using the nucleic acid molecules, primers, vectors, host cells, polypeptides, antibodies and other compositions of the invention, for example in methods of synthesizing nucleic acid molecules (e.g., via amplification such as via PCR), in methods of cloning nucleic acid molecules (preferably via recombinational cloning as described herein), and the like.

# Optimization of Recombinational Cloning System

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The usefulness of a particular nucleic acid molecule, or vector comprising a nucleic acid molecule, of the invention in methods of recombinational cloning may be determined by any one of a number of assay methods. For example, Entry and Destination vectors of the present invention may be assessed for their ability to function (*i.e.*, to mediate the transfer of a nucleic acid molecule, DNA segment, gene, cDNA molecule or library from a cloning vector to an Expression Vector) by carrying out a recombinational cloning reaction as described in more detail in the Examples below and as described in U.S. Application Nos. 08/663,002, filed

June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12, 1998, 09/177,387, filed October 23, 1998, and 60/108,324, filed November 13, 1998, the disclosures of which are incorporated by reference herein in their entireties. Alternatively, the functionality of Entry and Destination Vectors prepared according to the invention may be assessed by examining the ability of these vectors to recombine and create cointegrate molecules, or to transfer a nucleic acid molecule of interest, using an assay such as that described in detail below in Example 19 Analogously, the formulation of compositions comprising one or more recombination proteins or combinations thereof, for example GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix and GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix, may be optimized using assays such as those described below in Example 18.

#### Uses

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There are a number of applications for the compositions, methods and kits of the present invention. These uses include, but are not limited to, changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences (e.g., promoters, enhancers, and the like), constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning, e.g., PCR products, genomic DNAs, and cDNAs. In addition, the nucleic acid molecules, vectors, and host cells of the invention may be used in the production of polypeptides encoded by the nucleic acid molecules, in recombinational cloning of desired nucleic acid sequences, and in other applications that may be enhanced or facilitated by the use of the nucleic acid molecules, vectors, and host cells of the invention.

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In particular, the nucleic acid molecules, vectors, host cells, polypeptides, antibodies, and kits of the invention may be used in methods of transferring one or more desired nucleic acid molecules or DNA segments, for example one or more genes, cDNA molecules or cDNA libraries, into a cloning or Expression Vector for use in transforming additional host cells for use in cloning or

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amplification of, or expression of the polypeptide encoded by, the desired nucleic acid molecule or DNA segment. Such recombinational cloning methods which may advantageously use the nucleic acid molecules, vectors, and host cells of the invention, are described in detail in the Examples below, and in commonly owned U.S. Application Nos. 08/486,139, filed June 7, 1995, 08/663,002, filed June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12, 1998, 09/177,387, filed October 23, 1998, and 60/108,324, filed November 13, 1998, the disclosures of all of which are incorporated by reference herein in their entireties.

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It will be understood by one of ordinary skill in the relevant arts that other suitable modifications and adaptations to the methods and applications described herein are readily apparent from the description of the invention contained herein in view of information known to the ordinarily skilled artisan, and may be made without departing from the scope of the invention or any embodiment thereof. Having now described the present invention in detail, the same will be more clearly understood by reference to the following examples, which are included herewith for purposes of illustration only and are not intended to be limiting of the invention.

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# Examples

# Example 1: Recombination Reactions of Bacteriophage $\lambda$

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The  $E.\ coli$  bacteriophage  $\lambda$  can grow as a lytic phage, in which case the host cell is lysed, with the release of progeny virus. Alternatively, lambda can integrate into the genome of its host by a process called lysogenization (see Figure 60). In this lysogenic state, the phage genome can be transmitted to daughter cells for many generations, until conditions arise that trigger its excision from the genome. At this point, the virus enters the lytic part of its life cycle. The control of the switch between the lytic and lysogenic pathways is one of the best understood processes in molecular biology (M. Ptashne,  $A\ Genetic\ Switch$ , Cell Press, 1992).

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The integrative and excisive recombination reactions of  $\lambda$ , performed in vitro, are the basis of Recombinational Cloning System of the present invention. They can be represented schematically as follows:

attB x attP ↔ attL x attR (where "x" signifies recombination)

The four att sites contain binding sites for the proteins that mediate the reactions. The wild type attP, attB, attL, and attR sites contain about 243, 25, 100, and 168 base pairs, respectively. The attB x attP reaction (hereinafter referred to as a "BP Reaction," or alternatively and equivalently as an "Entry Reaction" or a "Gateward Reaction") is mediated by the proteins Int and IHF. The attL x attR reaction (hereinafter referred to as an "LR Reaction," or alternatively and equivalently as a "Destination Reaction") is mediated by the proteins Int, IHF, and Xis. Int (integrase) and Xis (excisionase) are encoded by the λ genome, while IHF (integration host factor) is an E. coli protein. For a general review of lambda recombination, see: A. Landy, Ann. Rev. Biochem. 58: 913-949 (1989).

# Example 2: Recombination Reactions of the Recombinational Cloning System

The LR Reaction — the exchange of a DNA segment from an Entry Clone to a Destination Vector — is the *in vitro* version of the  $\lambda$  excision reaction:

 $attL \times attR \Rightarrow attB + attP$ .

There is a practical imperative for this configuration: after an LR Reaction in one configuration of the present method, an att site usually separates a functional motif (such as a promoter or a fusion tag) from a nucleic acid molecule of interest in an Expression Clone, and the 25 bp attB site is much smaller than the attP, attL, and attR sites.

Note that the recombination reaction is conservative, i.e., there is no net synthesis or loss of base pairs. The DNA segments that flank the recombination

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sites are merely switched. The wild type  $\lambda$  recombination sites are modified for purposes of the GATEWAY<sup>TM</sup> Cloning System, as follows:

To create certain preferred Destination Vectors, a part (43 bp) of attR was removed, to make the excisive reaction irreversible and more efficient (W. Bushman et al., *Science 230*: 906, 1985). The attR sites in preferred Destination Vectors of the invention are 125 bp in length. Mutations were made to the core regions of the att sites, for two reasons: (1) to eliminate stop codons, and (2) to ensure specificity of the recombination reactions (i.e., attR1 reacts only with attL1, attR2 reacts only with attL2, etc.).

Other mutations were introduced into the short (5 bp) regions flanking the 15 bp core regions of the attB sites to minimize secondary structure formation in single-stranded forms of attB plasmids, e.g., in phagemid ssDNA or in mRNA. Sequences of attB1 and attB2 to the left and right of a nucleic acid molecule of interest after it has been cloned into a Destination Vector are given in Figure 6.

Figure 61 illustrates how an Entry Clone and a Destination Vector recombine in the LR Reaction to form a co-integrate, which resolves through a second reaction into two daughter molecules. The two daughter molecules have the same general structure regardless of which pair of sites, attL1 and attR1 or attL2 and attR2, react first to form the co-integrate. The segments change partners by these reactions, regardless of whether the parental molecules are both circular, one is circular and one is linear, or both are linear. In this example, selection for ampicillin resistance carried on the Destination Vector, which also carries the death gene ccdB, provides the means for selecting only for the desired attB product plasmid.

# Example 3: Protein Expression in the Recombinational Cloning System

Proteins are expressed *in vivo* as a result of two processes, transcription (DNA into RNA), and translation (RNA into protein). For a review of protein expression in prokaryotes and eukaryotes, see Example 13 below. Many vectors (pUC, BlueScript, pGem) use interruption of a transcribed lacZ gene for bluewhite screening. These plasmids, and many Expression Vectors, use the lac promoter to control expression of cloned genes. Transcription from the lac

promoter is turned on by adding the inducer IPTG. However, a low level of RNA is made in the absence of inducer, i.e., the lac promoter is never completely off. The result of this "leakiness" is that genes whose expression is harmful to *E. coli* may prove difficult or impossible to clone in vectors that contain the lac promoter, or they may be cloned only as inactive mutants.

In contrast to other gene expression systems, nucleic acid molecules cloned into an Entry Vector may be designed *not* to be expressed. The presence of the strong transcriptional terminator *rrnB* (Orosz, et al., *Eur. J. Biochem. 201*: 653, 1991) just upstream of the attL1 site keeps transcription from the vector promoters (drug resistance and replication origin) from reaching the cloned gene. However, if a toxic gene is cloned into a Destination Vector, the host may be sick, just as in other expression systems. But the reliability of subcloning by *in vitro* recombination makes it easier to recognize that this has happened -- and easier to try another expression option in accordance with the methods of the invention, if necessary.

## Example 4: Choosing the Right Entry Vector

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There are two kinds of choices that must be made in choosing the best Entry Vector, dictated by (1) the particular DNA segment that is to be cloned, and (2) what is to be accomplished with the cloned DNA segment. These factors are critical in the choice of Entry Vector used, because when the desired nucleic acid molecule of interest is moved from the Entry Vector to a Destination Vector, all the base pairs between the nucleic acid molecule of interest and the Int cutting sites in attL1 and attL2 (such as in Figure 6) move into the Destination Vector as well. For genomic DNAs that are not expressed as a result of moving into a Destination Vector, these decisions are not as critical.

For example, if an Entry Vector with certain translation start signals is used, those sequences will be translated into amino acids if an amino-terminal fusion to the desired nucleic acid molecule of interest is made. Whether the desired nucleic acid molecule of interest is to be expressed as fusion protein, native protein, or both, dictates whether translational start sequences must be included between the attB sites of the clone (native protein) or, alternatively, supplied by the Destination

Vector (fusion protein). In particular, Entry Clones that include translational start sequences may prove less suitable for making fusion proteins, as internal initiation of translation at these sites can decrease the yield of N-terminal fusion protein. These two types of expression afforded by the compositions and methods of the invention are illustrated in Figure 62.

No Entry Vector is likely to be optimal for all applications. The nucleic acid molecule of interest may be cloned into any of several optimal Entry Vectors.

As an example, consider pENTR7 (Figure 16) and pENTR11 (Figure 20), which are useful in a variety of applications, including (but not limited to):

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•Cloning cDNAs from most of the commercially available libraries. The sites to the left and right of the ccdB death gene have been chosen so that directional cloning is possible if the DNA to be cloned does not have two or more of these restriction sites.

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•Cloning of genes directionally: SalI, BamHI, XmnI (blunt), or KpnI on the left of ccdB; NotI, XhoI, XbaI, or EcoRV (blunt), on the right.

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•Cloning of genes or gene fragments with a blunt amino end at the *Xmn*I site. The *Xmn*I site has four of the six most favored bases for eukaryotic expression (see Example 13, below), so that if the first three bases of the DNA to be cloned are ATG, the open reading frame (ORF) will be expressed in eukaryotic cells (e.g., mammalian cells, insect cells, yeast cells) when it is transcribed in the appropriate Destination Vector. In addition, in pENTR11, a Shine-Dalgarno sequence is situated 8 bp upstream, for initiating protein synthesis in a prokaryotic host cell (particularly a bacterial cell, such as *E. coli*) at an ATG.

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•Cleaving off amino terminal fusions (e.g., His<sub>6</sub>, GST, or thioredoxin) using the highly specific TEV (Tobacco Etch Virus) protease (available from Life Technologies, Inc.). If the nucleic acid molecule of interest is cloned at the

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blunt XmnI site, TEV cleavage will leave two amino acids on the amino end of the expressed protein.

•Selecting against uncut or singly cut Entry Vector molecules during cloning with restriction enzymes and ligase. If the ccdB gene is not removed with a double digest, it will kill any recipient *E. coli* cell that does not contain a mutation that makes the cell resistant to ccdB (see U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, the disclosure of which is incorporated by reference herein in its entirety).

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• Allowing production of amino fusions with ORFs in all cloning sites. There are no stop codons (in the attL1 reading frame) upstream of the ccdB gene.

In addition, pENTR11 is also useful in the following applications:

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•Cloning cDNAs that have an *NcoI* site at the initiating ATG into the *NcoI* site. Similar to the *XmnI* site, this site has four of the six most favored bases for eukaryotic expression. Also, a Shine-Dalgarno sequence is situated 8 bp upstream, for initiating protein synthesis in a prokaryotic host cell (particularly a bacterial cell, such as *E. coli*) at an ATG.

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•Producing carboxy fusion proteins with ORFs positioned in phase with the reading frame convention for carboxy-terminal fusions (see Figure 20A).

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Table 1 lists some non-limiting examples of Entry Vectors and their characteristics, and Figures 10-20 show their cloning sites. All of the Entry Vectors listed in Table 1 are available commercially from Life Technologies, Inc., Rockville, Maryland. Other Entry Vectors not specifically listed here, which comprise alternative or additional features may be made by one of ordinary skill using routine methods of molecular and cellular biology, in view of the disclosure contained herein.

Table 1 Examples of Entry Vectors

Designation	Mnemonic	Class of	Distinctive	Amino	Native Protein in	Native	Protein	_
	Name	Entry	Cloning Sites	Fusions	E.coli	Protein in	Synthesis	
		Vector				Eukaryotic Cells	Features	
pENTR-	Minimal	Alternative	Reading frame A,	Good	Poor	Good	Minimal amino	
3, 3C	blunt RF	Reading	B, or C; blunt cut				acids between	
	A, B, C	Frame	closest to attL1				tag and protein;	
		Vectors					no SD	
pENTR4	Minimal	Restr. Enz.	Nco I site	Good	Poor	Good	Good Kozac; no	
	Nco	Cleavage	(common in euk.				SD	
		Vectors	cDNAs) closest					
			to attL1					
pENTR5	Minimal	Restr. Enz.	Ndel site closest	Good	Poor	Poor at Nde I,	No SD; poor	
	Nde	Cleavage	to attL1			Good at Xmn	Kozac at Nde,	
		Vectors					good at Xmn	
pENTR6	Minimal	Restr. Enz.	Sph I site closest	Good	Poor	Poor at Sph I,	No SD; poor	
	Sph	Cleavage	to attL1			Good at Xmn	Kozac at Sph,	
		Vectors				I	good at Xmn	
pENTR7	TEV Blunt		Xmn I (blunt) is	Good	Poor	Good at Xmn	TEV protease	
		e Site	first cloning site			I site	leaves Gly-Thr	
		Present	after TEV site	_			on amino end of	_
							protein; no SD	_
pENTR8	TEV Nco	TEV	Nco I is first	Good	Poor	Good	TEV protease	
		Cleavage Site	cloning site after				leaves Gly-Thr	
		Present	TEV site				on amino end of	
					•	_	nrotein, no SD	

pENTR9	TEV Nde	e Site	Nde I is first cloning site after	Good	Poor	Poor	TEV protease leaves Gly-Thr on amino end of
		rieselli	Alexander of the same of the s				protein; no SD, poor Kozac
pENTR10 Nde with	Nde with	Good SD for	Good SD for Strong SD; Nde I Poor	Poor	Good	Poor	Strong SD,
	SD	E.coli	site, no TEV				internal starts in
		Expression					amino fusions.
		•				•	Poor Kz. No
							TEV
pENTR11	2 X	Good SD for	Xmn I (blunt)	Good	Good	Good	Strong SD/Koz
	SD+Kozac		and Nco I sites				Internal starts in
		Expression	each preceded by				armino fusions.
		4	SD and Kozac				No TEV

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Entry vectors pENTR1A (Figures 10A and 10B), pENTR2B (Figures 11A and 11B), and pENTR3C (Figures 12A and 12B) are almost identical, except that the restriction sites are in different reading frames. Entry vectors pENTR4 (Figures 13A and 13B), pENTR5 (Figures 14A and 14B), and pENTR6 (Figures 15A and 15B) are essentially identical to pENTR1A, except that the blunt *DraI* site has been replaced with sites containing the ATG methionine codon: *NcoI* in pENTR4, *NdeI* in pENTR5, and *SphI* in pENTR6. Nucleic acid molecules that contain one of these sites at the initiating ATG can be conveniently cloned in these Entry vectors. The *NcoI* site in pENTR4 is especially useful for expression of nucleic acid molecules in eukaryotic cells, since it contains many of the bases that give efficient translation (*see* Example 13, below). (Nucleic acid molecules of interest cloned into the *NdeI* site of pENTR5 are not expected to be highly expressed in eukaryotic cells, because the cytosine at position -3 from the initiating ATG is rare in eukaryotic genes.)

Entry vectors pENTR7 (Figures 16A and 16B), pENTR8 (Figures 17A and 17B), and pENTR9 (Figures 18A and 18B) contain the recognition site for the TEV protease between the attL1 site and the cloning sites. Cleavage sites for XmnI (blunt), NcoI, and NdeI, respectively, are the most 5' sites in these Entry vectors. Amino fusions can be removed efficiently if nucleic acid molecules are cloned into these Entry vectors. TEV protease is highly active and highly specific.

#### Example 5: Controlling Reading Frame

One of the trickiest tasks in expression of cloned nucleic acid molecules is making sure the reading frame is correct. (Reading frame is important if fusions are being made between two ORFs, for example between a nucleic acid molecule of interest and a His6 or GST domain.) For purposes of the present invention, the following convention has been adopted: The reading frame of the DNA cloned into any Entry Vector must be in phase with that of the attB1 site shown in Figure 16A, pENTR7. Notice that the six As of the attL1 site are split into two lysine codons (aaa aaa). The Destination Vectors that make amino fusions were constructed such that they enter the attR1 site in this reading frame.

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Destination Vectors for carboxy terminal fusions were also constructed, including those containing His<sub>6</sub> (pDEST23; Figure 43), GST (pDEST24; Figure 44), or thioredoxin (pDEST25; Figure 45) C-terminal fusion sequences.

Therefore, if a nucleic acid molecule of interest is cloned into an Entry Vector so that the aaa aaa reading frame within the attL1 site is in phase with the nucleic acid molecule's ORF, amino terminal fusions will automatically be correctly phased, for all the fusion tags. This is a significant improvement over the usual case, where each different vector can have different restriction sites and different reading frames.

See Example 15 for a practical example of how to choose the most appropriate combinations of Entry Vector and Destination Vector.

#### Materials

Unless otherwise indicated, the following materials were used in the remaining Examples included herein:

# 5X LR Reaction Buffer:

200-250 mM (preferably 250 mM) Tris-HCl, pH 7.5
250-350 mM (preferably 320 mM) NaCl
1.25-5 mM (preferably 4.75 mM) EDTA
12.5-35 mM (preferably 22-35 mM, and most preferably 35 mM)
Spermidine-HCl

1 mg/ml bovine serum albumin

#### GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix:

### per 4 µl of 1X LR Reaction Buffer:

150 ng carboxy-His6-tagged Int (see U.S. Appl. Nos. 60/108,324, filed November 13, 1998, and 09/438,358, filed November 12, 1999, both entirely incorporated by reference herein)

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25 ng carboxy-His6-tagged Xis (see U.S. Appl. Nos. 60/108,324, filed November 13, 1998, and 09/438,358, filed November 12, 1999, both entirely incorporated by reference herein)

30 ng IHF

50% glycerol

### 5X BP Reaction Buffer:

125 mM Tris-HCl, pH 7.5

110 mM NaCl

25 mM EDTA

25 mM Spermidine-HCl

5 mg/ml bovine serum albumin

# GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix:

per 4 µl of 1X BP Reaction Buffer:

200 ng carboxy-His6-tagged Int (see U.S. Appl. Nos. 60/108,324, filed November 13, 1998, and 09/438,358, filed November 12, 1999, both entirely incorporated by reference herein)

80 ng IHF

50% glycerol

# 10X Clonase Stop Solution:

50 mM Tris-HCl, pH 8.0

1 mM EDTA

2 mg/ml Proteinase K

# Example 6: LR ("Destination") Reaction

To create a new Expression Clone containing the nucleic acid molecule of interest (and which may be introduced into a host cell, ultimately for production of the polypeptide encoded by the nucleic acid molecule), an Entry Clone or Vector containing the nucleic acid molecule of interest, prepared as described

herein, is reacted with a Destination Vector. In the present example, a  $\beta$ -Gal gene flanked by attL sites is transferred from an Entry Clone to a Destination Vector.

### Materials needed:

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- 5 X LR Reaction buffer
- Destination Vector (preferably linearized), 75-150 ng/μl
- Entry Clone containing nucleic acid molecule of interest, 100-300 ng in  $\leq$  8  $\mu$ l TE buffer
- Positive control Entry Clone (pENTR-β-Gal) DNA (See note, below)
- Positive control Destination Vector, pDEST1 (pTrc), 75 ng/μl
- GATEWAY™ LR Clonase™ Enzyme Mix (stored at 80° C)
- 10X Clonase Stop solution
- pUC19 DNA, 10 pg/μl
- Chemically competent E. coli cells (competence: ≥1x10<sup>7</sup> CFU/μg), 400 μl.
- LB Plates containing ampicillin (100  $\mu$ g/ml) and methicillin (200  $\mu$ g/ml)  $\pm$  X-gal and IPTG (See below)

### Notes:

Preparation of the Entry Clone DNA: Miniprep DNA that has been treated with RNase works well. A reasonably accurate quantitation (±50%) of the DNA to be cloned is advised, as the GATEWAY<sup>TM</sup> reaction appears to have an optimum of about 100-300 ng of Entry Clone per 20 μl of reaction mix.

The positive control Entry Clone, pENTR- $\beta$ -Gal, permits functional analysis of clones based on the numbers of expected blue vs. white colonies on LB plates containing IPTG+Bluo-gal (or X-gal), in addition to ampicillin (100  $\mu$ g/ml) and methicillin (200  $\mu$ g/ml). Because  $\beta$ -Galactosidase is a large protein, it often yields a less prominent band than many smaller proteins do on SDS protein gels.

In the Positive Control Entry Vector pENTR- $\beta$ -Gal, the coding sequence of  $\beta$ -Gal has been cloned into pENTR11 (Figures 20A and 20B), with translational start signals permitting expression in E. coli, as well as in eukaryotic

cells. The positive control Destination Vector, for example pDEST1 (Figure 21), is preferably linearized.

To prepare X-gal + IPTG plates, either of the following protocols may be used:

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A. With a glass rod, spread over the surface of an LB agar plate: 40  $\mu$ l of 20 mg/ml X-gal (or Bluo-gal) in DMF plus 4  $\mu$ l 200 mg/ml IPTG. Allow liquid to adsorb into agar for 3-4 hours at 37° C before plating cells.

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B. To liquid LB agar at ~45°C, add: X-gal (or Bluo-Gal) (20 mg/ml in DMF) to make 50 μg/ml and IPTG (200 mM in water) to make 0.5-1 mM, just prior to pouring plates. Store X-gal and Bluo-Gal in a light-shielded container.

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Colony color may be enhanced by placing the plates at 5°C for a few hours after the overnight incubation at 37°C. Protocol B can give more consistent colony color than A, but A is more convenient when selection plates are needed on short notice.

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Recombination in Clonase reactions continues for many hours. While incubations of 45-60 minutes are usually sufficient, reactions with large DNAs, or in which both parental DNAs are supercoiled, or which will be transformed into cells of low competence, can be improved with longer incubation times, such as 2-24 hours at 25°C.

### Procedure:

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1. Assemble reactions as follows (combine all components at room temperature, except GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix ("Clonase LR"), before removing Clonase LR from frozen storage):

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	Tube 1	Tube 2	Tube 3	Tube 4
Component	Neg.	Pos.	Neg.	Test
p-Gate-βGal, (Positive control	4 µl	4 μl		
Entry Clone) 75 ng/µl		1	1	
pDEST1 (Positive control	4 μl	4 µl		
Destination Vector), 75 ng/µl				
Your Entry Clone (100-300 ng)			1 - 8 µl	1 - 8 µl
Destination Vector for your nucleic			4 μl	4 μl
acid molecule, 75 ng/µl				
5 X LR Reaction Buffer	4 µl	4 µl	4 μl	4 µl
TE	8 µ1	4 μl	То 20 µl	То 16 µl
GATEWAY™ LR Clonase™ Enzyme Mix (store at - 80° C, add last)		4 µl		4 µl
Total Volume	20 µl	20 µl	20 µl	20 μl

- 2. Remove the GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix from the -80° C freezer, place immediately on ice. The Clonase takes only a few minutes to thaw.
- 3. Add 4 µl of GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix to reactions #2 and #4;
- 4. Return GATEWAY™ LR Clonase™ Enzyme Mix to 80° C freezer.
- 5. Incubate tubes at 25° for at least 60 minutes.
- Add 2 μl Clonase Stop solution to all reactions. Incubate for 20 min at 37°C.
   (This step usually increases the total number of colonies obtained by 10-20 fold.)
- 7. Transform 2 μl into 100 μl competent *E. coli*. Select on plates containing ampicillin at 100 μg/ml.

### Example 7: Transformation of E. coli

To introduce cloning or Expression Vectors prepared using the recombinational cloning system of the invention, any standard *E. coli* transformation protocol should be satisfactory. The following steps are recommended for best results:

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1. Let the mixture of competent cells and Recombinational Cloning System reaction product stand on ice at least 15 minutes prior to the heat-shock step. This gives time for the recombination proteins to dissociate from the DNA, and improves the transformation efficiency.

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2. Expect the reaction to be about 1%-5% efficient, i.e., 2  $\mu$ l of the reaction should contain at least 100 pg of the Expression Clone plasmid (taking into account the amounts of each parental plasmid in the reaction, and the subsequent dilution). If the E. coli cells have a competence of  $10^7$  CFU/ $\mu$ g, 100 pg of the desired clone plasmid will give about 1000 colonies, or more, if the entire transformation is spread on one ampicillin plate.

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3. Always do a control pUC DNA transformation. If the number of colonies is not what you expect, the pUC DNA transformation gives you an indication of where the problem was.

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### Example 8: Preparation of attB-PCR Product

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For preparation of attB-PCR products in the PCR cloning methods described in Example 9 below, PCR primers containing attB1 and attB2 sequences are used. The attB1 and attB2 primer sequences are as follows:

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attB1: 5'-GGGGACAAGTTTGTACAAAAAAGCAGGCT-(template-specific sequence)-3'

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attB2: 5'-GGGGACCACTTTGTACAAGAAAGCTGGGT-(template-specific sequence)-3'

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The attB1 sequence should be added to the amino primer, and the attB2 sequence to the carboxy primer. The 4 guanines at the 5' ends of each of these primers enhance the efficiency of the minimal 25 bp attB sequences as substrates for use in the cloning methods of the invention.

Standard PCR conditions may be used to prepare the PCR product. The following suggested protocol employs PLATINUM Taq DNA Polymerase High

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Fidelity®, available commercially from Life Technologies, Inc. (Rockville, MD). This enzyme mix eliminates the need for hot starts, has improved fidelity over Taq, and permits synthesis of a wide range of amplicon sizes, from 200 bp to 10 kb, or more, even on genomic templates.

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#### Materials needed:

• PLATINUM Taq DNA Polymerase High Fidelity® (Life Technologies, Inc.)

•attB1- and attB2- containing primer pair (see above) specific for your template

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- •DNA template (linearized plasmid or genomic DNA)
- •10X High Fidelity PCR Buffer
- •10 mM dNTP mix
- •PEG/MgCl<sub>2</sub> Mix (30% PEG 8000, 30 mM MgCl<sub>2</sub>)

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### Procedure:

### 1.) Assemble the reaction as follows:

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\* Use of higher amounts of plasmid template may permit fewer cycles (10-15) of PCR

Component Reaction with Reaction with Genomic Plasmid Target Target 10X High Fidelity PCR Buffer 5 µl 5 μΙ dNTP Mix 10 mM l µl l µl MgSO<sub>4</sub>, 50mM  $2 \mu l$  $2 \mu l$ attB1 Primer, 10 µM  $2 \mu l$ l µl attB2 Primer, 10 µM  $2 \mu l$  $l \mu l$ Template DNA 1-5 ng\* ≥100 ng PLATINUM Taq High Fidelity  $2 \mu l$ l μl Water to 50 µl to 50 µl

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- 2.) Add 2 drops mineral oil, as appropriate.
- 3.) Denature for 30 sec. at 94°C.
- 4.) Perform 25 cycles:

94°C for 15 sec-30 sec

55°C for 15 sec-30 sec

68°C for 1 min per kb of template.

5.) Following the PCR reaction, apply 1-2 µl of the reaction mixture to an agarose gel, together with size standards (e.g., 1 Kb Plus Ladder, Life Technologies, Inc.) and quantitation standards (e.g., Low Mass Ladder, Life Technologies, Inc.), to assess the yield and uniformity of the product.

Purification of the PCR product is recommended, to remove attB primer dimers which can clone efficiently into the Entry Vector. The following protocol is fast and will remove DNA <300 bp in size:

- 6.) Dilute the 50 µl PCR reaction to 200 µl with TE.
- 7.) Add 100 μl PEG/MgCl<sub>2</sub> Solution. Mix and centrifuge immediately at 13,000 RPM for 10 min at room temperature. Remove the supernatant (pellet is clear and hard to see).
- 8.) Dissolve the pellet in 50 µl TE and check recovery on a gel.

If the starting PCR template is a plasmid that contains the gene for Kan<sup>r</sup>, it is advisable to treat the completed PCR reaction with the restriction enzyme DpnI, to degrade the plasmid since unreacted residual starting plasmid is a potential source of false-positive colonies from the transformation of the GATEWAY<sup>TM</sup> Cloning System reaction. Adding ~5 units of DpnI to the completed PCR reaction and incubating for 15 min at 37°C will eliminate this potential problem. Heat inactivate the DpnI at 65°C for 15 min, prior to using the PCR product in the GATEWAY<sup>TM</sup> Cloning System reaction.

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# Example 9: Cloning attB-PCR products into Entry Vectors via the BP ("Gateward") Reaction

The addition of 5'-terminal attB sequences to PCR primers allows synthesis of a PCR product that is an efficient substrate for recombination with a Donor (attP) Plasmid in the presence of GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix. This reaction produces an Entry Clone of the PCR product (See Figure 8).

The conditions of the Gateward Cloning reaction with an attB PCR substrate are similar to those of the BP Reaction (see Example 10 below), except that the attB-PCR product (see Example 8) substitutes for the Expression Clone, and the attB-PCR positive control (attB-tet) substitutes for the Expression Clone Positive Control (GFP).

### Materials needed:

- 5 X BP Reaction Buffer
- •. Desired attB-PCR product DNA, 50-100 ng in ≤ 8 µl TE.
- Donor (attP) Plasmid (Figures 49-54), 75 ng/μl, supercoiled DNA
- attB-tet<sup>r</sup> PCR product positive control, 25 ng/μl
- GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix (stored at 80° C)
- 10x Clonase Stop Solution
- pUC19 DNA, 10 pg/μl.
- Chemically competent E.coli cells (competence: ≥1x10<sup>7</sup> CFU/µg), 400 µl

### Notes:

- •Preparation of attB-PCR DNA: see Example 8.
- •The Positive Control attB-tet<sup>r</sup>PCR product contains a functional copy of the tet<sup>r</sup> gene of pBR322, with its own promoter. By plating the transformation of the control BP Reaction on kanamycin (50 µg/ml) plates (if kan<sup>r</sup> Donor Plasmids are used; see Figures 49-52) or an alternative selection agent (e.g., gentamycin, if gen<sup>r</sup> Donor Plasmids are used; see Figure 54), and then picking about 50 of these colonies onto plates with tetracycline (20 µg/ml), the

percentage of Entry Clones containing functional tet<sup>r</sup> among the colonies from the positive control reaction can be determined (% Expression Clones = (number of tet<sup>r</sup> + kan<sup>r</sup> (or gen<sup>r</sup>) colonies/kan<sup>r</sup> (or gen<sup>r</sup>) colonies).

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### Procedure:

1. Assemble reactions as follows. Combine all components except GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix, before removing GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix from frozen storage.

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	Neg.	Pos.	Test
Component	Tube 1	Tube 2	Tube 3
attB-PCR product, 50-100 ng			1 - 8 μ1
Donor (attP) Plasmid 75 ng/μl	2 µl	2 µl	2 μl
attB-PCR tet control DNA (75 ng/μl)		4 μl	
5 X BP Reaction Buffer	4 μl	4 μΙ	4 μΙ
TE	10 µl	6 µl	То 16 µl
GATEWAY™ BP Clonase™ Enzyme Mix (store at -80° C, add last)	4 µ1	4 μΙ	4 μl
Total Volume	20 µl	20 µl	20 μl

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- 2. Remove the GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix from the -80° C freezer, place immediately on ice. The Clonase takes only a few minutes to thaw.
- 3. Add 4 μl of GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix to the subcloning reaction, mix.
- 4. Return GATEWAY™ BP Clonase™ Enzyme Mix to 80° C freezer.
- 5. Incubate tubes at 25° for at least 60 minutes.

- 6. Add 2 μl Proteinase K (2 μg/μl) to all reactions. Incubate for 20 min at 37°C.
- Transform 2 μl into 100 μl competent E. coli, as per 3.2, above. Select on LB plates containing kanamycin, 50 μg/ml.

### Results:

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In initial experiments, primers for amplifying tetR and ampR from pBR322 were constructed containing only the tetR- or ampR-specific targeting sequences, the targeting sequences plus attB1 (for forward primers) or attB2 (for reverse primers) sequences shown in Figure 9, or the attB1 or attB2 sequences with a 5' tail of four guanines. The construction of these primers is depicted in Figure 65. After PCR amplification of tetR and ampR from pBR322 using these primers and cloning the PCR products into host cells using the recombinational cloning system of the invention, the results shown in Figure 66 were obtained. These results demonstrated that primers containing attB sequences provided for a somewhat higher number of colonies on the tetracycline and ampicillin plates. However, inclusion of the 5' extensions of four or five guanines on the primers in addition to the attB sequences provided significantly better cloning results, as shown in Figures 66 and 67. These results indicate that the optimal primers for cloning of PCR products using recombinational cloning will contain the recombination site sequences with a 5' extension of four or five guanine bases.

To determine the optimal stoichiometry between attB-containing PCR products and attP-containing Donor plasmid, experiments were conducted where the amount of PCR product and Donor plasmid were varied during the BP Reaction. Reaction mixtures were then transformed into host cells and plated on tetracycline plates as above. Results are shown in Figure 68. These results indicate that, for optimal recombinational cloning results with a PCR product in the size range of the tet gene, the amounts of attP-containing Donor plasmids are between about 100-500 ng (most preferably about 200-300 ng), while the optimal concentrations of attB-containing PCR products is about 25-100 ng (most preferably about 100 ng), per 20 µl reaction.

Experiments were then conducted to examine the effect of PCR product size on efficiency of cloning via the recombinational cloning approach of the invention.

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PCR products containing attB1 and attB2 sites, at sizes 256 bp, 1 kb, 1.4 kb, 3.4 kb, 4.6 kb, 6.9 kb and 10.1 kb were prepared and cloned into Entry vectors as described above, and host cells were transformed with the Entry vectors containing the cloned PCR products. For each PCR product, cloning efficiency was calculated relative to cloning of pUC19 positive control plasmids as follows:

The results of these experiments are depicted in Figures 69A-69C (for 256 bp PCR fragments), 70A-70C (for 1 kb PCR fragments), 71A-71C (for 1.4 kb PCR fragments), 72A-72C (for 3.4 kb PCR fragments), 73A-73C (for 4.6 kb PCR fragments), 74 (for 6.9 kb PCR fragments), and 75-76 (for 10.1 kb PCR fragments). The results shown in these figures are summarized in Figure 77, for different weights and moles of input PCR DNA.

Together, these results demonstrate that attB-containing PCR products ranging in size from about 0.25 kb to about 5 kb clone relatively efficiently in the recombinational cloning system of the invention. While PCR products larger than about 5 kb clone less efficiently (apparently due to slow resolution of cointegrates), longer incubation times during the recombination reaction appears to improve the efficiency of cloning of these larger PCR fragments. Alternatively, it may also be possible to improve efficiency of cloning of large (> about 5 kb) PCR fragments by using lower levels of input attP Donor plasmid and perhaps attB-containing PCR product, and/or by adjusting reaction conditions (e.g., buffer conditions) to favor more rapid resolution of the cointegrates.

### Example 10: The BP Reaction

One purpose of the Gateward ("Entry") reaction is to convert an Expression Clone into an Entry Clone. This is useful when you have isolated an individual Expression Clone from an Expression Clone cDNA library, and you wish to transfer the nucleic acid molecule of interest into another Expression Vector, or

to move a population of molecules from an attB or attL library. Alternatively, you may have mutated an Expression Clone and now wish to transfer the mutated nucleic acid molecule of interest into one or more new Expression Vectors. In both cases, it is necessary first to convert the nucleic acid molecule of interest to an Entry Clone.

### Materials needed:

- 5 X BP Reaction Buffer
- Expression Clone DNA, 100-300 ng in ≤ 8 µl TE.
- Donor (attP) Vector, 75 ng/µl, supercoiled DNA
- Positive control attB-tet-PCR DNA, 25 ng/µl
- GATEWAY™ BP Clonase™ Enzyme Mix (stored at 80°C)
- Clonase Stop Solution (Proteinase K, 2 μg/μl).

#### Notes:

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Preparation of the Expression Clone DNA: Miniprep DNA treated with RNase works well.

1. As with the LR Reaction (see Example 14), the BP Reaction is strongly influenced by the topology of the reacting DNAs. In general, the reaction is most efficient when one of the DNAs is linear and the other is supercoiled, compared to reactions where the DNAs are both linear or both supercoiled. Further, linearizing the attB Expression Clone (anywhere within the vector) will usually give more colonies than linearizing the Donor (attP) Plasmid. If finding a suitable cleavage site within your Expression Clone vector proves difficult, you may linearize the Donor (attP) Plasmid between the attP1 and attP2 sites (for example, at the *NcoI* site), avoiding the ccdB gene. Maps of Donor (attP) Plasmids are given in Figures 49-54.

### Procedure:

1. Assemble reactions as follows. Combine all components at room temperature, except GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix, before removing GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix from freezer.

	Neg.	Pos.	Test
Component	Tube 1	Tube 2	Tube 3
Positive Control, attB-tet-PCR DNA, 25 ng/µl	4 µl	4 μΙ	
Desired attB Expression Clone DNA (100ng) linearized			1 - 8 μl
Donor (attP) Plasmid, 75 ng/µl	2 μΙ	2 μl	2 μl
5 X BP Reaction Buffer	4 µl	4 μl	4 μl
TE	10 μl	6 µl	To 16 µl
GATEWAY™ BP Clonase™ Enzyme Mix (store at - 80° C, add last)		4 µl	4 μ1
Total Volume	20 μl	20 µl	20 µl

- 2. Remove the GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix from the -80°C freezer, place immediately on ice. The mixture takes only a few minutes to thaw.
- 3. Add 4  $\mu l$  of GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix to the subcloning reaction, mix.
- 4. Return GATEWAY™ BP Clonase™ Enzyme Mix to 80° C freezer.
- 5. Incubate tubes at 25° for at least 60 minutes. If both the attB and attP DNAs are supercoiled, incubation for 2-24 hours at 25°C is recommended.
- 6. Add 2 µl Clonase Stop Solution. Incubate for 10 min at 37°C.
- Transform 2 μl into 100 μl competent E. coli, as above. Select on LB plates containing 50 μg/ml kanamycin.

# Example 11: Cloning PCR Products into Entry Vectors using Standard Cloning Methods

### Preparation of Entry Vectors for Cloning of PCR Products

All of the Entry Vectors of the invention contain the death gene ccdB as a stuffer between the "left" and "right" restriction sites. The advantage of this arrangement is that there is virtually no background from vector that has not been cut with both restriction enzymes, because the presence of the ccdB gene will kill

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all standard E. coli strains. Thus it is necessary to cut each Entry Vector twice, to remove the ccdB fragment.

We strongly recommend that, after digestion of the Entry Vector with the second restriction enzyme, you treat the reaction with phosphatase (calf intestine alkaline phosphatase, CIAP or thermosensitive alkaline phosphatase, TSAP). The phosphatase can be added directly to the reaction mixture, incubated for an additional time, and inactivated. This step dephosphorylates both the vector and ccdB fragments, so that during subsequent ligation there is less competition between the ccdB fragment and the DNA of interest for the termini of the Entry Vector.

### Blunt Cloning of PCR products

Generally PCR products do not have 5' phosphates (because the primers are usually 5' OH), and they are not necessarily blunt. (On this latter point, see Brownstein, et al., *BioTechniques 20*: 1006, 1996 for a discussion of how the sequence of the primers affects the addition of single 3' bases.) The following protocol repairs these two defects.

In a 0.5 ml tube, ethanol precipitate about 40 ng of PCR product (as judged from an agarose gel).

- Dissolve the precipitated DNA in 10 μl comprising 1 μl 10 mM rATP, 1 μl mixed 2 mM dNTPs (i.e., 2 mM each dATP, dCTP, dTTP, and dGTP), 2 μl 5x T4 polynucleotide kinase buffer (350 mM Tris HCl (pH7.6), 50 mM MgCl<sub>2</sub>, 500mM KCl, 5 mM 2-mercaptoethanol) 10 units T4 polynucleotide kinase, 1 μl T4 DNA polymerase, and water to 10 μl.
- 2. Incubate the tube at 37° for 10 minutes, then at 65° for 15 minutes, cool, centrifuge briefly to bring any condensate to the tip of the tube.
- 3. Add 5 μl of the PEG/MgCl<sub>2</sub> solution, mix and centrifuge at room temperature for 10 minutes. Discard supernatant.
- 4. Dissolve the invisible precipitate in 10 μl containing 2 μl 5x T4 DNA ligase buffer (Life Technologies, Inc.), 0.5 units T4 DNA ligase, and about 50 ng of blunt, phosphatase-treated Entry Vector.

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- Incubate at 25° for 1 hour, then 65° for 10 minutes. Add 90 μl TE, transform
   μl into 50 100 μl competent E. coli cells.
- 6. Plate on kanamycin.

Note: In the above protocol, steps b-c simultaneously polish the ends of the PCR product (through the exonuclease and polymerase activities of T4 DNA polymerase) and phosphorylate the 5' ends (using T4 polynucleotide kinase). It is necessary to inactivate the kinase, so that the blunt, dephosphorylated vector in step e cannot self ligate. Step d (the PEG precipitation) removes all small molecules (primers, nucleotides), and has also been found to improve the yield of cloned PCR product by 50 fold.

### Cloning PCR Products after Digestion with Restriction Enzymes

Efficient cloning of PCR products that have been digested with restriction enzymes includes three steps: inactivation of *Taq* DNA polymerase, efficient restriction enzyme cutting, and removal of small DNA fragments.

Inactivation of Tag DNA Polymerase: Carryover of Taq DNA polymerase and dNTPs into a RE digestion significantly reduces the success in cloning a PCR product (D. Fox et al., FOCUS 20(1):15, 1998), because Taq DNA polymerase can fill in sticky ends and add bases to blunt ends. Either TAQQUENCH<sup>TM</sup> (obtainable from Life Technologies, Inc.; Rockville, Maryland) or extraction with phenol can be used to inactivate the Taq.

Efficient Restriction Enzyme Cutting: Extra bases on the 5' end of each PCR primer help the RE cut near ends of PCR products. With the availability of cheap primers, adding 6 to 9 bases on the 5' sides of the restriction sites is a good investment to ensure that most of the ends are digested. Incubation of the DNA with a 5-fold excess of restriction enzyme for an hour or more helps ensure success.

<u>Removal of Small Molecules before Ligation</u>: Primers, nucleotides, primer dimers, and small fragments produced by the restriction enzyme digestion,

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can all inhibit or compete with the desired ligation of the PCR product to the cloning vector. This protocol uses PEG precipitation to remove small molecules.

## Protocol for cutting the ends of PCR products with restriction enzyme(s):

1. Inactivation of Taq DNA polymerase in the PCR product:

### Option A: Extraction with Phenol

- A1. Dilute the PCR reaction to 200  $\mu$ l with TE. Add an equal volume of phenol:chloroform:isoamyl alcohol, vortex vigorously for 20 seconds, and centrifuge for 1 minute at room temperature. Discard the lower phase.
- A2. Extract the phenol from the DNA and concentrate as follows. Add an equal volume of 2-butanol (colored red with "Oil Red O" from Aldrich, if desired), vortex briefly, centrifuge briefly at room temperature. Discard the upper butanol phase. Repeat the extraction with 2-butanol. This time the volume of the lower aqueous phase should decrease significantly. Discard the upper 2-butanol phase.
- A3. Ethanol precipitate the DNA from the aqueous phase of the above extractions. Dissolve in a 200  $\mu$ l of a suitable restriction enzyme (RE) buffer.

### Option B: Inactivation with TagOuench

- B1. Ethanol precipitate an appropriate amount of PCR product (100 ng to 1  $\mu$ g), dissolve in 200  $\mu$ l of a suitable RE buffer.
- B2. Add 2 µl TaqQuench.
- 2. Add 10 to 50 units of restriction enzyme and incubate for at least 1 hour. Ethanol precipitate if necessary to change buffers for digestion at the other end of the PCR product.

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3. Add ½ volume of the PEG/MgCl<sub>2</sub> mix to the RE digestion. Mix well and immediately centrifuge at room temperature for 10 minutes. Discard the supernatant (pellet is usually invisible), centrifuge again for a few seconds, discard any remaining supernatant.

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4. Dissolve the DNA in a suitable volume of TE (depending on the amount of PCR product in the original amplification reaction) and apply an aliquot to an agarose gel to confirm recovery. Apply to the same gel 20-100 ng of the appropriate Entry Vector that will be used for the cloning.

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# Example 12: Determining The Expected Size of the GATEWAY<sup>TM</sup> Cloning Reaction Products

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If you have access to a software program that will electronically cut and splice sequences, you can create electronic clones to aid you in predicting the sizes and restriction patterns of GATEWAY<sup>TM</sup> Cloning System recombination products.

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The cleavage and ligation steps performed by the enzyme Int in the GATEWAY<sup>TM</sup> Cloning System recombination reactions mimic a restriction enzyme cleavage that creates a 7-bp 5'-end overhang followed by a ligation step that reseals the ends of the daughter molecules. The recombination proteins present in the Clonase cocktails (see Example 19 below) recognize the 15 bp core sequence present within all four types of att sites (in addition to other flanking sequences characteristic of each of the different types of att sites).

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By treating these sites in your software program as if they were restriction sites, you can cut and splice your Entry Clones with various Destination Vectors and obtain accurate maps and sequences of the expected results from your GATEWAY<sup>TM</sup> Cloning System reactions.

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### Example 13: Protein Expression

### Brief Review of Protein Expression

Transcription: The most commonly used promoters in E. coli Expression Vectors are variants of the lac promoter, and these can be turned on by adding

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IPTG to the growth medium. It is usually good to keep promoters off until expression is desired, so that the host cells are not made sick by the overabundance of some heterologous protein. This is reasonably easy in the case of the lac promoters used in E. coli. One needs to supply the *lac* I gene (or its more productive relative, the *lac* I<sup>q</sup> gene) to make *lac* repressor protein, which binds near the promoter and keeps transcription levels low. Some Destination Vectors for E. coli expression carry their own *lac*I<sup>q</sup> gene for this purpose. (However, lac promoters are always a little "on," even in the absence of IPTG.)

Controlling transcription in eukaryotic cells is not nearly so straightforward or efficient. The tetracycline system of Bujard and colleagues is the most successful approach, and one of the Destination Vectors (pDEST11; Figure 31) has been constructed to supply this function.

Translation: Ribosomes convert the information present in mRNA into protein. Ribosomes scan RNA molecules looking for methionine (AUG) codons, which begin nearly all nascent proteins. Ribosomes must, however, be able to distinguish between AUG codons that code for methionine in the middle of proteins from those at the start. Most often ribosomes choose AUGs that are 1) first in the RNA (toward the 5' end), and 2) have the proper sequence context. In E. coli the favored context (first recognized by Shine and Dalgarno, Eur. J. Biochem. 57: 221 (1975)) is a run of purines (As and Gs) from five to 12 bases upstream of the initiating AUG, especially AGGAGG or some variant.

In eukaryotes, a survey of translated mRNAs by Kozak (*J. Biol. Chem.* 266: 19867 (1991)) has revealed a preferred sequence context, gcc Acc ATGG, around the initiating methionine, with the A at -3 being most important, and a purine at +4 (where the A of the ATG is +1), preferably a G, being next most influential. Having an A at -3 is enough to make most ribosomes choose the first AUG of an mRNA, in plants, insects, yeast, and mammals. (For a review of initiation of protein synthesis in eukaryotic cells, see: Pain, V.M. Eur.J. Biochem. 236:747-771, 1996.)

Consequences of Translation Signals for GATEWAY<sup>TM</sup> Cloning System: First, translation signals (Shine-Dalgarno in E. coli, Kozak in eukaryotes) have to be close to the initiating ATG. The attB site is 25 base pairs long. Thus if

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translation signals are desired near the natural ATG of the nucleic acid molecule of interest, they must be present in the Entry Clone of that nucleic acid molecule of interest. Also, when a nucleic acid molecule of interest is moved from an Entry Clone to a Destination vector, any translation signals will move along. The result is that the presence or absence of Shine-Dalgarno and/or Kozak sequences in the Entry Clone must be considered, with the eventual Destination Vectors to be used in mind.

Second, although ribosomes choose the 5' ATG most often, internal ATGs are also used to begin protein synthesis. The better the translation context around this internal ATG, the more internal translation initiation will be seen. This is important in the GATEWAY<sup>TM</sup> Cloning System, because you can make an Entry Clone of your nucleic acid molecule of interest, and arrange to have Shine-Dalgarno and/or Kozak sequences near the ATG. When this cassette is recombined into a Destination Vector that transcribes your nucleic acid molecule of interest, you get native protein. If you want, you can make a fusion protein in a different Destination Vector, since the Shine-Dalgarno and/or Kozak sequences do not contain any stop signals in the same reading frame. However, the presence of these internal translation signals may result in a significant amount of native protein being made, contaminating, and lowering the yield of, your fusion protein. This is especially likely with short fusion tags, like His6.

A good compromise can be recommended. If an Entry Vector like pENTR7 (Figure 16) or pENTR8 (Figure 17) is chosen, the Kozak bases are present for native eukaryotic expression. The context for E. coli translation is poor, so the yield of an amino-terminal fusion should be good, and the fusion protein can be digested with the TEV protease to make near-native protein following purification.

Recommended Conditions for Synthesis of Proteins in E. coli: When making proteins in E. coli it is advisable, at least initially, to incubate your cultures at 30°C, instead of at 37°C. Our experience indicates that proteins are less likely to form aggregates at 30°C. In addition, the yields of proteins from cells grown at 30°C frequently are improved.

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The yields of proteins that are difficult to express may also be improved by inducing the cultures in mid-log phase of growth, using cultures begun in the morning from overnight growths, as opposed to harvesting directly from an overnight culture. In the latter case, the cells are preferably in late log or stationary growth, which can favor the formation of insoluble aggregates.

### Example 14: Constructing Destination Vectors from Existing Vectors

Destination Vectors function because they have two recombination sites, attR1 and attR2, flanking a chloramphenicol resistance (CmR) gene and a death gene, ccdB. The GATEWAY<sup>TM</sup> Cloning System recombination reactions exchange the entire Cassette (except for a few bases comprising part of the attB sites) for the DNA segment of interest from the Entry Vector. Because attR1, CmR, ccdB gene, and attR2 are contiguous, they can be moved on a single DNA segment. If this Cassette is cloned into a plasmid, the plasmid becomes a Destination Vector. Figure 63 shows a schematic of the GATEWAY<sup>TM</sup> Cloning System Cassette; attR cassettes in all three reading frames contained in vectors pEZC15101, pEZC15102 and pEZC15103 are shown in Figures 64A, 64B, and 64C, respectively.

The protocol for constructing a Destination Vector is presented below. Keep in mind the following points:

- Destination Vectors must be constructed and propagated in one of the DB strains of E. coli (e.g., DB3.1, and particularly E. coli LIBRARY EFFICIENCY® DB3.1™ Competent Cells) available from Life Technologies, Inc. (and described in detail in U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, which is incorporated herein by reference), because the ccdB death gene will kill any E. coli strain that has not been mutated such that it will survive the presence of the ccdB gene.
- If your Destination Vector will be used to make a fusion protein, a GATEWAY<sup>TM</sup> Cloning System cassette with the correct reading frame must be used. The nucleotide sequences of the ends of the cassettes are shown in Figure 78. The reading frame of the fusion protein domain must

be in frame with the core region of the attR1 site (for an amino terminal fusion) so that the six As are translated into two lysine codons. For a C-terminal fusion protein, translation through the core region of the attR2 site should be in frame with -TAC-AAA-, to yield -Tyr-Lys-.

- Note that each reading frame Cassette has a different unique restriction site between the chloramphenicol resistance and ccdB genes (MluI for reading frame A, BglII for reading frame B, and XbaI for reading frame C; see Figure 63).
- Most standard vectors can be converted to Destination Vectors, by inserting the Entry Cassette into the MCS of that vector.

### Protocol for Making a Destination Vector

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- 1. If the vector will make an amino fusion protein, it is necessary to keep the "aaa aaa" triplets in attR1 in phase with the triplets of the fusion protein. Determine which Entry cassette to use as follows:
  - a.) Write out the nucleotide sequence of the existing vector near the restriction site into which the Entry cassette will be cloned. These <u>must</u> be written in triplets corresponding to the amino acid sequence of the fusion domain.
  - b.) Draw a vertical line through the sequence that corresponds to the restriction site end, after it has been cut and made blunt, i.e., after filling in a protruding 5' end or polishing a protruding 3' end.
  - c.) Choose the appropriate reading frame cassette:
    - If the coding sequence of the blunt end ends after a complete codon triplet, use the reading frame A cassette. See Figures 78, 79 and 80.

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- •If the coding sequence of the blunt end ends in a single base, use the reading frame B cassette. See Figures 78, 79 and 81.
- •If the coding sequence of the blunt end ends in two bases, use the reading frame C cassette. See Figures 78, 79, 82A-B, and 83A-C.
- 2. Cut one to five micrograms of the existing plasmid at the position where you wish your nucleic acid molecule of interest (flanked by att sites) to be after the recombination reactions. **Note**: it is better to remove as many of the MCS restriction sites as possible at this step. This makes it more likely that restriction enzyme sites within the GATEWAY<sup>TM</sup> Cloning System Cassette will be unique in the new plasmid, which is important for linearizing the Destination Vector (Example 14, below).
- 3. Remove the 5' phosphates with alkaline phosphatase. While this is not mandatory, it increases the probability of success.
- 4. Make the end(s) blunt with fill-in or polishing reactions. For example, to 1 μg of restriction enzyme-cut, ethanol-precipitated vector DNA, add:
  - i. 20 μl 5x T4 DNA Polymerase Buffer (165 mM Tris-acetate (pH 7.9), 330 mM Na acetate, 50 mM Mg acetate, 500 μg/ml BSA, 2.5 mM DTT)
  - ii. 5 µl 10mM dNTP mix
  - iii. 1 Unit of T4 DNA Polymerase
  - iv. Water to a final volume of 100 µl
  - v. Incubate for 15 min at 37°C.
- 5. Remove dNTPs and small DNA fragments: Ethanol precipitate (add three volumes of room temperature ethanol containing 0.1 M sodium acetate, mix well, immediately centrifuge at room temperature 5 10 minutes), dissolve wet precipitate in 200 μl TE, add 100 μl 30% PEG 8000, 30 mM MgCl<sub>2</sub>, mix well,

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immediately centrifuge for 10 minutes at room temperature, discard supernatant, centrifuge again a few seconds, discard any residual liquid.

- 6. Dissolve the DNA to a final concentration of 10 50 ng per microliter. Apply 20 100 ng to a gel next to supercoiled plasmid and linear size standards to confirm cutting and recovery. The cutting does not have to be 100% complete, since you will be selecting for the chloramphenical marker on the Entry cassette.
- 7. In a 10 μl ligation reaction combine 10 50 ng vector, 10 20 ng of Entry Cassette (Figure 79), and 0.5 units T4 DNA ligase in ligase buffer. After one hour (or overnight, whichever is most convenient), transform 1 μl into one of the DB strains of competent *E. coli* cells with a *gyr*A462 mutation (See U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, which is incorporated herein by reference), preferably DB3.1, and most preferably *E. coli* LIBRARY EFFICIENCY® DB3.1<sup>TM</sup> Competent Cells. The ccdB gene on the Entry Cassette will kill other strains of *E. coli* that have not been mutated so as to survive the presence of the ccdB gene.
- 8. After expression in SOC medium, plate 10  $\mu$ l and 100  $\mu$ l on chloramphenicol-containing (30  $\mu$ g / ml) plates, incubate at 37° C.
- 9. Pick colonies, make miniprep DNA. Treat the miniprep with RNase A and store in TE. Cut with the appropriate restriction enzyme to determine the orientation of the Cassette. Choose clones with the attR1 site next to the amino end of the protein expression function of the plasmid.

### Notes on Using Destination Vectors

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• We have found that about ten-fold more colonies result from a GATEWAY<sup>TM</sup> Cloning System reaction if the Destination Vector is linear or relaxed. If the competent cells you use are highly competent (>10<sup>8</sup> per microgram), linearizing the Destination Vector is less essential.

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- The site or sites used for the linearization must be within the Entry Cassette.
   Sites that cut once or twice within each cassette are shown in Figures 80-82.
- Minipreps of Destination Vectors will work fine, so long as they have been treated with RNase. Since most DB strains are endA- (See U.S. Provisional Application No. 60/122,392, filed on March 2, 1999, which is incorporated herein by reference), minipreps can be digested with restriction enzymes without a prior phenol extraction.
- Reading the OD<sub>260</sub> of miniprep DNA is inaccurate unless the RNA and ribonucleotides have been removed, for example, by a PEG precipitation.

# Example 15: Some Options in Choosing Appropriate Entry Vectors and Destination Vectors: An Example

In some applications, it may be desirable to express a nucleic acid molecule of interest in two forms: as an amino-terminal fusion in *E. coli*, and as a native protein in eukaryotic cells. This may be accomplished in any of several ways:

Option 1: Your choices depend on your nucleic acid molecule of interest and the fragment that contains it, as well as the available Entry Vectors. For eukaryotic translation, you need consensus bases according to Kozak (*J. Biol. Chem. 266*:19867, 1991) near the initiating methionine (ATG) codon. All of the Entry Vectors offer this motif upstream of the *XmnI* site (blunt cutter). One option is to amplify your nucleic acid molecule of interest, with its ATG, by PCR, making the amino end blunt and the carboxy end containing the natural stop codon followed by one of the "right side" restriction sites (*EcoRI*, *NotI*, *XhoI*, *EcoRV*, or *XbaI* of the pENTR vectors).

If you know your nucleic acid molecule of interest does not have, for example, an XhoI site, you can make a PCR product that has this structure:

#### Xho I

- 5' ATG nnn nnn --- nnn TAA ctc gag nnn nnn 3'
- 3' tac nnn nnn --- nnn att gag ctc nnn nnn 5'

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After cutting with XhoI, the fragment is ready to clone:

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5' ATG nnn nnn --- nnn TAA c 3'
3' tac nnn nnn --- nnn att gag ct 5'
(If you follow this example, don't forget to put a phosphate on the amino oligo.)
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Option 2: This PCR product could be cloned into two Entry Vectors to give the desired products, between the *Xmn*I and *Xho*I sites: pENTR1A (Figures 10A, 10B) or pENTR7 (Figures 16A, 16B). If you clone into pENTR1A, amino fusions will have the minimal number of amino acids between the fusion domain and your nucleic acid molecule of interest, but the fusion cannot be removed with TEV protease. The converse is true of clones in pENTR7, i.e., an amino fusion can be cleaved with TEV protease, at the cost of more amino acids between the fusion and your nucleic acid molecule of interest.

In this example, let us choose to clone our hypothetical nucleic acid molecule of interest into pENTR7, between the *Xmn*I and *Xho*I sites. Once this is accomplished, several optional protocols using the Entry Clone pENTR7 may be followed:

Option 3: Since the nucleic acid molecule of interest has been amplified with PCR, it may be desirable to sequence it. To do this, transfer the nucleic acid molecule of interest from the Entry Vector into a vector that has priming sites for the standard sequencing primers. Such a vector is pDEST6 (Figures 26A, 26B). This Destination Vector places the nucleic acid molecule of interest in the opposite orientation to the lac promoter (which is leaky -- see Example 3 above). If the gene product is toxic to *E. coli*, this Destination Vector will minimize its toxicity.

Option 4: While the sequencing is going on, you might wish to check the expression of the nucleic acid molecule of interest in, for example, CHO cells, by recombining the nucleic acid molecule of interest into a CMV promoter vector (pDEST7, Figure 27; or pDEST12, Figure 32), or into a baculovirus vector (pDEST8, Figure 28; or pDEST10, Figure 30) for expression in insect cells. Both

of these vectors will transcribe the coding sequence of your nucleic acid molecule of interest, and translate it from the ATG of the PCR product using the Kozak bases upstream of the *Xmn*I site.

Option 5: If you wish to purify protein, for example to make antibodies, you can clone the nucleic acid molecule of interest into a His6 fusion vector, pDEST2 (Figure 22). Since the nucleic acid molecule of interest is cloned downstream of the TEV protease cleavage domain of pENTR7 (Figure 16), the amino acid sequence of the protein produced will be:

[----- attB1 -----] <u>TEV protease</u> NH2- MSYYHHHHHHGITSLYKKAGF*ENLYFO*! *G*TM----COOH

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The attB site and the restriction sites used to make the Destination and Entry Vectors are translated into the underlined 11 amino acids (GITSLYKKAGF). Cleavage with TEV protease (arrow) leaves two amino acids, GT, on the amino end of the gene product.

See Figure 55 for an example of a nucleic acid molecule of interest, the chloramphenical acetyl transferase (CAT) gene, cloned into pENTR7 (Figure 16) as a blunt (amino)-XhoI (carboxy) fragment, then cloned by recombination into the His6 fusion vector pDEST2 (Figure 22).

**Option 6:** If the His6 fusion protein is insoluble, you may go on and try a GST fusion. The appropriate Destination vector is pDEST3 (Figure 23).

Option 7: If you need to make RNA probes and prefer SP6 RNA polymerase, you can make the top strand RNA with your nucleic acid molecule of interest cloned into pSPORT+ (pDEST5 (Figures 25A, 25B)), and the bottom strand RNA with the nucleic acid molecule of interest cloned into pSPORT(-) (pDEST6 (Figures 26A, 26B)). Opposing promoters for T7 RNA polymerase and SP6 RNA polymerase are also present in these clones.

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Option 8: It is often worthwhile to clone your nucleic acid molecule of interest into a variety of Destination Vectors in the same experiment. For example, if the number of colonies varies widely when the various recombination reactions are transformed into *E. coli*, this may be an indication that the nucleic acid molecule of interest is toxic in some contexts. (This problem is more clearly evident when a positive control gene is used for each Destination Vector.) Specifically, if many more colonies are obtained when the nucleic acid molecule of interest is recombined into pDEST6 than in pDEST5, there is a good chance that leakiness of the lac promoter is causing some expression of the nucleic acid molecule of interest in pSPORT "+" (which is not harmful in pDEST6 because the nucleic acid molecule of interest is in the opposite orientation).

# Example 16: Demonstration of a One-tube Transfer of a PCR Product (or Expression Clone) to Expression Clone via a Recombinational Cloning Reaction

In the BxP recombination (Entry or Gateward) reaction described herein, a DNA segment flanked by attB1 and attB2 sites in a plasmid conferring ampicillin resistance was transferred by recombination into an attP plasmid conferring kanamycin resistance, which resulted in a product molecule wherein the DNA segment was flanked by attL sites (attL1 and attL2). This product plasmid comprises an "attL Entry Clone" molecule, because it can react with a "attR Destination Vector" molecule via the LxR (Destination) reaction, resulting in the transfer of the DNA segment to a new (ampicillin resistant) vector. In the previously described examples, it was necessary to transform the BxP reaction products into E. coli, select kanamycin resistant colonies, grow those colonies in liquid culture, and prepare miniprep DNA, before reacting this DNA with a Destination Vector in an LxR reaction.

The goal of the following experiment was to eliminate the transformation and miniprep DNA steps, by adding the BxP Reaction products directly to an LxR Reaction. This is especially appropriate when the DNA segment flanked by attB sites is a PCR product instead of a plasmid, because the PCR product cannot give

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produced:

ampicillin-resistant colonies upon transformation, whereas attB plasmids (in general) carry an ampicillin resistance gene. Thus use of a PCR product flanked by attB sites in a BxP Reaction allows one to select for the ampicillin resistance encoded by the desired attB product of a subsequent LxR Reaction.

Two reactions were prepared: Reaction A, negative control, no attB PCR

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product, (8 μl) contained 50 ng pEZC7102 (attP Donor plasmid, confers kanamycin resistance) and 2 μl BxP Clonase (22 ng / μl Int protein and 8 ng/μl IHF protein) in BxP buffer (25 mM Tris HCl, pH 7.8, 70 mM KCl, 5 mM spermidine, 0.5 mM EDTA, 250 μg / ml BSA). Reaction B (24 μl) contained 150 ng pEZC7102, 6 μl BxP Clonase, and 120 ng of the attB -tet-PCR product in the same buffer as reaction A. The attB - tet - PCR product comprised the tetracycline resistance gene of plasmid pBR322, amplified with two primers containing either attB1 or attB2 sites, and having 4 Gs at their 5' ends, as described earlier.

The two reactions were incubated at 25°C for 30 minutes. Then aliquots

of these reactions were added to new components that comprised LxR Reactions or appropriate controls for the LxR Reaction. Five new reactions were thus

Reaction 1: 5 μl of reaction A was added to a 5 μl LxR Reaction containing 25 ng *Nco*I-cut pEZC8402 (the attR Destination Vector plasmid) in LxR buffer (37.5 mM Tris HCl, pH 7.7, 16.5 mM NaCl, 35 mM KCl, 5 mM spermidine, 375 μg/ml BSA), and 1 μl of GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix (total volume of 10 μl).

Reaction 2: Same as reaction 1, except 5 µl of reaction B (positive) were added instead of reaction A (negative).

**Reaction 3:** Same as reaction 2, except that the amounts of Nco-cut pEZC8402 and GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix were doubled, to 50 ng and 2  $\mu$ l, respectively.

Reaction 4: Same as reaction 2, except that 25 ng of pEZ11104 (a positive control attL Entry Clone plasmid) were added in addition to the aliquot of reaction B.

Reaction 5: Positive control LxR Reaction, containing 25 ng NcoI-cut pEZC8402, 25 ng pEZ11104, 37.5 mM Tris HCl pH 7.7, 16.5 mM NaCl, 35 mM KCl, 5 mM spermidine, 375 μg / ml BSA and 1 μl GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix in a total volume of 5 μl.

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All five reactions were incubated at 25°C for 30 minutes. Then, 1  $\mu$ l aliquots of each of the above five reactions, plus 1  $\mu$ l from the remaining volume of Reaction B, the standard BxP Reaction, were used to transform 50  $\mu$ l competent DH5 $\alpha$  *E. coli*. DNA and cells were incubated on ice for 15 min., heat shocked at 42°C for 45 sec., and 450  $\mu$ l SOC were added. Each tube was incubated with shaking at 37°C for 60 min. Aliquots of 100  $\mu$ l and 400  $\mu$ l of each transformation were plated on LB plates containing either 50  $\mu$ g/ml kanamycin or 100  $\mu$ g/ml ampicillin (see Table 2). A transformation with 10 pg of pUC19 DNA (plated on LB-amp<sub>100</sub>) served as a control on the transformation efficiency of the DH5 $\alpha$  cells. Following incubation overnight at 37°C, the number of colonies on each plate was determined.

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Results of these reactions are shown in Table 2.

Table 2\*

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Reaction No.:	1	2	3	4	5	6
	Number of Colonies					
Vol. plated:	Neg Control BxP Reaction	1X pEZC8402 and LR Clonase™	2X pEZC8402 and LR Clonase <sup>TM</sup>	LxR Reaction with Pos. Control DNA	LxR Reaction alone	BxP Reaction alone
100 µl	2	1	8	9	~1000	~1000
400 μl	5	10	35	62	>2000	>2000
Selection:	Kan	Amp	Amn	Amp	Amp	Kan

\*(Transformation with pUC 19 DNA yielded 1.4 x 10° CFU/µg DNA.)

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34 of the 43 colonies obtained from Reaction 3 were picked into 2 ml Terrific Broth with 100 μg/ml ampicillin and these cultures were grown overnight, with shaking, at 37°C. 27 of the 34 cultures gave at least moderate growth, and of these 24 were used to prepare miniprep DNA, using the standard protocol. These 24 DNAs were initially analyzed as supercoiled (SC) DNA on a 1% agarose gel to identify those with inserts and to estimate the sizes of the inserts. Fifteen of the 24 samples displayed SC DNA of the size predicted (5553 bp) if tetx7102 had correctly recombined with pEZC8402 to yield tetx8402. One of these samples contained two plasmids, one of ~5500 bp and a one of ~3500 bp. The majority of the remaining clones were approximately 4100 bp in size.

All 15 of the clones displaying SC DNA of predicted size (~5500 bp) were analyzed by two different double digests with restriction endonucleases to confirm the structure of the expected product: **tetx8402**. (See plasmid maps, Figures 57-59) In one set of digests, the DNAs were treated with Not I and Eco RI, which should cut the predicted product just outside both attB sites, releasing the tet<sup>r</sup> insert on a fragment of 1475 bp. In the second set of digests, the DNAs were digested with *Not*I and with *Nru*I. *Nru*I cleaves asymmetrically within the subcloned tet<sup>r</sup> insert, and together with *Not*I will release a fragment of 1019 bp.

Of the 15 clones analyzed by double restriction digestion, 14 revealed the predicted sizes of fragments for the expected product.

### Interpretation:

The DNA components of Reaction B, pEZC7102 and attB-tet-PCR, are shown in Figure 56. The desired product of BxP Reaction B is tetx7102, depicted in Figure 57. The LxR Reaction recombines the product of the BxP Reaction, tetx7102 (Figure 57), with the Destination Vector, pEZC8402, shown in Figure 58. The LxR Reaction with tetx7102 plus pEZC8402 is predicted to yield the desired product tetx8402, shown in Figure 59.

Reaction 2, which combined the BxP Reaction and LxR Reaction, gave few colonies beyond those of the negative control Reaction. In contrast, Reaction 3, with twice the amount of pEZC8402 (Figure 58) and LxR Clonase, yielded a

larger number of colonies. These colonies were analyzed further, by restriction digestion, to confirm the presence of expected product. Reaction 4 included a known amount of attL Entry Clone plasmid in the combined BxP-plus-LxR reaction. But reaction 4 yielded only about 1% of the colonies obtained when the same DNA was used in a LxR reaction alone, Reaction 6. This result suggests that the LxR reaction may be inhibited by components of the BxP reaction.

Restriction endonuclease analysis of the products of Reaction 3 revealed that a sizeable proportion of the colonies (14 of the 34 analyzed) contained the desired tet<sup>r</sup> subclone, tetx8402 (Figure 59).

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The above results establish the feasibility of performing first a BxP recombination reaction followed by a LxR recombination reaction -- in the same tube -- simply by adding the appropriate buffer mix, recombination proteins, and DNAs to a completed BxP reaction. This method should prove useful as a faster method to convert attB-containing PCR products into different Expression Clones, eliminating the need to isolate first the intermediate attL-PCR insert subclones, before recombining these with Destination Vectors. This may prove especially valuable for automated applications of these reactions.

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This same one-tube approach allows for the rapid transfer of nucleic acid molecules contained in attB plasmid clones into new functional vectors as well. As in the above examples, attL subclones generated in a BxP Reaction can be recombined directly with various Destination Vectors in a LxR reaction. The only additional requirement for using attB plasmids, instead of attB-containing PCR products, is that the Destination Vector(s) employed must contain a different selection marker from the one present on the attB plasmid itself and the attP vector.

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Two alternative protocols for a one-tube reaction have also proven useful and somewhat more optimal than the conditions described above.

### Alternative 1:

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Reaction buffer contained 50 mM Tris-HCl (pH 7.5), 50 mM NaCl, 0.25 mM EDTA, 2.5 mM spermidine, and 200  $\mu$ g/ml BSA. After a 16 (or 3) hour incubation of the PCR product (100 ng) + attP Donor plasmid (100 ng) +

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GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix + Destination Vector (100 ng), 2 µl of GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix (per 10 µl reaction mix) was added and the mixture was incubated an additional 6 (or 2) hours at 25°C. Stop solution was then added as above and the mixture was incubated at 37°C as above and transformed by electroporation with 1 µl directly into electrocompetent host cells. Results of this series of experiments demonstrated that longer incubation times (16 hours vs. 3 hours for the BP Reaction, 6 hours vs. 2 hours for the LR Reaction) resulted in about twice as many colonies being obtained as for the shorter incubation times. With two independent genes, 10/10 colonies having the correct cloning patterns were obtained.

### Alternative 2:

A standard BP Reaction under the reaction conditions described above for Alternative 1 was performed for 2 hours at 25 °C. Following the BP Reaction, the following components were added to the reaction mixture in a total volume of 7  $\mu$ l:

20 mM Tris-HCl, pH 7.5 100 mM NaCl 5 μg/ml Xis-His6 15% glycerol

~1000 ng of Destination Vector

The reaction mixture was then incubated for 2 hours at 25°C, and 2.5 µl of stop solution (containing 2 µg/ml proteinase K) was added and the mixture was incubated at 37°C for an additional 10 minutes. Chemically competent host cells were then transformed with 2 µl of the reaction mixture, or electrocompetent host cells (e.g., EMax DH10B cells; Life Technologies, Inc.) were electroporated with 2 µl of the reaction mixture per 25-40 µl of cells. Following transformation, mixtures were diluted with SOC, incubated at 37°C, and plated as described above on media selecting for the selection markers on the Destination Vector and the Entry clone (B x P reaction product). Analogous results to those described for Alternative 1 were obtained with these reaction conditions -- a higher level of colonies containing correctly recombined reaction products were observed.

# Example 17: Demonstration of a One-tube Transfer of a PCR Product (or Expression Clone) to Expression Clone via a Recombinational Cloning Reaction

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Single-tube transfer of PCR product DNA or Expression Clones into Expression Clones by recombinational cloning has also been accomplished using a procedure modified from that described in Example 16. This procedure is as follows:

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•Perform a standard BP (Gateward) Reaction (see Examples 9 and 10) in 20 μl volume at 25°C for 1 hour.

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•After the incubation is over, take a 10 µl aliquot from the 20 µl total volume and add 1 µl of Proteinase K (2 mg/ml) and incubate at 37°C for 10 minutes. This first aliquot can be used for transformation and gel assay of BP reaction analysis. Plate BP reaction transformation on LB plates with Kanamycin (50 ug/ml).

•Add the following reagents to the remaining 10 µl aliquot of the BP reaction:

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- 1 µl of 0.75 M NaCl
- 2 μl of destination vector (150 ng/μl)
- 4 μl of LR Clonase<sup>TM</sup> (after thawing and brief mixing)

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•Mix all reagents well and incubate at 25°C for 3 hours. Stop the reaction at the end of incubation with 1.7  $\mu$ l of Proteinase K (2 mg/ml) and incubate at 37°C for 10 minutes.

•Transform 2 µl of the completed reaction into 100 µl of competent cells.

Plate 100 µl and 400 µl on LB plates with Ampicilin (100 µg/ml).

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#### Notes:

•If your competent cells are less than 108 CFU/µg, and you are concerned about getting enough colonies, you can improve the yield several fold by incubating the

BP reaction for 6-20 hours. Electroporation also can yield better colony output than chemical transformation.

•PCR products greater than about 5-6 kb show significantly lower cloning efficiency in the BP reaction. In this case, we recommend using longer incubation times for both BP and LR steps.

•If you want to move your insert gene into several destination vectors simultaneously, then scale up the initial BP reaction volume so that you have a 10 µl aliquot for adding each destination vector.

## Example 18: Optimization of GATEWAY<sup>TM</sup> Clonase<sup>TM</sup> Enzyme Compositions

The enzyme compositions containing Int and IHF (for BP Reactions) were optimized using a standard functional recombinational cloning reaction (a BP reaction) between attB-containing plasmids and attP-containing plasmids, according to the following protocol:

### Materials and Methods:

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Substrates:

AttP - supercoiled pDONR201

AttB - linear ~ 1Kb [3H]PCR product amplified from pEZC7501

Proteins:

IntH6 -- His<sub>6</sub>-carboxy- tagged λ Integrase

IHF -- Integration Host Factor

Clonase:

50 ng/μl IntH6 and 20 ng/μl IHF, admixed in 25 mM Tris-HCl (pH 7.5), 22 mM NaCl, 5 mM EDTA, 1 mg/ml BSA, 5 mM Spermidine, and 50% glycerol.

Reaction Mixture (total volume of 40 μl):
1000 ng AttP plasmid
600 ng AttB [³H] PCR product
8 μl Clonase (400 ng IntH6, 160 ng IHF) in 25 mM Tris-HCl (pH 7.5),
22 mM NaCl, 5 mM EDTA, 1 mg/ml BSA, 5 mM Spermidine, 5 mM
DTT.

Reaction mixture was incubated for 1 hour at 25°C, 4 µl of 2 µg/µl proteinase K was added and mixture was incubated for an additional 20 minutes at 37°C. Mixture was then extracted with an equal volume of Phenol/Chloroform/ Isoamyl alcohol. The aqueous layer was then collected, and 0.1 volumes of 3 M sodium acetate and 2 volumes of cold 100% ethanol were added. Tubes were then spun in a microcentrifuge at maximum RPM for 10 minutes at room temperature. Ethanol was decanted, and pellets were rinsed with 70% ethanol and re-centrifuged as above. Ethanol was decanted, and pellets were allowed to air dry for 5-10 minutes and then dissolved in 20 µl of 33 mM Tris-Acetate (pH 7.8), 66 mM potassium acetate, 10 mM magnesium acetate, 1 mM DTT, and 1mM ATP. 2 units of exonuclease V (e.g., Plasmid Safe; EpiCentre, Inc., Madison, WI) was then added, and the mixture was incubated at 37°C for 30 minutes.

Samples were then TCA-washed by spotting 30  $\mu$ l of reaction mixture onto a Whatman GF/C filter, washing filters once with 10% TCA + 1% NaPPi for 10 minutes, three times with 5% TCA for 5 minutes each, and twice with ethanol for 5 minutes each. Filters were then dried under a heat lamp, placed into a scintillation vial, and counted on a  $\beta$  liquid scintillation counter (LSC).

The principle behind this assay is that, after exonuclease V digestion, only double-stranded circular DNA survives in an acid-insoluble form. All DNA substrates and products that have free ends are digested to an acid-soluble form and are not retained on the filters. Therefore, only the <sup>3</sup>H-labeled attB linear DNA which ends up in circular form after both inter- and intramolecular integration is complete is resistant to digestion and is recovered as acid-insoluble product. Optimal enzyme and buffer formulations in the Clonase compositions therefore are those that give the highest levels of circularized <sup>3</sup>H-labeled attB-containing

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sequences, as determined by highest cpm in the LSC. Although this assay was designed for optimization of GATEWAY<sup>TM</sup> BP Clonase<sup>TM</sup> Enzyme Mix compositions (Int + IHF), the same type of assay may be performed to optimize GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix compositions (Int + IHF + Xis), except that the reaction mixtures would comprise 1000 ng of AttR (instead of AttP) and 600 ng of AttL (instead of AttB), and 40 ng of His<sub>6</sub>-carboxy- tagged Xis (XisH6) in addition to the IntH6 and IHF.

### Example 19: Testing Functionality of Entry and Destination Vectors

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As part of assessment of the functionality of particular vectors of the invention, it is important to functionally test the ability of the vectors to recombine. This assessment can be carried out by performing a recombinational cloning reaction (as schematized in Figures 2, 4, and 5A and 5B, and as described herein and in commonly owned U.S. Application Nos. 08/486,139, filed June 7, 1995, 08/663,002, filed June 7, 1996 (now U.S. Patent No. 5,888,732), 09/005,476, filed January 12, 1998, and 09/177,387, filed October 23, 1998, the disclosures of all of which are incorporated by reference herein in their entireties), by transforming E. coli and scoring colony forming units. However, an alternative assay may also be performed to allow faster, more simple assessment of the functionality of a given Entry or Destination Vector by agarose gel electrophoresis. The following is a description of such an in vitro assay.

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### Materials and Methods:

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Plasmid templates pEZC1301 (Figure 84) and pEZC1313 (Figure 85), each containing a single wild type att site, were used for the generation of PCR products containing attL or attR sites, respectively. Plasmid templates were linearized with AlwNI, phenol extracted, ethanol precipitated and dissolved in TE to a concentration of 1 ng/µl.

### PCR primers (capital letters represent base changes from wildtype):

attL1 gggg agcct gcttttttGtacAaa gttggcatta taaaaaagca ttgc

attL2 gggg agcct gctttCttGtacAaa gttggcatta taaaaaagca ttgc

attL right tgttgccggg aagctagagt aa

attR1

gggg Acaag ttTgtaCaaaaaagc tgaacgaga aacgtaaaat

attR2

gggg Acaag ttTgtaCaaGaaagc tgaacgaga aacgtaaaat

attR right

ca gacggcatga tgaacctgaa

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PCR primers were dissolved in TE to a concentration of 500 pmol/µl. Primer mixes were prepared, consisting of attL1 + attLright primers, attL2 + attLright primers, attR1 + attRright primers, and attR2 + attRright primers, each mix containing 20 pmol/µl of each primer.

### PCR reactions:

1 μl plasmid template (1 ng)

1 μl primer pairs (20 pmoles of each)

 $3 \mu l \text{ of } H_20$ 

45 µl of Platinum PCR SuperMix® (Life Technologies, Inc.)

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Cycling conditions (performed in MJ thermocycler):

95°C/2 minutes

94°C/30 seconds

25 cycles of 58°C/30 seconds and 72°C/1.5 minutes

72°C/5 minutes

5°C/hold

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The resulting attL PCR product was 1.5 kb, and the resulting attR PCR product was 1.0 kb.

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PCR reactions were PEG/MgCl<sub>2</sub> precipitated by adding 150  $\mu$ l H<sub>2</sub>O and 100  $\mu$ l of 3x PEG/MgCl<sub>2</sub> solution followed by centrifugation. The PCR products were dissolved in 50  $\mu$ l of TE. Quantification of the PCR product was performed by gel electrophoresis of 1  $\mu$ l and was estimated to be 50-100 ng/ $\mu$ l.

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Recombination reactions of PCR products containing attL or attR sites with GATEWAY<sup>TM</sup> plasmids was performed as follows:

- 8 ul of H<sub>2</sub>0
- 2 μl of attL or attR PCR product (100-200 ng)
- 2 μl of GATEWAY<sup>TM</sup> plasmid (100 ng)
- 4 ul of 5x Destination buffer
- 4 μl of GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix

 $20 \,\mu l$  total volume (the reactions can be scaled down to a 5  $\mu l$  total volume by adjusting the volumes of the components to about ¼ of those shown above, while keeping the stoichiometries the same).

Clonase reactions were incubated at 25°C for 2 hours. 2 µl of proteinase K (2 mg/ml) was added to stop the reaction. 10 µl was then run on a 1 % agarose gel. Positive control reactions were performed by reacting attL1 PCR product (1.0 kb) with attR1 PCR product (1.5 kb) and by similarly reacting attL2 PCR product with attR2 PCR product to observe the formation of a larger (2.5 kb) recombination product. Negative controls were similarly performed by reacting attL1 PCR product with attR2 PCR product and vice versa or reactions of attL PCR product with an attL plasmid, etc.

In alternative assays, to test attB Entry vectors, plasmids containing single attP sites were used. Plasmids containing single att sites could also be used as recombination substrates in general to test all Entry and Destination vectors (*i.e.*, those containing attL, attR, attB and attP sites). This would eliminate the need to do PCR reactions.

#### Results:

Destination and Entry plasmids when reacted with appropriate att-containing PCR products formed linear recombinant molecules that could be easily visualized on an agarose gel when compared to control reactions containing no attL or attR PCR product. Thus, the functionality of Destination and Entry vectors constructed according to the invention may be determined either by carrying out the Destination or Entry recombination reactions as depicted in

Figures 2, 4, and 5A and 5B, or more rapidly by carrying out the linearization assay described in this Example.

PCR Cloning System (Life Technologies, Inc.; Rockville, MD) requires the

As described herein, the cloning of PCR products using the GATEWAY™

# Example 20: PCR Cloning Using Universal Adapter-Primers

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addition of attB sites (attB1 and attB2) to the ends of gene-specific primers used in the PCR reaction. The protocols described in the preceding Examples suggest that the user add 29 bp (25 bp containing the attB site plus four G residues) to the gene-specific primer. It would be advantageous to high volume users of the GATEWAY<sup>TM</sup> PCR Cloning System to generate attB-containing PCR product using universal attB adapter-primers in combination with shorter gene-specific primers containing a specified overlap to the adapters. The following experiments demonstrate the utility of this strategy using universal attB adapter-primers and gene-specific primers containing overlaps of various lengths from 6 bp to 18 bp. The results demonstrate that gene-specific primers with overlaps of 10 bp to 18 bp can be used successfully in PCR amplifications with universal attB adapter-primers to generate full-length PCR products. These PCR products can then be successfully cloned with high fidelity in a specified orientation using the GATEWAY<sup>TM</sup> PCR Cloning System.

#### Methods and Results:

To demonstrate that universal attB adapter-primers can be used with genespecific primers containing partial attB sites in PCR reactions to generate fulllength PCR product, a small 256 bp region of the human hemoglobin cDNA was chosen as a target so that intermediate sized products could be distinguished from full-length products by agarose gel electrophoresis.

The following oligonucleotides were used:

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B1-Hgb: GGGG ACA AGT TTG TAC AAA AAA GCA GGC T-5'-Hgb\* B2-Hgb:GGGG ACC ACT TTG TAC AAG AAA GCT GGG T-3'-Hgb\*\*

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	18B1-Hgb:	TG	TAC A	AA AAA	GCA GGC	T-5'-Hg	b
	18B2-Hgb:	TG	TAC A	AG AAA	GCT GGG	T-3'-Hg	b
	15B1-Hgb:		AC AA	A AAA (	GCA GGC	T-5'-Hgh	)
	15B2-Hgb:		AC AA	G AAA	GCT GGG	T-3'-Hgk	)
5	12B1-Hgb:		A	A AAA	GCA GGC	T-5'-Hgh	)
	12B2-Hgb:		A	G AAA	GCT GGG	T-3'-Hgh	)
	11B1-Hgb:		i	A AAA	GCA GGC	T-5'-Hgk	)
	11B2-Hgb:		(	g aaa	GCT GGG	T-3'-Hgk	5
	10B1-Hgb:			AAA G	CA GGC	r-5'-Hgb	
10	10B2-Hgb:			AAA	GCT GGG	T-3'-Hgl	C
	9B1-Hgb:			AA G	CA GGC '	r-5'-Hgb	
	9B2-Hgb:			AA G	CT GGG '	I-3'-Hgb	
	8B1-Hgb:			A G	CA GGC '	r-5'-Hgb	
	8B2-Hgb:			A G	CT GGG '	r-3'-Hgb	
15	7B1-Hgb:			G	CA GGC	r-5'-Hgb	
	7B2-Hgb:			G	CT GGG	r-3'-Hgb	
	6B1-Hgb:			C	A GGC T	-5'-Hgb	
	6B2-Hgb:			C	T GGG T	-3'-Hgb	
20	attB1 adapter: GGG	G ACA	AGT TT	G TAC	AAA AAA	GCA GGC	Τ
	no l	0 700		ייט מייז ייט	<b>776 777</b>	CCT CCC	т

Т attB2 adapter: GGGG ACC ACT TTG TAC AAG AAA GCT GGG T

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-5'-Hgb = GTC ACT AGC CTG TGG AGC AAG A
** -3'-Hgb = AGG ATG GCA GAG GGA GAC GAC A
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The aim of these experiments was to develop a simple and efficient universal adapter PCR method to generate attB containing PCR products suitable for use in the GATEWAYTM PCR Cloning System. The reaction mixtures and thermocycling conditions should be simple and efficient so that the universal adapter PCR method could be routinely applicable to any PCR product cloning application.

PCR reaction conditions were initially found that could successfully amplify predominately full-length PCR product using gene-specific primers containing 18bp and 15 bp overlap with universal attB primers. These conditions are outlined below:

-146-

10 pmoles of gene-specific primers

10 pmoles of universal attB adapter-primers

1 ng of plasmid containing the human hemoglobin cDNA.

100 ng of human leukocyte cDNA library DNA.

5 μl of 10x PLATINUM Taq HiFi® reaction buffer (Life Technologies, Inc.)

2 μl of 50 mM MgSO<sub>4</sub>

1 μl of 10 mM dNTPs

0.2 µl of PLATINUM Taq HiFi® (1.0 unit)

H<sub>2</sub>O to 50 µl total reaction volume

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## Cycling conditions:

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To assess the efficiency of the method, 2  $\mu$ l (1/25) of the 50  $\mu$ l PCR reaction was electrophoresed in a 3 % Agarose-1000 gel. With overlaps of 12 bp or less, smaller intermediate products containing one or no universal attB adapter predominated the reactions. Further optimization of PCR reaction conditions was obtained by titrating the amounts of gene-specific primers and universal attB adapter-primers. The PCR reactions were set up as outlined above except that the amounts of primers added were:

- 0, 1, 3 or 10 pmoles of gene-specific primers
- 0, 10, 30 or 100 pmoles of adapter-primers

Cycling conditions:

The use of limiting amounts of gene-specific primers (3 pmoles) and excess adapter-primers (30 pmoles) reduced the amounts of smaller intermediate products. Using these reaction conditions the overlap necessary to obtain predominately full-length PCR product was reduced to 12 bp. The amounts of gene-specific and adapter-primers was further optimized in the following PCR reactions:

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0, 1, 2 or 3 pmoles of gene-specific primers

0, 30, 40 or 50 pmoles of adapter-primers

# Cycling conditions:

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The use of 2 pmoles of gene-specific primers and 40 pmoles of adapter-primers further reduced the amounts of intermediate products and generated predominately full-length PCR products with gene-specific primers containing an 11 bp overlap. The success of the PCR reactions can be assessed in any PCR application by performing a no adapter control. The use of limiting amounts of gene-specific primers should give faint or barely visible bands when 1/25 to 1/10 of the PCR reaction is electrophoresed on a standard agarose gel. Addition of the

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universal attB adapter-primers should generate a robust PCR reaction with a much higher overall yield of product.

PCR products from reactions using the 18 bp, 15 bp, 12 bp, 11 bp and 10 bp overlap gene-specific primers were purified using the CONCERT® Rapid PCR Purification System (PCR products greater than 500 bp can be PEG precipitated). The purified PCR products were subsequently cloned into an attP containing plasmid vector using the GATEWAY<sup>TM</sup> PCR Cloning System (Life Technologies, Inc.; Rockville, MD) and transformed into *E. coli*. Colonies were selected and counted on the appropriate antibiotic media and screened by PCR for correct inserts and orientation.

Raw PCR products (unpurified) from the attB adapter PCR of a plasmid clone of part of the human beta-globin (Hgb) gene were also used in GATEWAY<sup>TM</sup> PCR Cloning System reactions. PCR products generated with the full attB B1/B2-Hgb, the 12B1/B2, 11B1/B2 and 10B1/B2 attB overlap Hgb primers were successfully cloned into the GATEWAY<sup>TM</sup> pENTR21 attP vector (Figure 49). 24 colonies from each (24 x 4 = 96 total) were tested and each was verified by PCR to contain correct inserts. The cloning efficiency expressed as cfu/ml is shown below:

Primer Used	cfu/ml
Hgb full attB	8,700
Hgb 12 bp overlap	21,000
Hgb 11 bp overlap	20,500
Hgb 10 bp overlap	13,500
GFP control	1.300

Interestingly, the overlap PCR products cloned with higher efficiency than did the full attB PCR product. Presumably, and as verified by visualization on agarose gel, the adapter PCR products were slightly cleaner than was the full attB PCR product. The differences in colony output may also reflect the proportion of PCR product molecules with intact attB sites.

Using the attB adapter PCR method, PCR primers with 12 bp attB overlaps were used to amplify cDNAs of different sizes (ranging from 1 to 4 kb)

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from a leukocyte cDNA library and from first strand cDNA prepared from HeLa total RNA. While three of the four cDNAs were able to be amplified by this method, a non-specific amplification product was also observed that under some conditions would interfere with the gene-specific amplification. This non-specific product was amplified in reactions containing the attB adapter-primers alone without any gene-specific overlap primers present. The non-specific amplification product was reduced by increasing the stringency of the PCR reaction and lowering the attB adapter PCR primer concentration.

These results indicate that the adapter-primer PCR approach described in this Example will work well for cloned genes. These results also demonstrate the development of a simple and efficient method to amplify PCR products that are compatible with the GATEWAY<sup>TM</sup> PCR Cloning System that allows the use of shorter gene-specific primers that partially overlap universal attB adapter-primers. In routine PCR cloning applications, the use of 12 bp overlaps is recommended. The methods described in this Example can thus reduce the length of gene-specific primers by up to 17 residues or more, resulting in a significant savings in oligonucleotide costs for high volume users of the GATEWAY<sup>TM</sup> PCR Cloning System. In addition, using the methods and assays described in this Example, one of ordinary skill can, using only routine experimentation, design and use analogous primer-adapters based on or containing other recombination sites or fragments thereof, such as *att*L, *att*R, *att*P, *lox*, FRT, etc.

Example 21: Mutational Analysis of the Bacteriophage Lambda attL and attR Sites: Determinants of att Site Specificity in Site-specific Recombination

To investigate the determinants of *att* site specificity, the bacteriophage lambda *att*L and *att*R sites were systematically mutagenized. As noted herein, the determinants of specificity have previously been localized to the 7 bp overlap region (TTTATAC, which is defined by the cut sites for the integrase protein and is the region where strand exchange takes place) within the 15 bp core region (GCTTTTTTATACTAA) which is identical in all four lambda *att* sites, *att*B, *att*P, *att*L and *att*R. This core region, however, has not heretofore been systematically

mutagenized and examined to define precisely which mutations produce unique changes in *att* site specificity.

Therefore, to examine the effect of att sequence on site specificity, mutant attL and attR sites were generated by PCR and tested in an in vitro site-specific recombination assay. In this way all possible single base pair changes within the 7 bp overlap region of the core att site were generated as well as five additional changes outside the 7 bp overlap but within the 15 bp core att site. Each attL PCR substrate was tested in the in vitro recombination assay with each of the attR PCR substrates.

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#### Methods

To examine both the efficiency and specificity of recombination of mutant attL and attR sites, a simple in vitro site-specific recombination assay was developed. Since the core regions of attL and attR lie near the ends of these sites, it was possible to incorporate the desired nucleotide base changes within PCR primers and generate a series of PCR products containing mutant attL and attR sites. PCR products containing attL and attR sites were used as substrates in an in vitro reaction with GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix (Life Technologies, Inc.; Rockville, MD). Recombination between a 1.5 kb attL PCR product and a 1.0 kb attR PCR product resulted in a 2.5 kb recombinant molecule that was monitored using agarose gel electrophoresis and ethidium bromide staining.

Plasmid templates pEZC1301 (Figure 84) and pEZC1313 (Figure 85), each containing a single wild type attL or attR site, respectively, were used for the generation of recombination substrates. The following list shows primers that were used in PCR reactions to generate the attL PCR products that were used as substrates in L x R Clonase reactions (capital letters represent changes from the wild-type sequence, and the underline represents the 7 bp overlap region within the 15 bp core att site; a similar set of PCR primers was used to prepare the attR PCR products containing matching mutations):

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GATEWAY<sup>TM</sup> sites (note: attL2 sequence in GATEWAY<sup>TM</sup> plasmids begins "accca" while the attL2 site in this example begins "agcct" to reflect wild-type attL outside the core region.):

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attL1: gggg agcct gcttttttGtacAaa gttggcatta taaaaaagca ttgc

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attL2: gggg agcct gctttCttGtacAaa gttggcatta taaaaaagca ttgc

# Wild-type:

attL0: gggg agcct gcttttttatactaa gttggcatta taaaaaagca ttgc

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# Single base changes from wild-type:

attLT1A: gggg agcct gctttAttatactaa gttggcatta taaaaaagca ttgc

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attLT1C: gggg agcct gctttCttatactaa gttggcatta taaaaaagca ttgc

attLT1G: gggg agcct gctttGttatactaa gttggcatta taaaaaagca ttgc

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attLT2A: gggg agcct gcttttAtatactaa gttggcatta taaaaaagca ttgc

30

attLT2C: gggg agcct gcttttCtatactaa gttggcatta taaaaaagca ttgc

attLT2G: gggg agcct gcttttGtatactaa gttggcatta taaaaaagca ttgc

	attLT3A: gggg agcct aagca ttgc	gcttt <u>ttAatac</u> taa	gttggcatta	taaaa-
5	attLT3C: gggg agcct aagca ttgc	gcttt <u>ttCatac</u> taa	gttggcatta	taaaa-
10	attLT3G: gggg agcct aagca ttgc	gcttt <u>ttGatac</u> taa	gttggcatta	taaaa-
15	attLA4C: gggg agcct aagca ttgc	gcttt <u>tttCtac</u> taa	gttggcatta	taaaa-
	attLA4G: gggg agcct aagca ttgc			
20	attLA4T: gggg agcct aagca ttgc	gcttt <u>tttTtac</u> taa	gttggcatta	taaaa-
25	attLT5A: gggg agcct aagca ttgc			
	attLT5C: gggg agcct aagca ttgc	gcttt <u>tttaCac</u> taa	gttggcatta	taaaa-
30	attLT5G: gggg agcct aagca ttgc	gcttt <u>tttaGac</u> taa	gttggcatta	taaaa-
35	attLA6C: gggg agcct aagca ttgc	gcttt <u>tttatCc</u> taa	gttggcatta	taaaa-

	attLA6G: gggg agcct gcttt <u>tttatGc</u> taa gttggcatta taaaa aagca ttgc
5 .	attLA6T: gggg agcct gcttt <u>tttatTc</u> taa gttggcatta taaaa aagca ttgc
10	attLC7A: gggg agcct gcttt <u>tttataA</u> taa gttggcatta taaaa aagca ttgc
15	attLC7G: gggg agcct gcttt <u>tttataG</u> taa gttggcatta taaaa-aagca ttgc
13	attLC7T: gggg agcct gcttt <u>tttataT</u> taa gttggcatta taaaa- aagca ttgc
20	Single base changes outside of the 7 bp overlap:  attL8: gggg agcct Acttttttatactaa gttggcatta taaaa- aagca ttgc
25	attL9: gggg agcct gcCtt <u>tttatac</u> taa gttggcatta taaaaa-agca ttgc
	attL10: gggg agcct gcttC <u>tttatac</u> taa gttggcatta taaaaa- agca ttgc
30	attL14: gggg agcct gcttt <u>tttatac</u> Caa gttggcatta taaaaa-agca ttgc

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Note: additional vectors wherein the first nine bases are gggg agcca (i.e., substituting an adenine for the thymine in the position immediately preceding the 15-bp core region), which may or may not contain the single base pair substitutions (or deletions) outlined above, can also be used in these experiments.

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Recombination reactions of attL- and attR-containing PCR products was performed as follows:

 $8 \mu l \text{ of } H_20$ 

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2 μl of attL PCR product (100 ng)

2 μl of attR PCR product (100 ng)

4 μl of 5x buffer

4 μl of GATEWAY<sup>TM</sup> LR Clonase<sup>TM</sup> Enzyme Mix

20 µl total volume

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Clonase reactions were incubated at 25°C for 2 hours.

 $2 \mu l$  of 10 X Clonase stop solution (proteinase K, 2 mg/ml) were added to stop the reaction.

10 μl were run on a 1 % agarose gel.

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#### Results

Each attL PCR substrate was tested in the in vitro recombination assay with each of the attR PCR substrates. Changes within the first three positions of the 7 bp overlap (TTTATAC) strongly altered the specificity of recombination. These mutant att sites each recombined as well as the wild-type, but only with their cognate partner mutant; they did not recombine detectably with any other att site mutant. In contrast, changes in the last four positions (TTTATAC) only partially altered specificity; these mutants recombined with their cognate mutant as well as wild-type att sites and recombined partially with all other mutant att sites except for those having mutations in the first three positions of the 7 bp

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overlap. Changes outside of the 7 bp overlap were found not to affect specificity of recombination, but some did influence the efficiency of recombination.

Based on these results, the following rules for att site specificity were determined:

- •Only changes within the 7 bp overlap affect specificity.
- •Changes within the first 3 positions strongly affect specificity.
- •Changes within the last 4 positions weakly affect specificity.

Mutations that affected the overall efficiency of the recombination reaction were also assessed by this method. In these experiments, a slightly increased (less than 2-fold) recombination efficiency with attLT1A and attLC7T substrates was observed when these substrates were reacted with their cognate attR partners. Also observed were mutations that decreased recombination efficiency (approximately 2-3 fold), including attLA6G, attL14 and attL15. These mutations presumably reflect changes that affect Int protein binding at the core att site.

The results of these experiments demonstrate that changes within the first three positions of the 7 bp overlap (TTTATAC) strongly altered the specificity of recombination (i.e., att sequences with one or more mutations in the first three thymidines would only recombine with their cognate partners and would not cross-react with any other att site mutation). In contrast, mutations in the last four positions (TTTATAC) only partially altered specificity (i.e., att sequences with one or more mutations in the last four base positions would cross-react partially with the wild-type att site and all other mutant att sites, except for those having mutations in one or more of the first three positions of the 7 bp overlap). Mutations outside of the 7 bp overlap were not found to affect specificity of recombination, but some were found to influence (i.e., to cause a decrease in) the efficiency of recombination.

# Example 22: Discovery of Att Site Mutations That Increase the Cloning Efficiency of GATEWAY<sup>TM</sup> Cloning Reactions

In experiments designed to understand the determinants of att site specificity, point mutations in the core region of attL were made. Nucleic acid molecules containing these mutated attL sequences were then reacted in an LR

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reaction with nucleic acid molecules containing the cognate attR site (i.e., an attR site containing a mutation corresponding to that in the attL site), and recombinational efficiency was determined as described above. Several mutations located in the core region of the att site were noted that either slightly increased (less than 2-fold) or decreased (between 2-4-fold) the efficiency of the recombination reaction (Table 3).

Effects of attL mutations on Recombination Reactions. Table 3.

10	Site	Sequence	Effect on
	attL0	agcctgcttttttatactaagttggcatta	Recombination
	attL5	agcctgctttAttatactaagttggcatta	slightly increased
	attL6	agcctgcttttttataTtaagttggcatta	slightly increased
15	attL13	agcctgcttttttatGctaagttggcatta	decreased
	attL14	agcctgcttttttatacCaagttggcatta	decreased
	attL15	agcctgcttttttatactaGgttggcatta	decreased
	consensus	CAACTTnnTnnnAnnAAGTTG	

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It was also noted that these mutations presumably reflected changes that either increased or decreased, respectively, the relative affinity of the integrase protein for binding the core att site. A consensus sequence for an integrase corebinding site (CAACTTNNT) has been inferred in the literature but not directly tested (see, e.g., Ross and Landy, Cell 33:261-272 (1983)). This consensus core integrase-binding sequence was established by comparing the sequences of each of the four core att sites found in attP and attB as well as the sequences of five non-att sites that resemble the core sequence and to which integrase has been shown to bind in vitro. These experiments suggest that many more att site mutations might be identified which increase the binding of integrase to the core att site and thus increase the efficiency of GATEWAYTM cloning reactions.

# Example 23: Effects of Core Region Mutations on Recombination Efficiency

To directly compare the cloning efficiency of mutations in the att site core region, single base changes were made in the attB2 site of an attB1-TET-attB2 PCR product. Nucleic acid molecules containing these mutated attB2 sequences were then reacted in a BP reaction with nucleic acid molecules containing noncognate attP sites (i.e., wildtype attP2), and recombinational efficiency was determined as described above The cloning efficiency of these mutant attB2 containing PCR products compared to standard attB1-TET-attB2 PCR product are shown in Table 4.

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Table 4. Efficiency of Recombination With Mutated attB2 Sites.

	Site	Sequence	Mutation	Cloning Efficiency
15	attB0	tcaagttagtataaaaaagcaggct		
	attB1	ggggacaagtttgtacaaaaaaagcaggct		
	attB2	ggggaccactttgtacaagaaagctgggt		100%
	attB2.1	ggggaAcactttgtacaagaaagctgggt	$C \rightarrow A$	40%
	attB2.2	ggggacAactttgtacaagaaagctgggt	C→A	131%
20	attB2.3	ggggaccCctttgtacaagaaagctgggt	A→C	4%
	attB2.4	ggggaccaAtttgtacaagaaagctgggt	C→A	11%
	attB2.5	ggggaccacGttgtacaagaaagctgggt	T→G	4%
	attB2.6	ggggaccactGtgtacaagaaagctgggt	T→G	6%
	attB2.7	ggggaccacttGgtacaagaaagctgggt	T→G	1%
25	attB2.8	ggggaccacttt <u>Ttacaag</u> aaagctgggt	G→T	0.5%

As noted above, a single base change in the attB2.2 site increased the cloning efficiency of the attB1-TET-attB2.2 PCR product to 131% compared to the attB1-TET-attB2 PCR product. Interestingly, this mutation changes the integrase core binding site of attB2 to a sequence that matches more closely the proposed consensus sequence.

Additional experiments were performed to directly compare the cloning efficiency of an attB1-TET-attB2 PCR product with a PCR product that contained attB sites containing the proposed consensus sequence (see Example 22) of an integrase core binding site. The following attB sites were used to amplify attB-TET PCR products:

attB1	ggggacaagttt <u>gtacaaa</u> aaagcaggct
attB1.6	ggggacaa $\mathbf{C}$ ttt $\underline{\mathtt{gtacaaa}}$ aaag $\mathbf{TT}$ ggct
attB2	ggggaccactttgtacaagaaagctgggt
attB2.10	ggggacAactttgtacaagaaagTtgggt

BP reactions were carried out between 300 ng (100 fmoles) of pDONR201 (Figure 49A) with 80 ng (80 fmoles) of attB-TET PCR product in a 20 µl volume with incubation for 1.5 hrs at 25 °C, creating pENTR201-TET Entry clones. A comparison of the cloning efficiencies of the above-noted attB sites in BP reactions is shown in Table 5.

Table 5. Cloning efficiency of BP Reactions.

PCR product	CFU/ml I	Fold Increase
B1-tet-B2	7,500	
B1.6-tet-B2	12,000	1.6 x
B1-tet-B2.10	20,900	2.8 x
B1.6-tet-B2.10	30,100	4.0 x

These results demonstrate that attB PCR products containing sequences that perfectly match the proposed consensus sequence for integrase core binding sites can produce Entry clones with four-fold higher efficiency than standard Gateway attB1 and attB2 PCR products.

The entry clones produced above were then transferred to pDEST20 (Figure 40A) via LR reactions (300 ng (64 fmoles) pDEST20 mixed with 50 ng (77 fmoles) of the respective pENTR201-TET Entry clone in 20 µl volume; incubated for 1 hr incubation at 25°C). The efficiencies of cloning for these reactions are compared in Table 6.

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Table 6. Cloning Efficiency of LR Reactions.

pENTR201-TET x pDEST20	CFU/ml	Fold Increase
L1-tet-L2	5,800	
L1.6-tet-L2	8,000	1.4
L1-tet-L2.10	10,000	1.7
L1.6-tet-L2.10	9,300	1.6

These results demonstrate that the mutations introduced into attB1.6 and attB2.10 that transfer with the gene into entry clones slightly increase the efficiency of LR reactions. Thus, the present invention encompasses not only mutations in attB sites that increase recombination efficiency, but also to the corresponding mutations that result in the attL sites created by the BP reaction.

To examine the increased cloning efficiency of the attB1.6-TET-attB2.10 PCR product over a range of PCR product amounts, experiments analogous to those described above were performed in which the amount of attB PCR product was titrated into the reaction mixture. The results are shown in Table 7.

Table 7. Titration of attB PCR products.

Amount of attB PCR product (ng)	PCR product	CFU/ml	Fold Increase
20	attB1-TET-attB2	3,500	6.1
	attB1.6-TET-attB2.10	21,500	
50	attB1-TET-attB2	9,800	5.0
	attB1.6-TET-attB2.10	49,000	
100	attB1-TET-attB2	18,800	2.8
	attB1.6-TET-attB2.10	53,000	
200	attB1-TET-attB2	19,000	2.5
	attB1.6-TET-attB2.10	48,000	

These results demonstrate that as much as a six-fold increase in cloning efficiency is achieved with the attB1.6-TET-attB2.10 PCR product as compared to the standard attB1-TET-attB2 PCR product at the 20 ng amount.

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# Example 24: Determination of attB Sequence Requirements for Optimum Recombination Efficiency

To examine the sequence requirements for attB and to determine which attB sites would clone with the highest efficiency from populations of degenerate attB sites, a series of experiments was performed. Degenerate PCR primers were designed which contained five bases of degeneracy in the B-arm of the attB site. These degenerate sequences would thus transfer with the gene into Entry clone in BP reactions and subsequently be transferred with the gene into expression clones in LR reactions. The populations of degenerate attB and attL sites could thus be cycled from attB to attL back and forth for any number of cycles. By altering the reaction conditions at each transfer step (for example by decreasing the reaction time and/or decreasing the concentration of DNA) the reaction can be made increasingly more stringent at each cycle and thus enrich for populations of attB and attL sites that react more efficiently.

The following degernerate PCR primers were used to amplify a 500 bp fragment from pUC18 which contained the lacZ alpha fragment (only the attB portion of each primer is shown):

GGGG ACAAGTTTGTACAAA AAAGC AGGCT attB1 attB1n16-20 GGGG ACAAGTTTGTACAAA nnnnn AGGCT attB1n21-25 GGGG ACAAGTTTGTACAAA AAAGC nnnnn GGGG ACCACTTTGTACAAG AAAGC TGGGT attB2 attB2n16-20 GGGG ACCACTTTGTACAAG nnnnn TGGGT 25 attB2n21-25 GGGG ACCACTTTGTACAAG AAAGC nnnnn

> The starting population size of degenerate att sites is 4<sup>5</sup> or 1024 molecules. Four different populations were transferred through two BP reactions and two LR reactions. Following transformation of each reaction, the population of transformants was amplified by growth in liquid media containing the appropriate selection antibiotic. DNA was prepared from the population of clones by alkaline

lysis miniprep and used in the next reaction. The results of the BP and LR cloning reactions are shown below.

BP-1, overnight reactions

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	cfu/ml	percent of control
attB1-LacZa-attB2	78,500	100 %
attB1n16-20-LacZa-attB2	1,140	1.5 %
attB1n21-25-LacZa-attB2	11,100	14 %
attB1-LacZa-attB2n16-20	710	0.9 %
attB1-LacZa-attB2n21-25	16,600	21 %

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LR-1, pENTR201-LacZa x pDEST20/EcoRI, 1hr reactions

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	cfu/ml	percent of control
attL1-LacZa-attL2	20,000	100 %
attLln16-20-LacZa-attL2	2,125	11 %
attL1n21-25-LacZa-attL2	2,920	15 %
attL1-LacZa-attL2n16-20	3,190	16 %
attL1-LacZa-attL2n21-25	1,405	7 %

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BP-2, pEXP20-LacZa/ScaI x pDONR 201, 1hr reactions

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	cfu/ml	percent of control
attB1-LacZa-attB2	48,600	100 %
attB1n16-20-LacZa-attB2	22,800	47 %
attB1n21-25-LacZa-attB2	31,500	65 %
attB1-LacZa-attB2n16-20	42,400	87 %
attB1-LacZa-attB2n21-25	34,500	71 %

LR-2, pENTR201-LacZa x pDEST6/NcoI, 1hr reactions

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	cfu/ml	percent of control
attL1-LacZa-attL2	23,000	100 %
attL1n16-20-LacZa-attL2	49,000	213 %
attL1n21-25-LacZa-attL2	18,000	80 %
attL1-LacZa-attL2n16-20	37,000	160 %
attL1-LacZa-attL2n21-25	57,000	250 %

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These results demonstrate that at each successive transfer, the cloning efficiency of the entire population of att sites increases, and that there is a great deal of flexibility in the definition of an attB site. Specific clones may be isolated from the above reactions, tested individually for recombination efficiency, and

sequenced. Such new specificities may then be compared to known examples to guide the design of new sequences with new recombination specificities. In addition, based on the enrichment and screening protocols described herein, one of ordinary skill can easily identify and use sequences in other recombination sites, e.g., other att sites, lox, FRT, etc., that result in increased specificity in the recombination reactions using nucleic acid molecules containing such sequences.

# Example 25: Design of att Site PCR Adapter-Primers

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Additional studies were performed to design gene-specific primers with 12bp of attB1 and attB2 at their 5'-ends. The optimal primer design for att-containing primers is the same as for any PCR primers: the gene-specific portion of the primers should ideally have a Tm of > 50°C at 50 mM salt (calculation of Tm is based on the formula 59.9 + 41(%GC) - 675/n).

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Primers:

12bp attB1: AA AAA GCA GGC TNN - forward gene-specific primer

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12bp attB2: A GAA AGC TGG GTN - reverse gene-specific primer

attB1 adapter primer: GGGGACAAGTTTGTACAAAAAAGCAGGCT

attB2 adapter primer: GGGGACCACTTTGTACAAGAAAGCTGGGT

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#### Protocol:

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(1) Mix 200 ng of cDNA library or 1 ng of plasmid clone DNA (alternatively, genomic DNA or RNA could be used) with 10 pmoles of gene specific primers in a 50 µl PCR reaction, using one or more polypeptides having DNA polymerase activity such as those described herein. (The addition of greater than 10 pmoles of gene-specific primers can decrease the yield of attB PCR product. In addition, if RNA is used, a standard reverse transcriptase-PCR (RT-

PCR) protocol should be followed; see, e.g., Gerard, G.F., et al., FOCUS 11:60 (1989); Myers, T.W., and Gelfand, D.H., Biochem. 30:7661 (1991); Freeman, W.N., et al., BioTechniques 20:782 (1996); and U.S. Application No. 09/064,057, filed April 22, 1998, the disclosures of all of which are incorporated herein by reference.)

## 1st PCR profile:

- (a) 95°C for 3 minutes
- (b) 10 cycles of:

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- (i) 94°C for 15 seconds
- (ii) 50°C\* for 30 seconds
- (iii) 68°C for 1 minute/kb of target amplicon
- (c) 68°C for 5 minutes
- (d) 10°C hold

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- \*The optimal annealing temperature is determined by the calculated Tm of the gene-specific part of the primer.
- (2) Transfer 10  $\mu$ l to a 40  $\mu$ l PCR reaction mix containing 35 pmoles each of the attB1 and attB2 adapter primers.

# 2<sup>nd</sup> PCR profile:

- (a) 95°C for 1 minute
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- (b) 5 cycles of:
  - (i) 94°C for 15 seconds
  - (ii) 45°C\* for 30 seconds
  - (iii) 68°C for 1 minute/kb of target amplicon
- (c) 15-20 cycles\*\* of:

- (i) 94°C for 15 seconds
- (ii) 55°C\* for 30 seconds

- (iii) 68°C for 1 minute/kb of target amplicon
- (d) 68°C for 5 minutes
- (e) 10°C hold
- \*The optimal annealing temperature is determined by the calculated Tm of the gene-specific part of the primer.
  - \*\*15 cycles is sufficient for low complexity targets.

#### Notes:

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- 1. It is useful to perform a no-adapter primer control to assess the yield of attB PCR product produced.
- Linearized template usually results in slightly greater yield of PCR product.

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# Example 26: One-Tube Recombinational Cloning Using the GATEWAY<sup>TM</sup> Cloning System

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To provide for easier and more rapid cloning using the GATEWAYTM cloning system, we have designed a protocol whereby the BP and LR reactions may be performed in a single tube (a "one-tube" protocol). The following is an example of such a one-tube protocol; in this example, an aliquot of the BP reaction is taken before adding the LR components, but the BP and LR reactions may be performed in a one-tube protocol without first taking the BP aliquot:

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Reaction Component	<u>Volume</u>
attB DNA (100-200 ng/25 µl reaction)	1-12.5 μl
attP DNA (pDONR201) 150 ng/µl	2.5 μl
5X BP Reaction Buffer	5.0 μ1
Tris-EDTA	(to 20 μl)
BP Clonase	<u>5.0 μl</u>
Total vol.	25 µl

After the above components were mixed in a single tube, the reaction mixtures were incubated for 4 hours at 25°C. A 5  $\mu$ l aliquot of reaction mixture was removed, and 0.5  $\mu$ l of 10X stop solution was added to this reaction mixture and incubated for 10 minutes at 37°C. Competent cells were then transformed with 1-2  $\mu$ l of the BP reaction per 100  $\mu$ l of cells; this transformation yielded colonies of Entry Clones for isolation of individual Entry Clones and for quantitation of the BP Reaction efficiency.

To the remaining 20  $\mu$ l of BP reaction mixture, the following components of the LR reaction were added:

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Reaction Component	Final Concentration	Volume Added
NaCl	0.75 M	1 μ1
Destination Vector	150 ng/ul	3 μ1
LR Clonase		<u>6 µl</u>
Total vol.		30 μl

After the above components were mixed in a single tube, the reaction mixtures were incubated for 2 hours at  $25^{\circ}$ C. 3  $\mu$ l of 10X stop solution was added, and the mixture was incubated for 10 minutes at  $37^{\circ}$ C. Competent cells were then transformed with 1-2  $\mu$ l of the reaction mixture per 100  $\mu$ l of cells

## Notes:

- 1. If desired, the Destination Vector can be added to the initial BP reaction.
- 2. The reactions can be scaled down by 2x, if desired.
- 3. Shorter incubation times for the BP and/or LR reactions can be used (scaled to the desired cloning efficiencies of the reaction), but a lower number of colonies will typically result.
- 4. To increase the number of colonies obtained by several fold, incubate the BP reaction for 6-20 hours and increase the LR reaction to 3 hours. Electroporation also works well with 1-2 ul of the PK-treated reaction mixture.

5. PCR products greater than about 5 kb may show significantly lower cloning efficiency in the BP reaction. In this case, we recommend using a one-tube reaction with longer incubation times (e.g., 6-18 hours) for both the BP and LR steps.

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# Example 27: Relaxation of Destination Vectors During the LR Reaction

To further optimize the LR Reaction, the composition of the LR Reaction buffer was modified from that described above and this modified buffer was used in a protocol to examine the impact of enzymatic relaxation of Destination Vectors during the LR Reaction.

LR Reactions were set up as usual (see, e.g., Example 6), except that 5X BP Reaction Buffer (see Example 5) was used for the LR Reaction. To accomplish Destination Vector relaxation during the LR Reaction, Topoisomerase I (Life Technologies, Inc., Rockville, MD; Catalogue No. 38042-016) was added to the reaction mixture at a final concentration of ~15U per µg of total DNA in the reaction (for example, for reaction mixtures with a total of 400ng DNA in the 20 µl LR Reaction, ~6units of Topoisomerase I was added). Reaction mixtures were set up as follows:

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Reaction Component	<u>Volume</u>
$ddH_2O$	6.5 µl
4X BP Reaction Buffer	5 μl
100ng single chain/linear pENTR CAT, 50 ng/µl	2 μl
300ng single chain/linear pDEST6, 150ng/ $\mu$ l	2 μl
Topoisomerase I, 15 U/ml	0.5 μl
LR Clonase	4 μΙ

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Reaction mixtures were incubated at 25°C for 1hour, and 2  $\mu$ l of 2  $\mu$ g/ $\mu$ l Proteinase K was then added and mixtures incubated for 10 minutes at 37°C to stop the LR Reaction. Competent cells were then transformed as described in the preceding examples. The results of these studies demonstrated that relaxation of

substrates in the LR reaction using Topoisomerase I resulted in a 2- to 10-fold increase in colony output compared to those LR reactions performed without including Topoisomerase I.

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Having now fully described the present invention in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious to one of ordinary skill in the art that the same can be performed by modifying or changing the invention within a wide and equivalent range of conditions, formulations and other parameters without affecting the scope of the invention or any specific embodiment thereof, and that such modifications or changes are intended to be encompassed within the scope of the appended claims.

All publications, patents and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains, and are herein incorporated by reference to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference.

	167.1		
Applicant's or agent's file reference number 0942 38PC03	International application No. the	00/05432	
OR OTHER BI	TO DEPOSITED MICROOR( OLOGICAL MATERIAL T Rule 13 <i>bis</i> )	GANISM REC'D 17 APR 2000	
A. The indications made below relate to the microorganis  31	m referred to in the description o	<del></del>	
B. IDENTIFICATION OF DEPOSIT	Further deposit	s are identified on an additional sheet 🛭	
Name of depositary institution Agricultural Research Culture Collection (NRRL) International Depository Authority			
Address of depositary institution (including postal code and could	ntry)		
1815 N. University Street Peoria, Illinois 61604 United States of America			
Date of deposit February 27, 1999	Accession Number NRRL B-30099		
C. ADDITIONAL INDICATIONS (leave blank if not app	licable) This information i	s continued on an additional sheet □	
Escherichia coli DB3.1(pAHPKan) or Escherichia coli DB3.1(pAttPKan)			
D. DESIGNATED STATES FOR WHICH INDICATI	ONS ARE MADE (if the indication	ns are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)			
The indications listed below will be submitted to the international "Accession Number of Deposit")	Bureau later (specify the general na	ture of the indications, e.g.,	
For receiving Office use only	For Internatio	nal Bureau use only	
This sheet was received with the international application	☐ This sheet was received by the I	nternational Bureau on:	
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	OR OTHER BI	TO DEPOSITED MICROORGANI OLOGICAL MATERIAL T Rule 13 <i>bis</i> )	REC'D 17 APR 2000
			WIPO PCT
A. The indications mad	e below relate to the microorganis	m referred to in the description on pag	e <del>55</del> , tine
B. IDENTIFICATION	N OF DEPOSIT	Further deposits are id	lentified on an additional sheet 🛭
Name of depositary institu Agricultural Research C International Depository	ulture Collection (NRRL)		
Address of depositary insti	tution (including postal code and cou	ntry)	
1815 N. University Stre Peoria, Illinois 61604 United States of Americ			
Date of deposit February 27, 1999		Accession Number NRRL B-30100	
C. ADDITIONAL IN	DICATIONS (leave blank if not app	olicable) This information is cont	inued on an additional sheet □
Escherichia coli DB3.1(pENTR-1A)			
D. DESIGNATED ST	ATES FOR WHICH INDICAT	IONS ARE MADE (if the indications are	not for all designated States)
E. SEPARATE FURN	VISHING OF INDICATIONS (lea	ave blank if not applicable)	
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Applicant's or agent's file reference number	0942.468PC03	International application No. tb	00/05432	
INDICATIONS RELATING TO DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL (PCT Rule 13bis) REC. 1 310				
A. The indications made	le below relate to the microorganism	n referred to in the description or		
B. IDENTIFICATION	N OF DEPOSIT	Further deposits	are identified on an additional sheet	
Name of depositary institu Agricultural Research C International Depository	Culture Collection (NRRL)			
Address of depositary insti	itution (including postal code and coun	(ראי)	·	
1815 N. University Stre Peoria, Illinois 61604 United States of Americ				
Date of deposit February 27, 1999		Accession Number NRRL B-30101		
C. ADDITIONAL INDICATIONS (leave blank if not applicable)  This information is continued on an additional sheet				
Escherichia coli DB3.1(pENTR-2B)				
D. DESIGNATED ST	ATES FOR WHICH INDICATION	ONS ARE MADE (if the indication	ns are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)				
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")				
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INDICATIONS RELA' OR OTH	TING TO DEPOSITED MICROORGANISM  ER BIOLOGICAL MATERIAL  (PCT Rule 13bis)  REC'D 1 7 APR 2000  WIPO PCT
A. The indications made below relate to the microcalle.	organism referred to in the description on page <u>55</u> , line
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet 🖾
Name of depositary institution Agricultural Research Culture Collection (NRRL) International Depository Authority	·
Address of depositary institution (including postal code of 1815 N. University Street Peoria, Illinois 61604 United States of America	and country)
Date of deposit February 27, 1999	Accession Number NRRL B-30102
C. ADDITIONAL INDICATIONS (leave blank i	if not applicable) This information is continued on an additional sheet
Escherichia coli DB3.1(pENTR-3C)	
D. DESIGNATED STATES FOR WHICH IN	DICATIONS ARE MADE (if the indications are not for all designated States)
E. SEPARATE FURNISHING OF INDICATI	IONS (leave blank if not applicable)
The indications listed below will be submitted to the interpretation of the interpretati	ternational Bureau later (specify the general nature of the indications, e.g.,
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Applicant's or agent's file reference number	0942.468PC03	International application No. tb	00/05432
	OR OTHER BI (PC	TO DEPOSITED MICROOR OLOGICAL MATERIAL T Rule 13 <i>bis</i> )	V <sub>c</sub> or
A. The indications mad	e below relate to the microorganis	m referred to in the description o	WIPO 2000
B. IDENTIFICATION	OF DEPOSIT	Further deposit	s are identified on an additional sheet 🖾
Name of depositary institut Agricultural Research C International Depository	ulture Collection (NRRL)		
Address of depositary instit	ution (including postal code and cou	ntry)	
1815 N. University Street Peoria, Illinois 61604 United States of America			·
Date of deposit February 27, 1999	·	Accession Number NRRL B-30103	
C. ADDITIONAL INI	C. ADDITIONAL INDICATIONS (leave blank if not applicable)  This information is continued on an additional sheet		
Escherichia coli DB3.1(pEZC15101)			
D. DESIGNATED STA	D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)		
E. SEPARATE FURN	E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)		
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")			
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Applicant's or agent's file reference number

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# INDICATIONS RELATING TO DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL WARD

(PC	T Rule 13bis)
A. The indications made below relate to the microorganism 9	n referred to in the description on page <u>54</u> , line
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet 🛭
Name of depositary institution Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and count	try)
1815 N. University Street Peoria, Illinois 61604 United States of America	-
Date of deposit February 27, 1999	Accession Number NRRL B-30104
C. ADDITIONAL INDICATIONS (leave blank if not appl.	icable) This information is continued on an additional sheet
D. DESIGNATED STATES FOR WHICH INDICATION	ONS ARE MADE (if the indications are not for all designated States)
E. SEPARATE FURNISHING OF INDICATIONS (leave	
The indications listed below will be submitted to the international "Accession Number of Deposit")	Bureau later (specify the general nature of the indications, e.g.,
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Applicant's or agent's file reference number 0942.468PC03	International application No. tt. 00/05432	
INDICATIONS RELATING TO DEPOSITED MICROORGARGEM '7 ARR '17 OR OTHER BIOLOGICAL MATERIAL (PCT Rule 13bis)		
A. The indications made below relate to the microorganism referred to in the description on page 54, line 9		
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet 🗵	
Name of depositary institution Agricultural Research Culture Collection (NRRL) International Depository Authority		
Address of depositary institution (including postal code and country)		
1815 N. University Street Peoria, Illinois 61604 United States of America	·	
Date of deposit February 27, 1999	Accession Number NRRL B-30105	
C. ADDITIONAL INDICATIONS (leave blank if not applicable)  This information is continued on an additional sheet		
Escherichia coli DB3.1(pEZC15103)		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)		
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)		
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")		
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Applicant's or agent's fil reference number	e 0942.408PC03	International application No. tl PCT/US 00/05432
INDICATIONS RELATING TO DEPOSITED MICROOPECANISM OR OTHER BIOLOGICAL MATERIAL (PCT Rule 13bis)		
A. The indications made below relate to the microorganism referred to in the description on page 51, line 20-21.		
B. IDENTIFICATIO	ON OF DEPOSIT	Further deposits are identified on an additional sheet 🛭
Name of depositary insti Agricultural Research International Deposito	Culture Collection (NRRL)	
Address of depositary institution (including postal code and country)		
1815 N. University Str Peoria, Illinois 61604 United States of Amer		
Date of deposit February 27, 1999		Accession Number NRRL B-30108
C. ADDITIONAL I	NDICATIONS (leave blank if not app	olicable) This information is continued on an additional sheet
Escherichia coli DB10	B(pCMVSport6)	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)		
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)		
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")		
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#### WHAT IS CLAIMED IS:

- 1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group of nucleotide sequences consisting of an attB1 nucleotide sequence as set forth in Figure 9, an attB2 nucleotide sequence as set forth in Figure 9, an attP1 nucleotide sequence as set forth in Figure 9, an attP2 nucleotide sequence as set forth in Figure 9, an attL1 nucleotide sequence as set forth in Figure 9, an attL1 nucleotide sequence as set forth in Figure 9, an attR1 nucleotide sequence as set forth in Figure 9, an attR2 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, and a mutant, fragment, or derivative thereof.
- 2. An isolated nucleic acid molecule comprising an attB1 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.
- 3. An isolated nucleic acid molecule comprising an attB2 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.
- 4. An isolated nucleic acid molecule comprising an attP1 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.
- 5. An isolated nucleic acid molecule comprising an attP2 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.
- 6. An isolated nucleic acid molecule comprising an attL1 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.

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7. An isolated nucleic acid molecule comprising an attL2 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.

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8. An isolated nucleic acid molecule comprising an attR1 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.

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9. An isolated nucleic acid molecule comprising an attR2 nucleotide sequence as set forth in Figure 9, a polynucleotide complementary thereto, or a mutant, fragment, variant or derivative thereof.

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10. The isolated nucleic acid molecule of claim 1, further comprising one or more functional or structural nucleotide sequences selected from the group consisting of one or more multiple cloning sites, one or more localization signals, one or more transcription termination sites, one or more transcriptional regulatory sequences, one or more translational signals, one or more origins of replication, one or more fusion partner peptide-encoding nucleic acid molecules, one or more protease cleavage sites, and one or more 5' polynucleotide extensions.

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11. The nucleic acid molecule of claim 10, wherein said transcriptional regulatory sequence is a promoter, an enhancer, or a repressor.

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12. The nucleic acid molecule of claim 10, wherein said fusion partner peptide-encoding nucleic acid molecule encodes glutathione S-transferase (GST), hexahistidine (His<sub>6</sub>), or thioredoxin (Trx).

The nucleic acid molecule of claim 10, wherein said 5'

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13.

14. The nucleic acid molecule of claim 13, wherein said 5' polynucleotide extension consists of four or five guanine nucleotide bases.

polynucleotide extension consists of from one to five nucleotide bases.

15. A primer nucleic acid molecule suitable for amplifying a target nucleotide sequence, comprising the isolated nucleic acid molecule of claim 1 or a portion thereof linked to a target-specific nucleotide sequence useful in amplifying said target nucleotide sequence.

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16. The primer nucleic acid molecule of claim 15, wherein said primer comprises an attB1 nucleotide sequence having the sequence shown in Figure 9 or a portion thereof, or a polynucleotide complementary to the sequence shown in Figure 9 or a portion thereof.

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17. The primer nucleic acid molecule of claim 15, wherein said primer comprises an attB2 nucleotide sequence having the sequence shown in Figure 9 or a portion thereof, or a polynucleotide complementary to the sequence shown in Figure 9 or a portion thereof.

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18. The primer nucleic acid molecule of claim 15, further comprising a 5' terminal extension of four or five guanine bases.

A vector comprising the isolated nucleic acid molecule of claim 1.

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19.

20. The vector of claim 19, wherein said vector is an Expression Vector.

21. A host cell comprising the isolated nucleic acid molecule of claim 1 or the vector of claim 19.

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22. A method of synthesizing or amplifying one or more nucleic acid molecules comprising:

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(a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity and at least a first primer comprising a template-specific sequence that is complementary to or capable of hybridizing to said templates and at least a second primer comprising all or a portion of a recombination site wherein said at least a portion of said second primer is homologous to or complementary to at least a portion of said first primer; and

(b) incubating said mixture under conditions sufficient to synthesize or amplify one or more nucleic acid molecules complementary to all or a portion of said templates and comprising one or more recombination sites or portions thereof at one or both termini of said molecules.

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23. A method of synthesizing or amplifying one or more nucleic acid molecules comprising:

- (a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity and at least a first primer comprising a template-specific sequence that is complementary to or capable of hybridizing to said templates and at least a portion of a recombination site, and at least a second primer comprising all or a portion of a recombination site wherein said at least a portion of said recombination site on said second primer is complementary to or homologous to at least a portion of said recombination site on said first primer; and
- (b) incubating said mixture under conditions sufficient to synthesize or amplify one or more nucleic acid molecules complementary to all or a portion of said templates and comprising one or more recombination sites or portions thereof at one or both termini of said molecules.
- A method of amplifying or synthesizing one or more nucleic acid molecules comprising:
  - (a) mixing one or more nucleic acid templates with at least one polypeptide having polymerase or reverse transcriptase activity

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and one or more first primers comprising at least a portion of a recombination site and a template-specific sequence that is complementary to or capable of hybridizing to said template;

- (b) incubating said mixture under conditions sufficient to synthesize or amplify one or more first nucleic acid molecules complementary to all or a portion of said templates wherein said molecules comprise at least a portion of a recombination site at one or both termini of said molecules;
- (c) mixing said molecules with one or more second primers comprising one or more recombination sites, wherein said recombination sites of said second primers are homologous to or complementary to at least a portion of said recombination sites on said first nucleic acid molecules; and
- (d) incubating said mixture under conditions sufficient to synthesize or amplify one or more second nucleic acid molecules complementary to all or a portion of said first nucleic acid molecules and which comprise one or more recombination sites at one or both termini of said molecules.
- 25. A polypeptide encoded by the isolated nucleic acid molecule of any one of claims 1-10.
- 26. An isolated nucleic acid molecule comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between said recombination site and a second att recombination site.
- 27. The isolated nucleic acid molecule of claim 26, wherein said mutation is at least one substitution mutation of at least one nucleotide in the seven basepair overlap region of said core region of said recombination site.

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- 28. The isolated nucleic acid molecule of claim 26, wherein said nucleic acid molecule comprises the sequence NNNATAC, wherein "N" refers to any nucleotide with the proviso that if one of the first three nucleotides in the consensus sequence is a T/U, then at least one of the other two of the first three nucleotides is not a T/U.
- 29. An isolated nucleic acid molecule comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising said mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with said mutated att recombination site.
- 30. The isolated nucleic acid molecule of claim 29, wherein said mutated *att* recombination site is a mutated *att*L site comprising a core region having the nucleotide sequence caacttnntnnnannaagttg, wherein "n" represents any nucleotide.
- 31. The isolated nucleic acid molecule of claim 30, wherein said mutated attL recombination site comprises a core region having a nucleotide sequence selected from agcctgctttattatactaagttggcatta (attL5) and agcctgctttttatattaagttggcatta (attL6).
- 32. The isolated nucleic acid molecule of claim 29, wherein said mutated att recombination site comprises a core region having a nucleotide sequence selected from the group consisting of ggggacaactttgtacaaaaaagttggct (attB1.6), ggggacaactttgtacaagaaagctgggt (attB2.2), and ggggacaactttgtacaagaaagttgggt (attB2.10).
- 33. A vector selected from the group consisting of pENTR1A, pENTR2B, pENTR3C, pENTR4, pENTR5, pENTR6, pENTR7, pENTR8, pENTR9, pENTR10, pENTR11, pDEST1, pDEST2, pDEST3, pDEST4,

pDEST5, pDEST6, pDEST7, pDEST8, pDEST9, pDEST10, pDEST11, pDEST12.2 (also known as pDEST12), pDEST13, pDEST14, pDEST15, pDEST16, pDEST17, pDEST18, pDEST19, pDEST20, pDEST21, pDEST22, pDEST23, pDEST24, pDEST25, pDEST26, pDEST27, pDEST28, pDEST29, pDEST30, pDEST31, pDEST32, pDEST33, pDEST34, pDONR201 (also known as pENTR21 attP vector or pAttPkan Donor Vector), pDONR202, pDONR203 (also known as pEZ15812), pDONR204, pDONR205, pDONR206 (also known as pENTR22 attP vector or pAttPgen Donor Vector), pDONR207, pMAB58, pMAB62, pMAB85 and pMAB86.

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- 34. A host cell comprising the vector of claim 33.
- 35. A polypeptide encoded by the vector of claim 33.

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36. A kit for use in synthesizing a nucleic acid molecule, said kit comprising the isolated nucleic acid molecule of any one of claims 1-10, 26 and 29.

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- 37. A kit for use in synthesizing a nucleic acid molecule, said kit comprising the primer of claim 15 or claim 18.
- 38. A kit for use in cloning a nucleic acid molecule, said kit comprising the vector of claim 19 or claim 33.

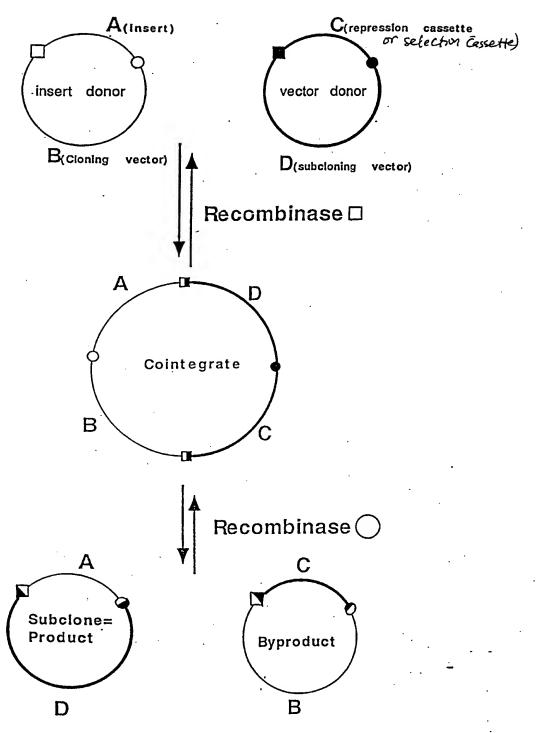
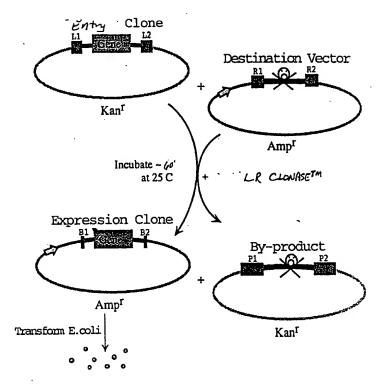
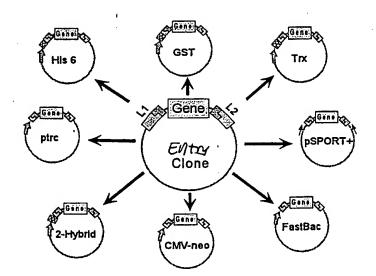


Figure 1

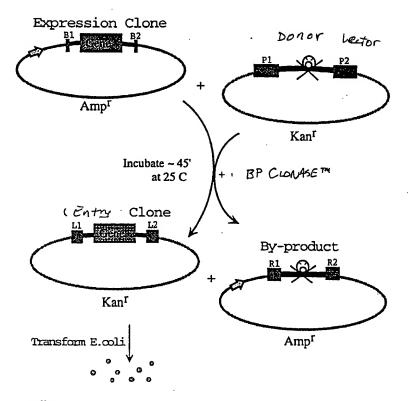


Amp<sup>r</sup> Colonies Next Day.

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Kan<sup>T</sup>Colonies Next Day

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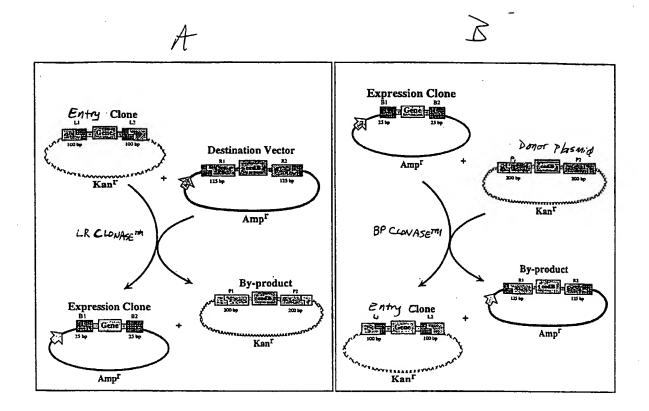
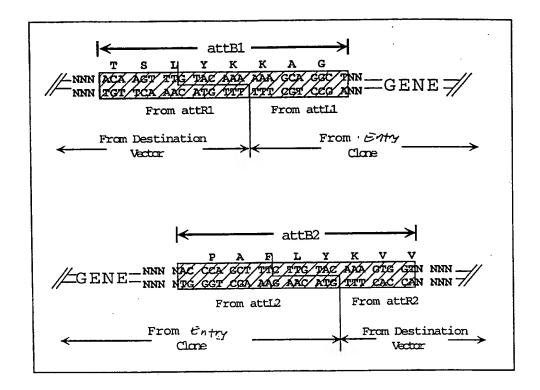
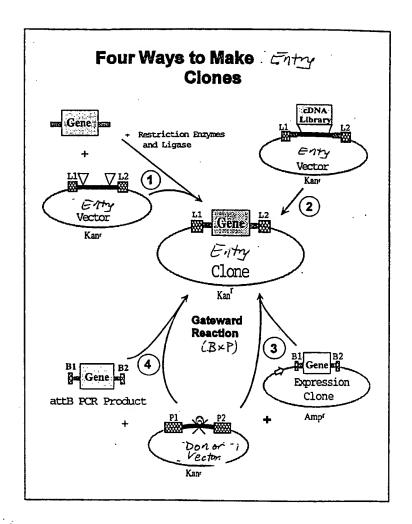


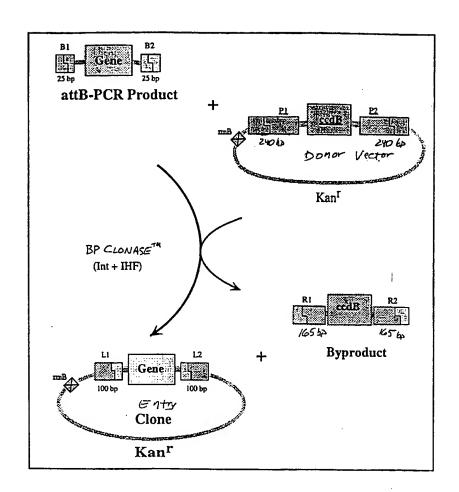
FIGURE 5



FEWRE 6



FOURT 7



FGURE 8

#### **Recombination Site Nucleotide Sequences**

- attB1: 5'-ACAAGTTTGTACAAAAAAGCAGGCT-3'
- attB2: 5'-ACCCAGCTTTCTTGTACAAAGTGGT-3'
- attP1: 5'-TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATG-TTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTA-ATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTTGTAC-AAAGTTGGCATTATAAAAAAGCATTGCTCATCAATTTGTTGCAACGAACA-GGTCACTATCAGTCAAAATAAAATCATTATTTG-3'
- attP2: 5'-CAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAACAAATTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA-3'
- <u>attR1</u>: 5'-ACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAA-TATCAATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATAC-TGTAAAACACAACATATCCAGTCACTATG-3'
- <u>attR2</u>: 5'-GCAGGTCGACCATAGTGACTGGATATGTTGTGTTTTACAGTATTAT-GTAGTCTGTTTTTATGCAAAATCTAATTTAATATATATTGATATTT-ATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTGGT-3'
- <u>attL1</u>: 5'-CAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAAC-AAATTGATAAGCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAA-GCAGGCT-3'
- <u>attL2</u>: 5'-CAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAACAA-ATTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGGGT-3'

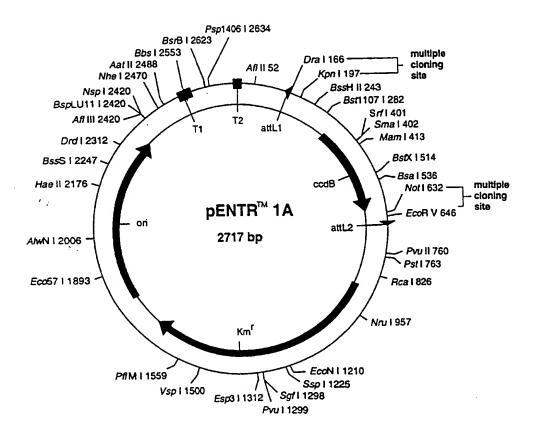
Figure 9

Figure 10A: Cloning sites of the : Entry Vector PENRIA (reading frame A)

ACT TTG TAC AAA AAA GCA GGC TTT AAA GGA ACC AAT TCA GTC GAC TGG ATC CGG TAC CGA ATT C TGA AAC ATG TTT TTT CGT CCG AAA TTT CCT TGG TTA AGT CAG CTIG ACC TAG GCT TAA G thr leu tyr lys lys ala gly phe lys gly thr asn ser val asp trp ile arg tyr arg ile

ECOR I NOT I XhO I ECOR V

GLAAT TCG CGG CCG CAC TCG AGA TAT CTA GAC CCA GCT TTC TTG TAC AAA
C TTA AGC GCC GGC GTG AGC TICT ATA GAT CTG GGT CGA AAG AAC ATG TTT



### pENTR1A 2717 bp

Base Nos.	Gene Encoded
67166	attL1
321626	ccdB
655754	attL2
8771686	KmR
17912364	ori

		GCCTTTTTGC				
		TAATGATTTT				
121		TTTTTATAAT				
181		GGATCCGGTA				
		ATTTTTGCGG				
		TGCTTCTAGA				
361	ATCGTCTGTT	TGTGGATGTA	CAGAGTGATA	TTATTGACAC	GCCCGGGCGA	CGGATAGTGA
421	TCCCCCTGGC	CAGTGCACGT	CTGCTGTCAG	ATAAAGTCTC	CCGTGAACTT	TACCCGGTGG
481	TGCATATCGG	GGATGAAAGC	TGGCGCATGA	TGACCACCGA	TATGGCCAGT	GTGCCGGTCT
541	CCGTTATCGG	GGAAGAAGTG	GCTGATCTCA	GCCACCGCGA	AAATGACATC	AAAAACGCCA
601	TTAACCTGAT	GTTCTGGGGA	ATATAGAATT	CGCGGCCGCA	CTCGAGATAT	CTAGACCCAG
661	CTTTCTTGTA	CAAAGTTGGC	ATTATAAGAA	AGCATTGCTT	ATCAATTTGT	TGCAACGAAC
721	AGGTCACTAT	CAGTCAAAAT	AAAATCATTA	TTTGCCATCC	AGCTGCAGCT	CTGGCCCGTG
781		TCTGATGTTA				
841		ACATAAACAG				
		GATTAAATTC				
		GGCAATCAGG				
		TGAAACATGG				
		GGCTGACGGA				
		CATGGTTACT				
		CTGATTCAGG				
		TTCCTGTTTG				
		CACGAATGAA				
		CTGTTGAACA				
		TCACTCATGG				
		GTATTGATGT				
		ACTGCCTCGG				
		ATAATCCTGA				
		AATTGGTTAA				
		CCGTAGAAAA				
		TGCAAACAAA				
		CTCTTTTTCC				
		TGTAGCCGTA				
1981	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG	GCTGCTGCCA	GTGGCGATAA	GTCGTGTCTT
		ACTCAAGACG				
		CACAGCCCAG				
		GAGAAAGCGC				
		TCGGAACAGG				
		CTGTCGGGTT				
		GGAGCCTATG				
		CTTTTGCTCA				
		CTAGCATGGA				
2521	CCAGGCATCA	AATAAAACGA	AAGGCTCAGT	CGGAAGACTG	GGCCTTTCGT	արդ դ. Հ.
		GAACGCTCTC				
		GCCCGGAGGG				
	CTAAGCAGAA					HOSCHICHMA

FIGURE 10B

## Figure UA: Cloning Sites of the Entry Vector pENTR2B (reading frame B)

Int	attL:	ı			E	EheI		3	(mn I		Sall		Ban	nHI	
TTG TA AAC AT	C AAA G TTT	AAA TTT	GCA CGT	GGC CCG	TGG ACC	CGC GCG	CGG GCC	AAC TTG	CAA	TTC AAG	ag <u>t</u> TCA	CGA GCT	CTG GAC	GAT CTA	CCG GGC
Leu Ty	r Lys	Lys	Ala	Gly	Trp	W Arg	Arg	Asn	Gln	Phe	Ser	Arg	Leu	Asp	Pro

KpnI EcoRI	EcoRI	NotI		EcoRV XbaI
GTA dCG AAT TC- CAT GGC TTA AG Val Pro Asn	ccdBG AAT C TTA	TCG CGG CCG AGC GCC GGC V Ser Arg Pro	CAC TCG GTG AGC His Ser	AGA TAT CTA GAC CCA TCT ATA GAT CTG GGT  Arg Tyr Leu Asp Pro

Int attL2

GCT TTC TTG TAC AAA G
CGA AAG AAC ATG TTT C

Ala Phe Leu Tyr Lys

# 13/240

### pENTR2B 2718 bp

Gene Encoded
attL1
ccdB
attL2
KmR
ori

1	CTGACGGATG	GCCTTTTTGC	GTTTCTACAA	ACTCTTCCTG	TTAGTTAGTT	ACTTAAGCTC
61	GGGCCCCAAA	TAATGATTTT	ATTTTGACTG	ATAGTGACCT	GTTCGTTGCA	ACAAATTGAT
121	AAGCAATGCT	TTTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTGGCG	CCGGAACCAA
181	TTCAGTCGAC	TGGATCCGGT	ACCGAATTCG	CTTACTAAAA	GCCAGATAAC	AGTATGCGTA
241	TTTGCGCGCT	GATTTTTGCG	GTATAAGAAT	ATATACTGAT	ATGTATACCC	GAAGTATGTC
301	AAAAAGAGGT	GTGCTTCTAG	AATGCAGTTT	AAGGTTTACA	CÇTATAAAAG	AGAGAGCCGT
361	TATCGTCTGT	TTGTGGATGT	ACAGAGTGAT	ATTATTGACA	CGCCCGGGCG	ACGGATGGTG
421	ATCCCCCTGG	CCAGTGCACG	TCTGCTGTCA	GATAAAGTCT	CCCGTGAACT	TTACCCGGTG
481	GTGCATATCG	GGGATGAAAG	CTGGCGCATG	ATGACCACCG	ATATGGCCAG	TGTGCCGGTC
541	TCCGTTATCG	GGGAAGAAGT	GGCTGATCTC	AGCCACCGCG	AAAATGACAT	CAAAAACGCC
601	ATTAACCTGA	TGTTCTGGGG	AATATAGAAT	TCGCGGCCGC	ACTCGAGATA	TCTAGACCCA
661	GCTTTCTTGT	ACAAAGTTGG	CATTATAAGA	AAGCATTGCT	TATCAATTTG	TTGCAACGAA
721	CAGGTCACTA	TCAGTCAAAA	TAAAATCATT	ATTTGCCATC	CAGCTGCAGC	TCTGGCCCGT
781	GTCTCAAAAT	CTCTGATGTT	ACATTGCACA	AGATAAAAAT	ATATCATCAT	GAACAATAAA
841	ACTGTCTGCT	TACATAAACA	GTAATACAAG	GGGTGTTATG	AGCCATATTC	AACGGGAAAC
901	GTCGAGGCCG	CGATTAAATT	CCAACATGGA	TGCTGATTTA	TATGGGTATA	AATGGGCTCG
961	CGATAATGTC	GGGCAATCAG	GTGCGACAAT	CTATCGCTTG	TATGGGAAGC	CCGATGCGCC
1021	AGAGTTGTTT	CTGAAACATG	GCAAAGGTAG	CGTTGCCAAT	GATGTTACAG	ATGAGATGGT
1081	CAGACTAAAC	TGGCTGACGG	AATTTATGCC	TCTTCCGACC	ATCAAGCATT	TTATCCGTAC
1141	TCCTGATGAT	GCATGGTTAC	TCACCACTGC	GATCCCCGGA	AAAACAGCAT	TCCAGGTATT
1201	AGAAGAATAT	CCTGATTCAG	GTGAAAATAT	TGTTGATGCG	CTGGCAGTGT	TCCTGCGCCG
1261	GTTGCATTCG	ATTCCTGTTT	GTAATTGTCC	TTTTAACAGC	GATCGCGTAT	TTCGTCTCGC
1321	TCAGGCGCAA	TCACGAATGA	ATAACGGTTT	GGTTGATGCG	AGTGATTTTG	ATGACGAGCG
1381	TAATGGCTGG	CCTGTTGAAC	AAGTCTGGAA	AGAAATGCAT	AAACTTTTGC	CATTCTCACC
	GGATTCAGTC					
1501	ATTAATAGGT	TGTATTGATG	TTGGACGAGT	CGGAATCGCA	GACCGATACC	AGGATCTTGC
1561	CATCCTATGG	AACTGCCTCG	GTGAGTTTTC	TCCTTCATTA	CAGAAACGGC	TTTTTCAAAA
	ATATGGTATT					
	TTTCTAATCA					
	AGCGTCAGAC					
	AATCTGCTGC					
1861	AGAGCTACCA	ACTCTTTTTC	CGAAGGTAAC	TGGCTTCAGC	AGAGCGCAGA	TACCAAATAC
	TGTTCTTCTA					
	ATACCTCGCT					
	TACCGGGTTG					
	GGGTTCGTGC					
	GCGTGAGCTA					
	AAGCGGCAGG					
2281	TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	TGTGATGCTC
	GTCAGGGGGG					
	CTTTTGCTGG					
	CCGTATTACC					
	GCCAGGCATC					
	TGTTTGTCGG					
	GTGAAGCAAC		GTGGCGGGCA	GGACGCCCGC	CATAAACTGC	CAGGCATCAA
2701	ACTAAGCAGA	AGGCCATC				

## Figure [2A: Cloning Sites of the Entry Vector pENTR3C (reading frame C)

Int	attL:	L		Dra		Xmn.	t	Sa	alI	I	BamH]	E	
TTG TA AAC AT				•		•				•		•	•

KpnI EcoRI PvuI EcoRI NotI XhoI EcoRV XbaI

Acc GAA TTC GAT CGC-- ccdB --G AAT TCG CGG CCG CAC TCG AGA TAT CTA
TGG CTT AAG CTA GCG

Thr Glu Phe Asn Ser Arg Pro His Ser Arg Tyr Leu

attL2 Int

GAC CCA GCT TTC TTG TAC AAA G CTG GGT CGA AAG AAC ATG TTT C

Asp Pro Ala Phe Leu Tyr Lys

### pENTR3C 2723 bp

Location (Base Nos.)	Gene Encoded
67166	attL1
327632	ccdB
661760	attL2
8831692	KmR
17972370	ori

		GCCTTTTTGC				
		TAATGATTTT				
121	AAGCAATGCT	TTTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTCTTT	AAAGGAACCA
181	ATTCAGTCGA	CTGGATCCGG	TACCGAATTC	GATCGCTTAC	TAAAAGCCAG	ATAACAGTAT
241	GCGTATTTGC	GCGCTGATTT	TTGCGGTATA	AGAATATATA	CTGATATGTA	TACCCGAAGT
		GAGGTGTGCT				
		TCTGTTTGTG				
421	TGGTGATCCC	CCTGGCCAGT	GCACGTCTGC	TGTCAGATAA	AGTCTCCCGT	GAACTTTACC
481	CGGTGGTGCA	TATCGGGGAT	GAAAGCTGGC	GCATGATGAC	CACCGATATG	GCCAGTGTGC
		TATCGGGGAA				
		CCTGATGTTC				
		CTTGTACAAA				
		CACTATCAGT				
		AAAATCTCTG				
		CTGCTTACAT				
		GGCCGCGATT				
		ATGTCGGGCA				
1021	GCGCCAGAGT	TGTTTCTGAA	ACATGGCAAA	GGTAGCGTTG	CCAATGATGT	TACAGATGAG
		TAAACTGGCT				
		ATGATGCATG				
		AATATCCTGA				
1261	CGCCGGTTGC	ATTCGATTCC	TGTTTGTAAT	TGTCCTTTTA	ACAGCGATCG	CGTATTTCGT
1321	CTCGCTCAGG	CGCAATCACG	AATGAATAAC	GGTTTGGTTG	ATGCGAGTGA	TTTTGATGAC
		GCTGGCCTGT				
1441	TCACCGGATT	CAGTCGTCAC	TCATGGTGAT	TTCTCACTTG	ATAACCTTAT	TTTTGACGAG
		TAGGTTGTAT				
1561	CTTGCCATCC	TATGGAACTG	CCTCGGTGAG	TTTTCTCCTT	CATTACAGAA	ACGGCTTTTT
1621	CAAAAATATG	GTATTGATAA	TCCTGATATG	AATAAATTGC	AGTTTCATTT	GATGCTCGAT
1681	GAGTTTTTCT	AATCAGAATT	GGTTAATTGG	TTGTAACATT	ATTCAGATTG	GGCCCCGTTC
1741	CACTGAGCGT	CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTCTG
		GCTGCTTGCA				
		TACCAACTCT				
		TTCTAGTGTA				
		TCGCTCTGCT				
2041	TGTCTTACCG	GGTTGGACTC	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA
.2101	ACGGGGGGTT	CGTGCACACA	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC
						GGACAGGTAT
						GGGAAACGCC
2281	TGGTATCTTT	TATAGTCCTGT	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA
						TTTACGGTTC
						TGATTCTGTG
	-					CGAGAGTAGG
						TTTCGTTTTA
						GCGGATTTGA
						ACTGCCAGGC
		A GCAGAAGGCC		. Journoone		
2101	. WICHWICIM	. CCACAAGGCC				

### Figure 13A: Cloning Sites of the Entry Vector pENTR4 =

Int attL1	NcoI	Kozak XmnI	SalI	BamHI
TTG TAC AAA AAA AAC ATG TTT TTT	GCA GGC TCC ACC ATC	GGA ACC AAT	TCA GTC GAC	TGG ATC CGG
Leu Tyr Lys Lys	Ala Gly Ser Thr Met	V V Gly Thr Asn	Ser Val Asp	Trp Ile Arg

Int attL2

TTC TTG TAC AAA G
AAG AAC ATG TTT C

Phe Leu Tyr Lys

#### pENTR4 2720 bp

Location (Base Nos.)	Gene Encoded
67166	attLl
324629	ccdB
658757	attL2
8801689	KmR
17942367	ori

1 CTGACGGATG GCCTTTTTGC GTTTCTACAA ACTCTTCCTG TTAGTTAGTT ACTTAAGCTC 61 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT 121 AAGCAATGCT TTTTTATAAT GCCAACTTTG TACAAAAAAG CAGGCTCCAC CATGGGAACC 181 AATTCAGTCG ACTGGATCCG GTACCGAATT CGCTTACTAA AAGCCAGATA ACAGTATGCG 241 TATTTGCGCG CTGATTTTTG CGGTATAAGA ATATATACTG ATATGTATAC CCGAAGTATG 301 TCAAAAAGAG GTGTGCTTCT AGAATGCAGT TTAAGGTTTA CACCTATAAA AGAGAGAGCC 361 GTTATCGTCT GTTTGTGGAT GTACAGAGTG ATATTATTGA CACGCCCGGG CGACGGATGG 421 TGATCCCCCT GGCCAGTGCA CGTCTGCTGT CAGATAAAGT CTCCCGTGAA CTTTACCCGG 481 TGGTGCATAT CGGGGATGAA AGCTGGCGCA TGATGACCAC CGATATGGCC AGTGTGCCGG 541 TCTCCGTTAT CGGGGAAGAA GTGGCTGATC TCAGCCACCG CGAAAATGAC ATCAAAAACG 601 CCATTAACCT GATGTTCTGG GGAATATAGA ATTCGCGGCC GCACTCGAGA TATCTAGACC 661 CAGCTTTCTT GTACAAAGTT GGCATTATAA GAAAGCATTG CTTATCAATT TGTTGCAACG 721 AACAGGTCAC TATCAGTCAA AATAAAATCA TTATTTGCCA TCCAGCTGCA GCTCTGGCCC 781 GTGTCTCAAA ATCTCTGATG TTACATTGCA CAAGATAAAA ATATATCATC ATGAACAATA 841 AAACTGTCTG CTTACATAAA CAGTAATACA AGGGGTGTTA TGAGCCATAT TCAACGGGAA 901 ACGTCGAGGC CGCGATTAAA TTCCAACATG GATGCTGATT TATATGGGTA TAAATGGGCT 961 CGCGATAATG TCGGGCAATC AGGTGCGACA ATCTATCGCT TGTATGGGAA GCCCGATGCG 1081 GTCAGACTAA ACTGGCTGAC GGAATTTATG CCTCTTCCGA CCATCAAGCA TTTTATCCGT 1141 ACTCCTGGTG ATGCATGGTT ACTCACCACT GCGATCCCCG GAAAAACAGC ATTCCAGGTA 1201 TTAGAAGAAT ATCCTGATTC AGGTGAAAAT ATTGTTGATG CGCTGGCAGT GTTCCTGCGC 1261 CGGTTGCATT CGATTCCTGT TTGTAATTGT CCTTTTAACA GCGATCGCGT ATTTCGTCTC 1321 GCTCAGGCGC AATCACGAAT GAATAACGGT TTGGTTGATG CGAGTGATTT TGATGACGAG 1381 CGTAATGGCT GGCCTGTTGA ACAAGTCTGG AAAGAAATGC ATAAACTTTT GCCATTCTCA 1441 CCGGATTCAG TCGTCACTCA TGGTGATTTC TCACTTGATA ACCTTATTTT TGACGAGGGG 1501 AAATTAATAG GTTGTATTGA TGTTGGACGA GTCGGAATCG CAGACCGATA CCAGGATCTT 1561 GCCATCCTAT GGAACTGCCT CGGTGAGTTT TCTCCTTCAT TACAGAAACG GCTTTTTCAA 1621 AAATATGGTA TTGATAATCC TGATATGAAT AAATTGCAGT TTCATTTGAT GCTCGATGAG 1681 TTTTTCTAAT CAGAATTGGT TAATTGGTTG TAACATTATT CAGATTGGGC CCCGTTCCAC 1741 TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC 1801 GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT 1861 CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT 1921 ACTGTTCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT 1981 ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT 2041 CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG 2101 GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA 2161 CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG 2221 GTAAGCGGCA GGGTCGGAAC AGGAGGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG 2281 TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC 2341 TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG 2401 GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT 2461 AACCGTATTA CCGCTAGCAT GGATCTCGGG GACGTCTAAC TACTAAGCGA GAGTAGGGAA 2521 CTGCCAGGCA TCAAATAAAA CGAAAGGCTC AGTCGGAAGA CTGGGCCTTT CGTTTTATCT 2581 GTTGTTTGTC GGTGAACGCT CTCCTGAGTA GGACAAATCC GCCGGGAGCG GATTTGAACG 2641 TTGTGAAGCA ACGGCCCGGA GGGTGGCGGG CAGGACGCCC GCCATAAACT GCCAGGCATC 2701 AAACTAAGCA GAAGGCCATC

Figure 14. Cloning sites of the Entry Vector PENTES

Int att 1 Me I Ka Xun I Sil I For tog tac and and god god ott cat atg god leto and ton god for and tac cot tog the age cag Leu Tur Lys Lys Ma Gly Pie His Met Gly The Asn Ser Val

gac top atc con tac con att coc --- Death --- and att coc ctg acc tag occ atg get taa geg --- (ccdB)--- tet taa geg.

Asp Trp Lie Arg Tyr Arg De

Mut I Mul Ectric Ma Int att 12

ggc cgc act cga gat atc tag acc cag ctt tcz zgr aca adg --ccg gcg tga gct cta tag atc tgg gtc gaa aga aca tgt ttz ---

#### pENTR5 2720 bp

Location (Base Nos.)	Gene Encoded
67166	attLl
324629	ccdB
658757	attL2
8801689	KmR
17942367	ori

1	CTGACGGATG	GCCTTTTTGC	GTTTCTACAA	ACTCTTCCTG	TTAGTTAGTT	ACTTAAGCTC
61	GGGCCCCAAA	TAATGATTTT	ATTTTGACTG	ATAGTGACCT	GTTCGTTGCA	ACAAATTGAT
121	AAGCAATGCT	TTTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTTTCA	TATGGGAACC
181	AATTCAGTCG	ACTGGATCCG	GTACCGAATT	CGCTTACTAA	AAGCCAGATA	ACAGTATGCG
241	TATTTGCGCG	CTGATTTTTG	CGGTATAAGA	ATATATACTG	ATATGTATAC	CCGAAGTATG
301	TCAAAAAGAG	GTGTGCTTCT	AGAATGCAGT	TTAAGGTTTA	CACCTATAAA	AGAGAGAGCC
361	GTTATCGTCT	GTTTGTGGAT	GTACAGAGTG	ATATTATTGA	CACGCCCGGG	CGACGGATGG
	TGATCCCCCT					
481	TGGTGCATAT	CGGGGATGAA	AGCTGGCGCA	TGATGACCAC	CGATATGGCC	AGTGTGCCGG
541	TCTCCGTTAT	CGGGGAAGAA	GTGGCTGATC	TCAGCCACCG	CGAAAATGAC	ATCAAAAACG
601	CCATTAACCT	GATGTTCTGG	GGAATATAGA	ATTCGCGGCC	GCACTCGAGA	TATCTAGACC
661	CAGCTTTCTT	GTACAAAGTT	GGCATTATAA	GAAAGCATTG	CTTATCAATT	TGTTGCAACG
	AACAGGTCAC					
781	GTGTCTCAAA	ATCTCTGATG	TTACATTGCA	CAAGATAAAA	ATATATCATC	ATGAACAATA
	AAACTGTCTG					
901	ACGTCGAGGC	CGCGATTAAA	TTCCAACATG	GATGCTGATT	${\tt TATATGGGTA}$	TAAATGGGCT
	CGCGATAATG					
	CCAGAGTTGT					
	GTCAGACTAA					
	ACTCCTGATG					
	TTAGAAGAAT					
	CGGTTGCATT					
	GCTCAGGCGC					
	CGTAATGGCT					
	CCGGATTCAG					
	AAATTAATAG					
	GCCATCCTAT					
	AAATATGGTA					
	TTTTTCTAAT					
1741	TGAGCGTCAG	ACCCCGTAGA	AAAGATCAAA	GGATCTTCTT	GAGATCCTTT	TTTTCTGCGC
1801	GTAATCTGCT	GCTTGCAAAC	AAAAAAACCA	CCGCTACCAG	CGGTGGTTTG	TTTGCCGGAT
	CAAGAGCTAC					
	ACTGTTCTTC					
	ACATACCTCG					
2041	CTTACCGGGT	TGGACTCAAG	ACGATAGTTA	CCGGATAAGG	CGCAGCGGTC	GGGCTGAACG
	GGGGGTTCGT					
2161	CAGCGTGAGC	TATGAGAAAG	CGCCACGCTT	CCCGAAGGGA	GAAAGGCGGA	CAGGTATCCG
	GTAAGCGGCA					
2281	TATCTTTATA	GTCCTGTCGG	GTTTCGCCAC	CTCTGACTTG	AGCGTCGATT	TTTGTGATGC
	TCGTCAGGGG					
	GCCTTTTGCT					
	AACCGTATTA					
	CTGCCAGGCA					
	GTTGTTTGTC					
2641	TTGTGAAGCA	ACGGCCCGGA	GGGTGGCGGG	CAGGACGCCC	GCCATAAACT	GCCAGGCATC
2701	AAACTAAGCA	GAAGGCCATC				

FIGURE 14B

Figure 1 7. Cloning sites of the Entry Vector PEUR 6

BunHI KonI EccRI EccRI

gac top atc cog tac cog att coc --- Death --- aga att coc

cog acc tag occ atg oct taa gog --- (cod8) --- tot taa gog

Ase Trp Ite Ary Tyr Ary The

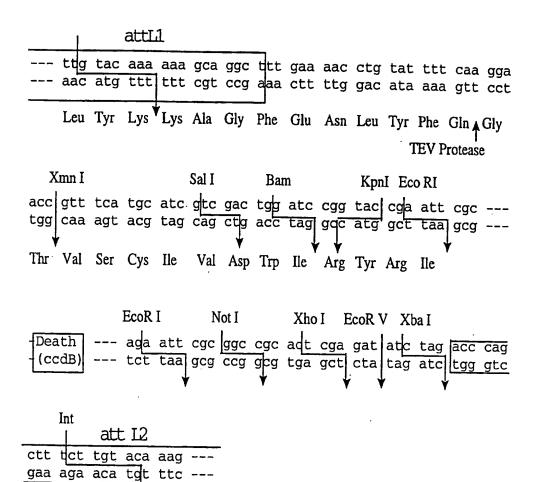
### pENTR6 2717 bp

Location (Base Nos.)	Gene Encoded
67166	attL1
321626	ccdB
655754	attL2
8771686	KmR
17912364	ori

1	CTGACGGATG	GCCTTTTTGC	GTTTCTACAA	ACTCTTCCTG	TTAGTTAGTT	ACTTAAGCTC
61	GGGCCCCAAA	TAATGATTTT	ATTTTGACTG	ATAGTGACCT	GTTCGTTGCA	ACAAATTGAT
121	AAGCAATGCT	TTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTGCAT	GCGAACCAAT
181	TCAGTCGACT	GGATCCGGTA	CCGAATTCGC	TTACTAAAAG	CCAGATAACA	GTATGCGTAT
241	TTGCGCGCTG					
301	AAAAGAGGTG					
361	ATCGTCTGTT					
421					CCGTGAACTT	
481	TGCATATCGG					
541					AAATGACATC	
601	TTAACCTGAT	GTTCTGGGGA	ATATAGAATT	CGCGGCCGCA	CTCGAGATAT	CTAGACCCAG
661	CTTTCTTGTA	CAAAGTTGGC	ATTATAAGAA	AGCATTGCTT	ATCAATTTGT	TGCAACGAAC
721	AGGTCACTAT					
781						
841	CTGTCTGCTT					
901	TCGAGGCCGC					
	GATAATGTCG					
	GAGTTGTTTC					
	AGACTAAACT					
	CCTGATGATG					
	GAAGAATATC					
1261	TTGCATTCGA	TTCCTGTTTG	TAATTGTCCT	TTTAACAGCG	ATCGCGTATT	TCGTCTCGCT
	CAGGCGCAAT					
1381	AATGGCTGGC	CTGTTGAACA	AGTCTGGAAA	GAAATGCATA	AACTTTTGCC	ATTCTCACCG
	GATTCAGTCG					
1501	TTAATAGGTT	GTATTGATGT	TGGACGAGTC	GGAATCGCAG	ACCGATACCA	GGATCTTGCC
1561	ATCCTATGGA					
1621					ATTTGATGCT	
	TTCTAATCAG					GTTCCACTGA
	GCGTCAGACC					TCTGCGCGTA
	ATCTGCTGCT					
1861	GAGCTACCAA					
1921					ACTCTGTAGC	
	TACCTCGCTC					
2041	ACCGGGTTGG					
2101					CCGAACTGAG	
	CGTGAGCTAT					
	AGCGGCAGGG					
	CTTTATAGTC					
2341					CCTTTTTACG	GTTCCTGGCC
2401		CTTTTGCTCA				TGTGGATAAC
2461	CGTATTACCG					
2521					GGCCTTTCGT	
2581	GTTTGTCGGT					
2641			TGGCGGGCAG	GACGCCCGCC	ATAAACTGCC	AGGCATCAAA
2701	CTAAGCAGAA	GGCCATC				

FIGURE 15B

Figure 16A: Cloning sites of the Entry Vector PENTRI



#### pENTR7 2738 bp

Location (Base Nos.)	Gene Encoded
67166	attLl
342647	ccdB
676775	attL2
8981707	KmR
18122385	ori

1 CTGACGGATG GCCTTTTTGC GTTTCTACAA ACTCTTCCTG TTAGTTAGTT ACTTAAGCTC 61 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT 121 AAGCAATGCT TTTTTATAAT GCCAACTTTG TACAAAAAAG CAGGCTTTGA AAACCTGTAT 181 TTTCAAGGAA CCGTTTCATG CATCGTCGAC TGGATCCGGT ACCGAATTCG CTTACTAAAA 241 GCCAGATAAC AGTATGCGTA TTTGCGCGCT GATTTTTGCG GTATAAGAAT ATATACTGAT 301 ATGTATACCC GAAGTATGTC AAAAAGAGGT GTGCTTCTAG AATGCAGTTT AAGGTTTACA 361 CCTATAAAAG AGAGAGCCGT TATCGTCTGT TTGTGGATGT ACAGAGTGAT ATTATTGACA 421 CGCCCGGGCG ACGGATAGTG ATCCCCCTGG CCAGTGCACG TCTGCTGTCA GATAAAGTCT 481 CCCGTGAACT TTACCCGGTG GTGCATATCG GGGATGAAAG CTGGCGCATG ATGACCACCG 541 ATATGGCCAG TGTGCCGGTC TCCGTTATCG GGGAAGAAGT GGCTGATCTC AGCCACCGCG 601 AAAATGACAT CAAAAACGCC ATTAACCTGA TGTTCTGGGG AATATAGAAT TCGCGGCCGC 661 ACTCGAGATA TCTAGACCCA GCTTTCTTGT ACAAAGTTGG CATTATAAGA AAGCATTGCT 721 TATCAATTG TTGCAACGAA CAGGTCACTA TCAGTCAAAA TAAAATCATT ATTTGCCATC 781 CAGCTGCAGC TCTGGCCCGT GTCTCAAAAT CTCTGATGTT ACATTGCACA AGATAAAAAT 841 ATATCATCAT GAACAATAAA ACTGTCTGCT TACATAAACA GTAATACAAG GGGTGTTATG 901 AGCCATATTC AACGGGAAAC GTCGAGGCCG CGATTAAATT CCAACATGGA TGCTGATTTA 961 TATGGGTATA AATGGGCTCG CGATAATGTC GGGCAATCAG GTGCGACAAT CTATCGCTTG 1021 TATGGGAAGC CCGATGCGCC AGAGTTGTTT CTGAAACATG GCAAAGGTAG CGTTGCCAAT 1081 GATGTTACAG ATGAGATGGT CAGACTAAAC TGGCTGACGG AATTTATGCC TCTTCCGACC 1141 ATCAAGCATT TTATCCGTAC TCCTGATGAT GCATGGTTAC TCACCACTGC GATCCCCGGA 1201 AAAACAGCAT TCCAGGTATT AGAAGAATAT CCTGATTCAG GTGAAAATAT TGTTGATGCG 1261 CTGGCAGTGT TCCTGCGCCG GTTGCATTCG ATTCCTGTTT GTAATTGTCC TTTTAACAGC 1321 GATCGCGTAT TTCGTCTCGC TCAGGCGCAA TCACGAATGA ATAACGGTTT GGTTGATGCG 1381 AGTGATTTTG ATGACGAGCG TAATGGCTGG CCTGTTGAAC AAGTCTGGAA AGAAATGCAT 1441 AAACTTTTGC CATTCTCACC GGATTCAGTC GTCACTCATG GTGATTTCTC ACTTGATAAC 1501 CTTATTTTTG ACGAGGGGAA ATTAATAGGT TGTATTGATG TTGGACGAGT CGGAATCGCA 1561 GACCGATACC AGGATCTTGC CATCCTATGG AACTGCCTCG GTGAGTTTTC TCCTTCATTA 1621 CAGAAACGGC TTTTTCAAAA ATATGGTATT GATAATCCTG ATATGAATAA ATTGCAGTTT 1681 CATTTGATGC TCGATGAGTT TTTCTAATCA GAATTGGTTA ATTGGTTGTA ACATTATTCA 1741 GATTGGGCCC CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA 1801 GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG 1861 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC 1921 AGAGCGCAGA TACCAAATAC TGTTCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG 1981 AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC 2041 AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG , 2101 CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC 2161 ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA 2221 AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT 2281 CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG 2341 CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG 2401 GCCTTTTAC GGTTCCTGGC CTTTTGCTGG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA 2461 TCCCCTGATT CTGTGGATAA CCGTATTACC GCTAGCATGG ATCTCGGGGA CGTCTAACTA 2521 CTAAGCGAGA GTAGGGAACT GCCAGGCATC AAATAAAACG AAAGGCTCAG TCGGAAGACT 2581 GGGCCTTTCG TTTTATCTGT TGTTTGTCGG TGAACGCTCT CCTGAGTAGG ACAAATCCGC 2641 CGGGAGCGGA TTTGAACGTT GTGAAGCAAC GGCCCGGAGG GTGGCGGGCA GGACGCCCGC 2701 CATAAACTGC CAGGCATCAA ACTAAGCAGA AGGCCATC

FIGURE 16B

Figure 17A: Cloning Sites of the EATY Vector PEARS

NeoI ha II Sa! BamHI KonI EcolI
ade atg bac eta get gat tog ate egg tac edg att ege --tgg tac etg gat cag etg ace tag get atg get taa geg --Thr Met Asp Leu Val Asp Trp IIe Arg Tyr Arg IIe

Death --- aga att cgc ggc cgc act cga gat atc tag acc cag --- tet taa gcg ccg dcg tga gct cta tag atc tgg gtc

Ctt tct/xot/aca aag/--gaa aga aca tgt ttc/---

## 25/240

#### pENTR8 2735 bp

Location (Base Nos.)	Gene Encoded
67166	attL1
339644	ccdB
673772	attL2
8951704	KmR
18092382	ori

1 CTGACGGATG GCCTTTTTGC GTTTCTACAA ACTCTTCCTG TTAGTTAGTT ACTTAAGCTC 61 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT 121 AAGCAATGCT TTTTTATAAT GCCAACTTTG TACAAAAAAG CAGGCTTTGA AAACCTGTAT 181 TTTCAAGGAA CCATGGACCT AGTCGACTGG ATCCGGTACC GAATTCGCTT ACTAAAAGCC 241 AGATAACAGT ATGCGTATTT GCGCGCTGAT TTTTGCGGTA TAAGAATATA TACTGATATG 301 TATACCCGAA GTATGTCAAA AAGAGGTGTG CTTCTAGAAT GCAGTTTAAG GTTTACACCT 361 ATAAAAGAGA GAGCCGTTAT CGTCTGTTTG TGGATGTACA GAGTGATATT ATTGACACGC 421 CCGGGCGACG GATAGTGATC CCCCTGGCCA GTGCACGTCT GCTGTCAGAT AAAGTCTCCC 481 GTGAACTTTA CCCGGTGGTG CATATCGGGG ATGAAAGCTG GCGCATGATG ACCACCGATA 541 TGGCCAGTGT GCCGGTCTCC GTTATCGGGG AAGAAGTGGC TGATCTCAGC CACCGCGAAA 601 ATGACATCAA AAACGCCATT AACCTGATGT TCTGGGGAAT ATAGAATTCG CGGCCGCACT 661 CGAGATATCT AGACCCAGCT TTCTTGTACA AAGTTGGCAT TATAAGAAAG CATTGCTTAT 721 CAATTIGTTG CAACGAACAG GTCACTATCA GTCAAAATAA AATCATTATT TGCCATCCAG 781 CTGCAGCTCT GGCCCGTGTC TCAAAATCTC TGATGTTACA TTGCACAAGA TAAAAATATA 841 TCATCATGAA CAATAAAACT GTCTGCTTAC ATAAACAGTA ATACAAGGGG TGTTATGAGC 901 CATATTCAAC GGGAAACGTC GAGGCCGCGA TTAAATTCCA ACATGGATGC TGATTTATAT 961 GGGTATAAAT GGGCTCGCGA TAATGTCGGG CAATCAGGTG CGACAATCTA TCGCTTGTAT 1021 GGGAAGCCCG ATGCGCCAGA GTTGTTTCTG AAACATGGCA AAGGTAGCGT TGCCAATGAT 1081 GTTACAGATG AGATGGTCAG ACTAAACTGG CTGACGGAAT TTATGCCTCT TCCGACCATC 1141 AAGCATTTTA TCCGTACTCC TGATGATGCA TGGTTACTCA CCACTGCGAT CCCCGGAAAA 1201 ACAGCATTCC AGGTATTAGA AGAATATCCT GATTCAGGTG AAAATATTGT TGATGCGCTG 1261 GCAGTGTCCC TGCGCCGGTT GCATTCGATT CCTGTTTGTA ATTGTCCTTT TAACAGCGAT 1321 CGCGTATTTC GTCTCGCTCA GGCGCAATCA CGAATGAATA ACGGTTTGGT TGATGCGAGT 1381 GATTTTGATG ACGAGCGTAA TGGCTGGCCT GTTGAACAAG TCTGGAAAGA AATGCATAAA 1441 CTTTTGCCAT TCTCACCGGA TTCAGTCGTC ACTCATGGTG ATTTCTCACT TGATAACCTT 1501 ATTTTTGACG AGGGGAAATT AATAGGTTGT ATTGATGTTG GACGAGTCGG AATCGCAGAC 1561 CGATACCAGG ATCTTGCCAT CCTATGGAAC TGCCTCGGTG AGTTTTCTCC TTCATTACAG 1621 AAACGGCTTT TTCAAAAATA TGGTATTGAT AATCCTGATA TGAATAAATT GCAGTTTCAT 1681 TTGATGCTCG ATGAGTTTTT CTAATCAGAA TTGGTTAATT GGTTGTAACA TTATTCAGAT 1741 TGGGCCCCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC TTCTTGAGAT 1801 CCTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAA AACCACCGCT ACCAGCGGTG 1861 GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA AGGTAACTGG CTTCAGCAGA 1921 GCGCAGATAC CAAATACTGT TCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 1981 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT 2041 GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA TAAGGCGCAG 2101 CGGTCGGCT GAACGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC GACCTACACC 2161 GAACTGAGAT ACCTACAGCG TGAGCTATGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG 2221 GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 2281 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT 2341 CGATTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG CAACGCGGCC 2401 TTTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC TGCGTTATCC 2461 CCTGATTCTG TGGATAACCG TATTACCGCT AGCATGGATC TCGGGGACGT CTAACTACTA 2521 AGCGAGAGTA GGGAACTGCC AGGCATCAAA TAAAACGAAA GGCTCAGTCG GAAGACTGGG 2581 CCTTTCGTTT TATCTGTTGT TTGTCGGTGA ACGCTCTCCT GAGTAGGACA AATCCGCCGG 2641 GAGCGGATTT GAACGTTGTG AAGCAACGGC CCGGAGGGTG GCGGGCAGGA CGCCCGCCAT 2701 AAACTGCCAG GCATCAAACT AAGCAGAAGG CCATC

FIGURE 17B

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Figure 18th: Cloning sites of the Entry Vector penteg

Int still

The still gas as ctg tat tit cas ggs recommendated to the control of t

NdeI ByII SolI BomHI Kan I EcokI

cat ato aga tot oto gao toto ato con tacjona att coc

gta tac tot aga can con acc tanj got atn got taaj gon

His Met Any Ser Val Asp Trp Ile Any Tyr Any Ile

Death --- aga att ege gge ege act ega get eta tag atc tag gtc cag

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### pENTR9 2735 bp

Location (Base Nos.)	Gene Encoded
67166	attL1
339644	ccdB
673772	attL2
8951704	KmR
18092382	ori

1	CTGACGGATG	GCCTTTTTGC	GTTTCTACAA	ACTCTTCCTG	TTAGTTAGTT	ACTTAAGCTC
61	GGGCCCCAAA	TAATGATTTT	ATTTTGACTG	ATAGTGACCT	GTTCGTTGCA	ACAAATTGAT
121	AAGCAATGCT	TTTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTTTGA	AAACCTGTAT
181	TTTCAAGGAC	ATATGAGATC	TGTCGACTGG	ATCCGGTACC	GAATTCGCTT	ACTAAAAGCC
241	AGATAACAGT	ATGCGTATTT	GCGCGCTGAT	TTTTGCGGTA	TAAGAATATA	TACTGATATG
301	TATACCCGAA	GTATGTCAAA	AAGAGGTGTG	CTTCTAGAAT	GCAGTTTAAG	GTTTACACCT
361	ATAAAAGAGA	GAGCCGTTAT	CGTCTGTTTG	TGGATGTACA	GAGTGATATT	ATTGACACGC
421	CCGGGCGACG	GATAGTGATC	CCCCTGGCCA	GTGCACGTCT	GCTGTCAGAT	AAAGTCTCCC
481	GTGAACTTTA	CCCGGTGGTG	CATATCGGGG	ATGAAAGCTG	GCGCATGATG	ACCACCGATA
541	TGGCCAGTGT	GCCGGTCTCC	GTTATCGGGG	AAGAAGTGGC	TGATCTCAGC	CACCGCGAAA
601	ATGACATCAA	AAACGCCATT	AACCTGATGT	TCTGGGGAAT	ATAGAATTCG	CGGCCGCACT
661	CGAGATATCT	AGACCCAGCT	TTCTTGTACA	AAGTTGGCAT	TATAAGAAAG	CATTGCTTAT
721	CAATTTGTTG	CAACGAACAG	GTCACTATCA	GTCAAAATAA	AATCATTATT	TGCCATCCAG
781	CTGCAGCTCT	GGCCCGTGTC	TCAAAATCTC	TGATGTTACA	TTGCACAAGA	TAAAAATATA
841	TCATCATGAA	CAATAAAACT	GTCTGCTTAC	ATAAACAGTA	ATACAAGGGG	TGTTATGAGC
901	CATATTCAAC	GGGAAACGTC	GAGGCCGCGA	TTAAATTCCA	ACATGGATGC	TGATTTATAT
961	GGGTATAAAT	GGGCTCGCGA	TAATGTCGGG	CAATCAGGTG	CGACAATCTA	TCGCTTGTAT
1021	GGGAAGCCCG	ATGCGCCAGA	GTTGTTTCTG	AAACATGGCA	AAGGTAGCGT	TGCCAATGAT
1081	GTTACAGATG	AGATGGTCAG	ACTAAACTGG	CTGACGGAAT	TTATGCCTCT	TCCGACCATC
1141	AAGCATTTTA	TCCGTACTCC	TGATGATGCA	TGGTTACTCA	CCACTGCGAT	CCCCGGAAAA
1201	ACAGCATTCC	AGGTATTAGA	AGAATATCCT	GATTCAGGTG	AAAATATTGT	TGATGCGCTG
1261	GCAGTGTCCC	TGCGCCGGTT	GCATTCGATT	CCTGTTTGTA	ATTGTCCTTT	TAACAGCGAT
1321	CGCGTATTTC	GTCTCGCTCA	GGCGCAATCA	CGAATGAATA	ACGGTTTGGT	TGATGCGAGT
1381	GATTTTGATG	ACGAGCGTAA	TGGCTGGCCT	GTTGAACAAG	TCTGGAAAGA	AATGCATAAA
1441	CTTTTGCCAT	TCTCACCGGA	TTCAGTCGTC	ACTCATGGTG	ATTTCTCACT	TGATAACCTT
1501	ATTTTTGACG	AGGGGAAATT	AATAGGTTGT	ATTGATGTTG	GACGAGTCGG	AATCGCAGAC
1561	CGATACCAGG	ATCTTGCCAT	CCTATGGAAC	TGCCTCGGTG	AGTTTTCTCC	TTCATTACAG
1621	AAACGGCTTT	TTCAAAAATA	TGGTATTGAT	AATCCTGATA	TGAATAAATT	GCAGTTTCAT
1681	TTGATGCTCG	ATGAGTTTTT	CTAATCAGAA	TTGGTTAATT	GGTTGTAACA	TTATTCAGAT
1741	TGGGCCCCGT	TCCACTGAGC	GTCAGACCCC	GTAGAAAAGA	TCAAAGGATC	TTCTTGAGAT
1801	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT	ACCAGCGGTG
1861	GTTTGTTTGC	CGGATCAAGA	GCTACCAACT	CTTTTTCCGA	AGGTAACTGG	CTTCAGCAGA
	GCGCAGATAC					
1981	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC	TGCTGCCAGT
	GGCGATAAGT					-
2101	CGGTCGGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	GACCTACACC
2161	GAACTGAGAT	ACCTACAGCG	TGAGCTATGA	GAAAGCGCCA	CGCTTCCCGA	AGGGAGAAAG
	GCGGACAGGT					
2281	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT
2341	CGATTTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG	CAACGCGGCC
	TTTTTACGGT					
	CCTGATTCTG					
	AGCGAGAGTA					
	CCTTTCGTTT				GAGTAGGACA	
	GAGCGGATTT				GCGGGCAGGA	CGCCCGCCAT
2701	AAACTGCCAG	GCATCAAACT	AAGCAGAAGG	CCATC		

Fame 188

Figure 19A: Cloning sites of the EATY Vector PENTRIO

Int still 5.D. - 12 Nde -- 12 Nde -- 12 Nde -- 13 Nde --

aty gga lace aat toa gto gao tob ato cog tac oda att coo --tac cot tog tta agt cay cay acc tag gop aty got taa gcg --Met Gly The Ash See Val Ash Trp Ile Asy Tyr Ag Ile

Death --- aga att ege gge ege adt ega gat ate tag acc cag (ccdB)--- tet taal geg eeg geg tga get eta tag ate tgg gte

GET THE MED ACA GAY TO THE GAA AGA ACA TOP THE

#### pENTR10 2738 bp

Location (Base Nos.)	Gene Encoded
67166	attL1
342647	ccdB
676775	attL2
8981707	KmR
18122385	ori

1 CTGACGGATG GCCTTTTTGC GTTTCTACAA ACTCTTCCTG TTAGTTAGTT ACTTAAGCTC 61 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT 121 AAGCAATGCT TTTTTATAAT GCCAACTTTG TACAAAAAAG CAGGCTTCGA ACTAAGGAAA 181 TACTTACATA TGGGAACCAA TTCAGTCGAC TGGATCCGGT ACCGAATTCG CTTACTAAAA 241 GCCAGATAAC AGTATGCGTA TTTGCGCGCT GATTTTTGCG GTATAAGAAT ATATACTGAT 301 ATGTATACCC GAAGTATGTC AAAAAGAGGT GTGCTTCTAG AATGCAGTTT AAGGTTTACA 361 CCTATAAAAG AGAGAGCCGT TATCGTCTGT TTGTGGATGT ACAGAGTGAT ATTATTGACA 421 CGCCCGGCC ACGGATGGTG ATCCCCCTGG CCAGTGCACG TCTGCTGTCA GATAAAGTCT 481 CCCGTGAACT TTACCCGGTG GTGCATATCG GGGATGAAAG CTGGCGCATG ATGACCACCG 541 ATATGGCCAG TGTGCCGGTC TCCGTTATCG GGGAAGAAGT GGCTGATCTC AGCCACCGCG 601 AAAATGACAT CAAAAACGCC ATTAACCTGA TGTTCTGGGG AATATAGAAT TCGCGGCCGC 661 ACTCGAGATA TCTAGACCCA GCTTTCTTGT ACAAAGTTGG CATTATAAGA AAGCATTGCT 721 TATCAATTG TTGCAACGAA CAGGTCACTA TCAGTCAAAA TAAAATCATT ATTTGCCATC 781 CAGCTGCAGC TCTGGCCCGT GTCTCAAAAT CTCTGATGTT ACATTGCACA AGATAAAAAT 841 ATATCATCAT GAACAATAAA ACTGTCTGCT TACATAAACA GTAATACAAG GGGTGTTATG 901 AGCCATATTC AACGGGAAAC GTCGAGGCCG CGATTAAATT CCAACATGGA TGCTGATTTA 961 TATGGGTATA AATGGGCTCG CGATAATGTC GGGCAATCAG GTGCGACAAT CTATCGCTTG 1021 TATGGGAAGC CCGATGCGCC AGAGTTGTTT CTGAAACATG GCAAAGGTAG CGTTGCCAAT 1081 GATGTTACAG ATGAGATGGT CAGACTAAAC TGGCTGACGG AATTTATGCC TCTTCCGACC 1141 ATCAAGCATT TTATCCGTAC TCCTGATGAT GCATGGTTAC TCACCACTGC GATCCCCGGA 1201 AAAACAGCAT TCCAGGTATT AGAAGAATAT CCTGATTCAG GTGAAAATAT TGTTGATGCG 1261 CTGGCAGTGT TCCTGCGCCG GTTGCATTCG ATTCCTGTTT GTAATTGTCC TTTTAACAGC 1321 GATCGCGTAT TTCGTCTCGC TCAGGCGCAA TCACGAATGA ATAACGGTTT GGTTGATGCG 1381 AGTGATTTTG ATGACGAGCG TAATGGCTGG CCTGTTGAAC AAGTCTGGAA AGAAATGCAT 1441 AAACTTTTGC CATTCTCACC GGATTCAGTC GTCACTCATG GTGATTTCTC ACTTGATAAC 1501 CTTATTTTG ACGAGGGAA ATTAATAGGT TGTATTGATG TTGGACGAGT CGGAATCGCA 1561 GACCGATACC AGGATCTTGC CATCCTATGG AACTGCCTCG GTGAGTTTTC TCCTTCATTA 1621 CAGAAACGGC TTTTTCAAAA ATATGGTATT GATAATCCTG ATATGAATAA ATTGCAGTTT 1681 CATTTGATGC TCGATGAGTT TTTCTAATCA GAATTGGTTA ATTGGTTGTA ACATTATTCA 1741 GATTGGGCCC CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA 1801 GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG 1861 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC 1921 AGAGCGCAGA TACCAAATAC TGTTCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG 1981 AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC 2041 AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG 2101 CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC 2161 ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA 2221 AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGGAGCGCAC GAGGGAGCTT 2281 CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG 2341 CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG 2401 GCCTTTTAC GGTTCCTGGC CTTTTGCTGG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA 2461 TCCCCTGATT CTGTGGATAA CCGTATTACC GCTAGCATGG ATCTCGGGGA CGTCTAACTA 2521 CTAAGCGAGA GTAGGGAACT GCCAGGCATC GAATAAAACG AAAGGCTCAG TCGGAAGACT 2581 GGGCCTTTCG TTTTATCTGT TGTTTGTCGG TGAACGCTCT CCTGAGTAGG ACAAATCCGC 2641 CGGGAGCGGA TTTGAACGTT GTGAAGCAAC GGCCCGGAGG GTGGCGGGCA GGACGCCCGC 2701 CATAAACTGC CAGGCATCAA ACTAAGCAGA AGGCCATC

FIGURE 19B

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## Figure 20A: Cloning Sites of the Entry Vector pENTR11

CAC TCG AGA TAT CTA GAC CCA GCT TTC TTG TAC AAA G
GTG AGC TCT ATA GAT CTG GGT CGA AAG AAC ATG TTT C

His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys

Int	:	att	L1				S	D.	_,	Koz	zak >	lam)			S.1	D.		
TTG AAC	TAC ATG	AAA TTT	AAA TTT	GCA CGT	GGC CCG	TTC AAG	GAA CTT	GGA CCT	GAT CTA	AGA TCT	ACC	AAT TTA	TCT AGA	CTA GAT-	AGG TCC	AAA	TAC ATG	
Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Glu	Gly	Asp	Arg	Thr	Asn	Ser	Leu	Arg	Lys	Туг	• •
Kozak	No.	οI	SalI		BamH	II		Kpn	I Ec	oRI				Eco	RI	N	otI	
TTA AAT	ACC TGG	ATG TAC	GTC CAG	GAC CTG	TCG ACC	ATC	CGG GGC	TAC ATG	CGA GCT	ATT	C G	ccċ	IB -	-G[z	AT 1	ice o	GG CC	G C
Leu	Thr	Met	Val	Asp	Trp	Ile	Arg	Tyr	Arg	Ile	,			P	sn S	Ψ Ser Æ	\rg Pr	0
XhoI	:	Eco	RV 3	(baI				Int	at	tL2								

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## pENTR11 2744 bp (rotated to position 2578)

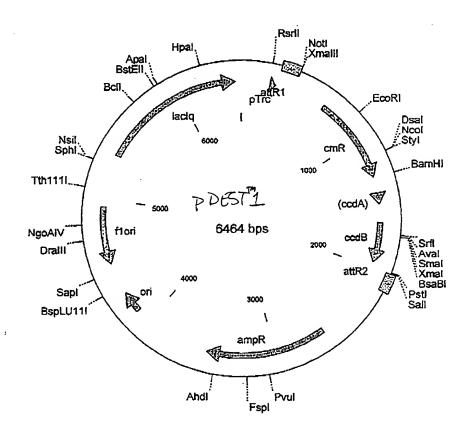
Location (Base Nos.)	Gene Encoded
67166	attL1
348653	ccdB
683781	attL2
9041713	KmR
18182391	ori

1	CTGACGGATG	GCCTTTTTGC	GTTTCTACAA	ACTCTTCCTG	TTAGTTAGTT	ACTTAAGCTC
61	GGGCCCCAAA	TAATGATTTT	ATTTTGACTG	ATAGTGACCT	GTTCGTTGCA	ACAAATTGAT
121	AAGCAATGCT	TTTTTTATAAT	GCCAACTTTG	TACAAAAAAG	CAGGCTTCGA	AGGAGATAGA
181	ACCAATTCTC	TAAGGAAATA	CTTAACCATG	GTCGACTGGA	TCCGGTACCG	AATTCGCTTA
241	CTAAAAGCCA	GATAACAGTA	TGCGTATTTG	CGCGCTGATT	TTTGCGGTAT	AAGAATATAT
301	ACTGATATGT	ATACCCGAAG	TATGTCAAAA	AGAGGTGTGC	TTCTAGAATG	CAGTTTAAGG
361	TTTACACCTA	TAAAAGAGAG	AGCCGTTATC	GTCTGTTTGT	GGATGTACAG	AGTGATATTA
421	TTGACACGCC	CGGGCGACGG	ATAGTGATCC	CCCTGGCCAG	TGCACGTCTG	CTGTCAGATA
481	AAGTCTCCCG	TGAACTTTAC	CCGGTGGTGC	ATATCGGGGA	TGAAAGCTGG	CGCATGATGA
541	CCACCGATAT	GGCCAGTGTG	CCGGTCTCCG	TTATCGGGGA	AGAAGTGGCT	GATCTCAGCC
601	ACCGCGAAAA	TGACATCAAA	AACGCCATTA	ACCTGATGTT	CTGGGGAATA	TAGAATTCGC
661	GGCCGCACTC	GAGATATCTA	GACCCAGCTT	TCTTGTACAA	AGTTGGCATT	ATAAGAAAGC
721	ATTGCTTATC	AATTTGTTGC	AACGAACAGG	TCACTATCAG	TCAAAATAAA	ATCATTATTT
781	GCCATCCAGC	TGCAGCTCTG	GCCCGTGTCT	CAAAATCTCT	GATGTTACAT	TGCACAAGAT
841	TATATAAAA	CATCATGAAC	AATAAAACTG	TCTGCTTACA	TAAACAGTAA	TACAAGGGGT
901	GTTATGAGCC	ATATTCAACG	GGAAACGTCG	AGGCCGCGAT	TAAATTCCAA	CATGGATGCT
961	GATTTATATG	GGTATAAATG	GGCTCGCGAT	AATGTCGGGC	AATCAGGTGC	GACAATCTAT
1021	CGCTTGTATG	GGAAGCCCGA	TGCGCCAGAG	TTGTTTCTGA	AACATGGCAA	AGGTAGCGTT
1081	GCCAATGATG	TTACAGATGA	GATGGTCAGA	CTAAACTGGC	TGACGGAATT	TATGCCTCTT
1141	CCGACCATCA	AGCATTTTAT	CCGTACTCCT	GATGATGCAT	GGTTACTCAC	CACTGCGATC
1201	CCCGGAAAAA	CAGCATTCCA	GGTATTAGAA	GAATATCCTG	ATTCAGGTGA	AAATATTGTT
1261	GATGCGCTGG	CAGTGTTCCT	GCGCCGGTTG	CATTCGATTC	CTGTTTGTAA	TTGTCCTTTT
1321	AACAGCGATC	GCGTATTTCG	TCTCGCTCAG	GCGCAATCAC	GAATGAATAA	CGGTTTGGTT
1381	GATGCGAGTG	ATTTTGATGA	CGAGCGTAAT	GGCTGGCCTG	TTGAACAAGT	CTGGAAAGAA
1441	ATGCATAAAC	TTTTGCCATT	CTCACCGGAT	TCAGTCGTCA	CTCATGGTGA	TTTCTCACTT
1501	GATAACCTTA	TTTTTGACGA	GGGGAAATTA	ATAGGTTGTA	TTGATGTTGG	ACGAGTCGGA
1561	ATCGCAGACC	GATACCAGGA	TCTTGCCATC	CTATGGAACT	GCCTCGGTGA	GTTTTCTCCT
1621	TCATTACAGA	AACGGCTTTT	TCAAAAATAT	GGTATTGATA	ATCCTGATAT	GAATAAATTG
1681	CAGTTTCATT	TGATGCTCGA	TGAGTTTTTC	TAATCAGAAT	TGGTTAATTG	GTTGTAACAT
1741	TATTCAGATT	GGGCCCCGTT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT
1801	TCTTGAGATC	CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAACAAAAAA	ACCACCGCTA
1861	CCAGCGGTGG	TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA	GGTAACTGGC
1921	TTCAGCAGAG	CGCAGATACC	AAATACTGTT	CTTCTAGTGT	AGCCGTAGTT	AGGCCACCAC
1981	TTCAAGAACT	CTGTAGCACC	GCCTACATAC	CTCGCTCTGC	TAATCCTGTT	ACCAGTGGCT
2041	GCTGCCAGTG	GCGATAAGTC	GTGTCTTACC	GGGTTGGACT	CAAGACGATA	GTTACCGGAT
2101	AAGGCGCAGC	GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCCAGCTT	GGAGCGAACG
2161	ACCTACACCG	AACTGAGATA	CCTACAGCGT	GAGCTATGAG	AAAGCGCCAC	GCTTCCCGAA
2221	GGGAGAAAGG	CGGACAGGTA	TCCGGTAAGC	GGCAGGGTCG	GAACAGGAGA	GCGCACGAGG
2281	GAGCTTCCAG	GGGGAAACGC	CTGGTATCTT	TATAGTCCTG	TCGGGTTTCG	CCACCTCTGA
2341	CTTGAGCGTC	GATTTTTGTG	ATGCTCGTCA	GGGGGGGGA	GCCTATGGAA	AAACGCCAGC
2401	AACGCGGCCT	TTTTACGGTT	CCTGGCCTTT	TGCTGGCCTT	TTGCTCACAT	GTTCTTTCCT
2461	GCGTTATCCC	CTGATTCTGT	GGATAACCGT	ATTACCGCTA	GCATGGATCT	CGGGGACGTC
2521	TAACTACTAA	GCGAGAGTAG	GGAACTGCCA	GGCATCAAAT	AAAACGAAAG	GCTCAGTCGG
2581	AAGACTGGGC	CTTTCGTTTT	ATCTGTTGTT	TGTCGGTGAA	CGCTCTCCTG	AGTAGGACAA
2641	ATCCGCCGGG	AGCGGATTTG	AACGTTGTGA	AGCAACGGCC	CGGAGGGTGG	CGGGCAGGAC
2701	${\tt GCCCGCCATA}$	AACTGCCAGG	CATCAAACTA	AGCAGAAGGC	CATC	

FGURE ZOB

Figure ZAPDEST1 Native Protein Expression in E. coli

- 1 atgagetget gacasttaat cateeggete geatautitg tggaattgtg ageggataac tactegacha etgytaatta gtaggeegag chtattacac acettaacac tegeetattg
- 61 aattteacac aggaaacaga caggtatagg atcacaagtt tgtacaada agetgaagga ttaaagtgtg teetttgtet gteeatatee tagtgtteaa acatgtttt pegacteget



### pDEST1 6464 bp

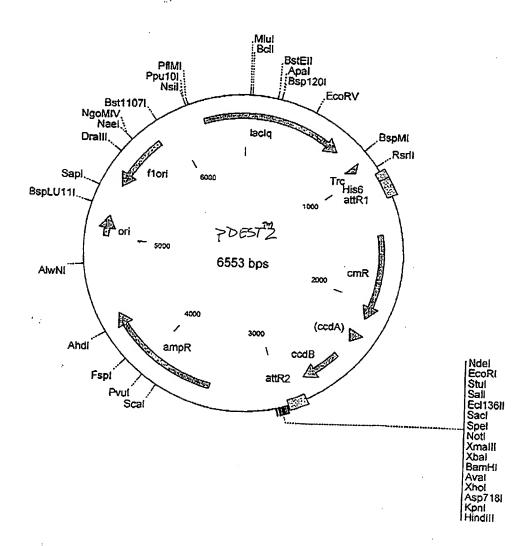
	Loc	ation (Base	Nos.)	Gene I	Encoded			
		21625 397273	7		Trc promoter			
		397273	3	attR1	attR1			
		647130	06	CmR				
		142615	510	inacti	inactivated ccdA			
		164819	953	ccdB				
		199421	L18 503	attR2				
		259835	503	ampR				
		410442	264	ori				
		450449		flori	(fl interge	enic region)		
		534064	120	lacIq				
1	GTTTGACAGC	TTATCATCGA	CTGCACGGTG	CACCAATGCT	TCTGGCGTCA	GGCAGCCATC		
61	GGAAGCTGTG	GTATGGCTGT	GCAGGTCGTA	AATCACTGCA	TAATTCGTGT	CGCTCAAGGC		
	GCACTCCCGT							
	TGAAATGAGC							
	ATAACAATTT							
	AAACGTAAAA							
361	CATAATACTG	TAAAACACAA	CATATCCAGT	CACTATGGCG	GCCGCTAAGT	TGGCAGCATC		
421	ACCCGACGCA	CTTTGCGCCG	AATAAATACC	TGTGACGGAA	GATCACTTCG	CAGAATAAAT		
	AAATCCTGGT							
	CGTTGATCGG							
601	CGTATTTTTT	GAGTTATCGA	GATTTTCAGG	AGCTAAGGAA	GCTAAAATGG	AGAAAAAAAT		
661	CACTGGATAT	ACCACCGTTG	ATATATCCCA	ATGGCATCGT	AAAGAACATT	TTGAGGCATT		
721	TCAGTCAGTT	GCTCAATGTA	CCTATAACCA	GACCGTTCAG	CTGGATATTA	CGGCCTTTTT		
	AAAGACCGTA							
	CCTGATGAAT							
901	GGATAGTGTT	CACCCTTGTT	ACACCGTTTT	CCATGAGCAA	ACTGAAACGT	TTTCATCGCT		
961	CTGGAGTGAA	TACCACGACG	ATTTCCGGCA	GTTTCTACAC	ATATATTCGC	AAGATGTGGC		
1021	GTGTTACGGT	GAAAACCTGG	CCTATTTCCC	TAAAGGGTTT	ATTGAGAATA	TGTTTTTCGT		
	CTCAGCCAAT							
	CTTCTTCGCC							
	GCCGCTGGCG							
1261	TAATGAATTA	CAACAGTACT	GCGATGAGTG	GCAGGGCGGG	GCGTAAACGC	GTGGATCCGG		
	CTTACTAAAA							
1381	ATATACTGAT	ATGTATACCC	GAAGTATGTC	AAAAAGAGGT	GTGCTATGAA	GCAGCGTATT		
1441	ACAGTGACAG	TTGACAGCGA	CAGCTATCAG	TTGCTCAAGG	CATATATGAT	GTCAATATCT		
1501	CCGGTCTGGT	AAGCACAACC	ATGCAGAATG	AAGCCCGTCG	TCTGCGTGCC	GAACGCTGGA		
1561	AAGCGGAAAA	TCAGGAAGGG	ATGGCTGAGG	TCGCCCGGTT	TATTGAAATG	AACGGCTCTT		
1621	TTGCTGACGA	GAACAGGGAC	TGGTGAAATG	CAGTTTAAGG	TTTACACCTA	TAAAAGAGAG		
1681	AGCCGTTATC	GTCTGTTTGT	GGATGTACAG	AGTGATATTA	TTGACACGCC	CGGGCGACGG		
1741	ATGGTGATCC	CCCTGGCCAG	TGCACGTCTG	CTGTCAGATA	AAGTCTCCCG	TGAACTTTAC		
1801	CCGGTGGTGC	ATATCGGGGA	TGAAAGCTGG	CGCATGATGA	CCACCGATAT	GGCCAGTGTG		
1861	CCGGTCTCCG	TTATCGGGGA	AGAAGTGGCT	GATCTCAGCC	ACCGCGAAAA	TGACATCAAA		
1921	AACGCCATTA	ACCTGATGTT	CTGGGGAATA	TAAATGTCAG	GCTCCCTTAT	ACACAGCCAG		
1981	TCTGCAGGTC	GACCATAGTG	ACTGGATATG	TTGTGTTTTA	CAGTATTATG	TAGTCTGTTT		
2041	TTTATGCAAA	ATCTAATTTA	ATATATTGAT	ATTTATATCA	TITTACGTTT	CTCGTTCAGC		
2101	TTTCTTGTAC	AAAGTGGTGA	TAGCTTGGCT	GTTTTGGCGG	ATGAGAGAAG	ATTTTCAGCC		
2161	TGATACAGAT	TAAATCAGAA	CGCAGAAGCG	GTCTGATAAA	ACAGAATTTG	CCTGGCGGCA		
2221	GTAGCGCGGT	GGTCCCACCT	GACCCCATGC	CGAACTCAGA	AGTGAAACGC	CGTAGCGCCG		
2281	ATGGTAGTGT	GGGGTCTCCC	CATGCGAGAG	TAGGGAACTG	CCAGGCATCA	AATAAAACGA		
2341	AAGGCTCAGT	CGAAAGACTG	GGCCTTTCGT	TTTATCTGTT	GTTTGTCGGT	GAACGCTCTC		
2401	CTGAGTAGGA	CAAATCCGCC	GGGAGCGGAT	TTGAACGTTG	CGAAGCAACG	GCCCGGAGGG		
2461	TGGCGGGCAG	GACGCCCGCC	ATAAACTGCC	AGGCATCAAA	TTAAGCAGAA	GGCCATCCTG		
25ZI	ACGGATGGCC	TITITGCGTT	TCTACAAACT	CTTTTTGTTT	ATTTTTCTAA	ATACATTCAA-		

	ATATGTATCC					
2641	AGAGTATGAG	TATTCAACAT	TTCCGTGTCG	CCCTTATTCC	CTTTTTTGCG	GCATTTTGCC
	TTCCTGTTTT					
	GTGCACGAGT					
	GCCCCGAAGA					
	TATCCCGTGT					
	ACTTGGTTGA					
	AATTATGCAG					
3061	CGATCGGAGG	ACCGAAGGAG	CTAACCGCTT	TTTTGCACAA	CATGGGGGAT	CATGTAACTC
	GCCTTGATCG					
3181	CGATGCCTAC	AGCAATGGCA	ACAACGTTGC	GCAAACTATT	AACTGGCGAA	CTACTTACTC
3241	TAGCTTCCCG	GCAACAATTA	ATAGACTGGA	TGGAGGCGGA	TAAAGTTGCA	GGACCACTTC
3301	TGCGCTCGGC	CCTTCCGGCT	GGCTGGTTTA	TTGCTGATAA	ATCTGGAGCC	GGTGAGCGTG
3361	GGTCTCGCGG	TATCATTGCA	GCACTGGGGC	CAGATGGTAA	GCCCTCCCGT	ATCGTAGTTA
3421	TCTACACGAC	GGGGAGTCAG	GCAACTATGG	ATGAACGAAA	TAGACAGATC	GCTGAGATAG
3481	GTGCCTCACT	GATTAAGCAT	TGGTAACTGT	CAGACCAAGT	TTACTCATAT	ATACTTTAGA
3541	TTGATTTAAA	ACTTCATTTT	TAATTTAAAA	GGATCTAGGT	GAAGATCCTT	TTTGATAATC
	TCATGACCAA					
3661	AGATCAAAGG	ATCTTCTTGA	GATCCTTTTT	TTCTGCGCGT	AATCTGCTGC	TTGCAAACAA
3721	AAAAACCACC	GCTACCAGCG	GTGGTTTGTT	TGCCGGATCA	AGAGCTACCA	VC.L.C.LaLaLaLaL.C.
3781	CGAAGGTAAC	TGGCTTCAGC	AGAGCGCAGA	TACCAAATAC	TGTCCTTCTA	GTGTAGCCGT
3841	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC
3901	TGTTACCAGT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	GACTCAAGAC
3961	GATAGTTACC	GGATAAGGCG	CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA
4021	GCTTGGAGCG	AACGACCTAC	ACCGAACTGA	GATACCTACA	GCGTGAGCTA	TGAGAAAGCG
4081	CCACGCTTCC	CGAAGGGAGA	AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG
4141	GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	CCTGTCGGGT
4201	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CCCACCCTAT
4261	GGAAAAACGC	CAGCAACGCG	GCCTTTTTAC	GGTTCCTGGC	CTTTTGCTGG	CCTTTTCCTC
4321	ACATGTTCTT	TCCTGCGTTA	TCCCCTGATT	CTGTGGATAA	CCGTATTACC	GCCTTTGACT
4381	GAGCTGATAC	CGCTCGCCGC	AGCCGAACGA	CCGAGCGCAG	CGAGTCAGTG	ACCCACCAAC
4441	CGGAAGAGCG	CCTGATGCGG	TATTTTCTCC	TTACGCATCT	GTGCGGTATT	TCACACCGCA
	TAATTTTGTT					
	CCGAAATCGG					
4621	TTCCAGTTTG	GAACAAGAGT	CCACTATTAA	AGAACGTGGA	CTCCAACGTC	AAAGGGCGAA
4681	AAACCGTCTA	TCAGGGCGAT	GGCCCACTAC	GTGAACCATC	ACCCTAATCA	ACTITITITIC
4741	GGTCGAGGTG	CCGTAAAGCA	CTAAATCGGA	ACCCTAAAGG	GAGCCCCCCA	TTTACACCTT
4801	GACGGGGAAA	GCCGCGAAC	GTGGCGAGAA	AGGAAGGGAA	GAAAGCGAAA	CCACCCCCCC
4861	CTAGGGCGCT	GGCAAGTGTA	GCGGTCACGC	TGCGCGTAAC	CACCACACCC	GCCCCCCTTA
4921	ATGCGCCGCT	ACAGGGCGCG	TCCATTCGCC	ATTCAGGCTG	CTATGGTGCA	CTCTCACTAC
4981	AATCTGCTCT	GATGCCGCAT	AGTTAAGCCA	GTACCAGTCA	CGTAGCGATA	TCCCACTAC
5041	TACACTCCGC	TATCGCTACG	TGACTGGGTC	ATGGCTGCGC	CCCGACACCC	CCCAACACCC
5101	GCTGACGCGC	CCTGACGGGC	TTGTCTGCTC	CCGCCATCCC	CTTACACACC	ACCTCTCT ACC
5161	GTCTCCGGGA	GCTGCATGTG	TCAGAGGTTT	TCACCGTCAT	CACCGAAACC	CCCCACCCAC
5221	CAGATCAATT	CGCGCGCGAA	GGCGAAGCGG	CATCCATTTA	CACCGAAACG	ATTCC A ATTCCT
5281	GCAAAACCTT	TCGCGGTATG	GCATGATAGC	GCCCGGAAGA	CACTCAATTC	ACCOMOCHON
5341	ATGTGAAACC	AGTAACGTTA	TACGATGTCG	CACACTATCC	CCCTCTCTCTCT	TATCACACC
5401	TTTCCCGCGT	GGTGAACCAG	GCCAGCCACG	TTTCTCCCAA	AACCCCCCAA	AAACTCCAAC
5461	CGGCGATGGC	GGAGCTGAAT	TACATTCCCA	ACCCCCTCCC	ACAACAACTC	CCCCCCAAAG
5521	AGTCGTTGCT	GATTGGCGTT	GCCACCTCCA	GTCTCCCCTGGC	CCACCCCCCCC	TCCCAAAC
5581	TCGCGGCGAT	TAAATCTCGC	GCCGATCAAC	TGCCTCCCAC	CCTCCTCCTC	TCGCAAATTG
5641	AACGAAGCGG	CGTCGAAGCC	TGTAAAGCCG	CCCTCCACAA	TCTTCTCCC	CAACCCCCCC
5701	GTGGGCTGAT	CATTAACTAT	CCCCTGGATG	ACCAGGGCACAA	CATTCTCGCG	CAACGCGTCA
5761	GCACTAATGT	TCCGGCGTTA	TALLULATION	TCTCTCACCA	CALIGUIGIG	AACACTATT
5821	TTTTCTCCCA	TGAAGACGGT	ACGCGACTGG	GCGTCCACCA	TOTOGOTOGO	AACAGTATTA
5881	AGCAAATCGC	GCTGTTAGCG	GGCCCACIGG	GTTCTCTCTCTCTC	CCCCCCCCCCC	1 TGGGTCACC
5941	GCTGGCATAA	ATATCTCACT	CGCAATCAAA	TTCACCCAT	ACCCCAACCC	CANCECCE
6001	GGAGTGCCAT	GTCCGGTTTTT	CAACAAACCA	TCCAAATCCT	CANTONOCOC	ATCGTTCCCA-
				- OCWWHIGE!	OUUTANGGGC	ATCGITCCCA-

6061	CTGCGATGCT	GGTTGCCAAC	GATCAGATGG	CGCTGGGCGC	AATGCGCGCC	ATTACCGAGT
6121	CCGGGCTGCG	CGTTGGTGCG	GATATCTCGG	TAGTGGGATA	CGACGATACC	GAAGACAGCT
6181	CATGTTATAT	CCCGCCGTTA	ACCACCATCA	AACAGGATTT	TCGCCTGCTG	GGGCAAACCA
6241	GCGTGGACCG	CTTGCTGCAA	CTCTCTCAGG	GCCAGGCGGT	GAAGGGCAAT	CAGCTGTTGC
6301	CCGTCTCACT	GGTGAAAAGA	AAAACCACCC	TGGCACCCAA	TACGCAAACC	GCCTCTCCCC
6361	GCGCGTTGGC	CGATTCATTA	ATGCAGCTGG	CACGACAGGT	TTCCCGACTG	GAAAGCGGGC
6421	AGTGAGCGCA	ACCCA ATTA A	TOTOACTTAC	CCCCAATTCA	TCTC	

Figure 22A: PDCST2

His6 fusions in E. coli



### pDEST2 6553 bp

	Loc	ation (Base	Nos.)	Gene E	ncoded			
		912962		Trc				
		122310	109	attR1	attRl			
		147321	.32	CmR	CmR			
		225223	36	inacti	inactivated ccdA			
		247427	79	ccdB				
		282029	144	attR2				
		350944	14	ampR				
		501551	.75	ori				
		541558			(fl interge	nic region)		
		622575	52	lacIq		-		
				-		`		
1	GGCGGTGCAC	AATCTTCTCG	CGCAACGCGT	CAGTGGGCTG	ATCATTAACT	ATCCGCTGGA		
61	TGACCAGGAT	GCCATTGCTG	TGGAAGCTGC	CTGCACTAAT	GTTCCGGCGT	TATTTCTTGA		
121	TGTCTCTGAC	CAGACACCCA	TCAACAGTAT	TATTTTCTCC	CATGAAGACG	GTACGCGACT		
181	GGGCGTGGAG	CATCTGGTCG	CATTGGGTCA	CCAGCAAATC	GCGCTGTTAG	CGGGCCCATT		
241	AAGTTCTGTC	TCGGCGCGTC	TGCGTCTGGC	TGGCTGGCAT	AAATATCTCA	CTCGCAATCA		
301	AATTCAGCCG	ATAGCGGAAC	GGGAAGGCGA	CTGGAGTGCC	ATGTCCGGTT	TTCAACAAAC		
361	CATGCAAATG	CTGAATGAGG	GCATCGTTCC	CACTGCGATG	CTGGTTGCCA	ACGATCAGAT		
421	GGCGCTGGGC	GCAATGCGCG	CCATTACCGA	GTCCGGGCTG	CGCGTTGGTG	CGGATATCTC		
481	GGTAGTGGGA	TACGACGATA	CCGAAGACAG	CTCATGTTAT	ATCCCGCCGT	CAACCACCAT		
541	CAAACAGGAT	TTTCGCCTGC	TGGGGCAAAC	CAGCGTGGAC	CGCTTGCTGC	AACTCTCTCA		
601	GGGCCAGGCG	GTGAAGGGCA	ATCAGCTGTT	GCCCGTCTCA	CTGGTGAAAA	GAAAAACCAC		
661	CCTGGCACCC	AATACGCAAA	CCGCCTCTCC	CCGCGCGTTG	GCCGATTCAT	TAATGCAGCT		
721	GGCACGACAG	GTTTCCCGAC	TGGAAAGCGG	GCAGTGAGCG	CAACGCAATT	AATGTGAGTT		
781	AGCGCGAATT	GATCTGGTTT	GACAGCTTAT	CATCGACTGC	ACGGTGCACC	AATGCTTCTG		
841	GCGTCAGGCA	GCCATCGGAA	GCTGTGGTAT	GGCTGTGCAG	GTCGTAAATC	ACTGCATAAT		
901	TCGTGTCGCT	CAAGGCGCAC	TCCCGTTCTG	GATAATGTTT	TTTGCGCCGA	CATCATAACG		
961	GTTCTGGCAA	ATATTCTGAA	ATGAGCTGTT	GACAATTAAT	CATCCGGTCC	GTATAATCTG		
1021	TGGAATTGTG	AGCGGATAAC	AATTTCACAC	AGGAAACAGA	CCATGTCGTA	CTACCATCAC		
1081	CATCACCATC	ACGGCATCAC	AAGTTTGTAC	AAAAAAGCTG	AACGAGAAAC	GTAAAATGAT		
1141	ATAAATATCA	ATATATTAAA	TTAGATTTTG	CATAAAAAAC	AGACTACATA	ATACTGTAAA		
1201	ACACAACATA	TCCAGTCACT	ATGGCGGCCG	CTAAGTTGGC	AGCATCACCC	GACGCACTTT		
1261	GCGCCGAATA	AATACCTGTG	ACGGAAGATC	ACTTCGCAGA	TAAATAAATA	CCTGGTGTCC		
1321	CTGTTGATAC	CGGGAAGCCC	TGGGCCAACT	TTTGGCGAAA	ATGAGACGTT	GATCGGCACG		
1381	TAAGAGGTTC	CAACTTTCAC	CATAATGAAA	TAAGATCACT	ACCGGGCGTA	TTTTTTGAGT		
1441	TATCGAGATT	TTCAGGAGCT	AAGGAAGCTA	AAATGGAGAA	AAAAATCACT	GGATATACCA		
1501	CCGTTGATAT	ATCCCAATGG	CATCGTAAAG	AACATTTTGA	GGCATTTCAG	TCAGTTGCTC		
	AATGTACCTA							
1621	AAAATAAGCA	CAAGTTTTAT	CCGGCCTTTA	TTCACATTCT	TGCCCGCCTG	ATGAATGCTC		
1681	ATCCGGAATT	CCGTATGGCA	ATGAAAGACG	GTGAGCTGGT	GATATGGGAT	AGTGTTCACC		
1741	CTTGTTACAC	CGTTTTCCAT	GAGCAAACTG	AAACGTTTTC	ATCGCTCTGG	AGTGAATACC		
	ACGACGATTT							
	ACCTGGCCTA							
	GGGTGAGTTT							
	TTTTCACCAT							
	AGGTTCATCA							
	AGTACTGCGA							
	GATAACAGTA							
	ATACCCGAAG							
	CAGCGACAGC							
	ACAACCATGC							
	GAAGGGATGG							
	AGGGACTGGT							
2521	GTTTGTGGAT	GTACAGAGTG	ATATTATTGA	CACGCCCGGG	CGACGGATGG	TGATCCCCCT-		

FIGURE ZZB

	GGCCAGTGCA					
2641	CGGGGATGAA	AGCTGGCGCA	TGATGACCAC	CGATATGGCC	AGTGTGCCGG	TCTCCGTTAT
2701	CGGGGAAGAA	GTGGCTGATC	TCAGCCACCG	CGAAAATGAC	ATCAAAAACG	CCATTAACCT
2761	GATGTTCTGG	GGAATATAAA	TGTCAGGCTC	CCTTATACAC	AGCCAGTCTG	CAGGTCGACC
2821	ATAGTGACTG	GATATGTTGT	GTTTTACAGT	ATTATGTAGT	CTGTTTTTTA	TGCAAAATCT
2881	AATTTAATAT	ATTGATATTT	ATATCATTTT	ACGTTTCTCG	TTCAGCTTTC	TTGTACAAAG
2941	TGGTGATGCC	CATATGGGAA	TTCAAAGGCC	TACGTCGACG	AGCTCACTAG	TCGCGGCCGC
3001	TTCTAGAGGA	TCCCTCGAGG	CATGCGGTAC	CAAGCTTGGC	TGTTTTGGCG	GATGAGAGAA
	GATTTTCAGC					
3121	GCCTGGCGGC	AGTAGCGCGG	TGGTCCCACC	TGACCCCATG	CCGAACTCAG	AAGTGAAACG
3181	CCGTAGCGCC	GATGGTAGTG	TGGGGTCTCC	CCATGCGAGA	GTAGGGAACT	GCCAGGCATC
	AAATAAAACG					
3301	TGAACGCTCT	CCTGAGTAGG	ACAAATCCGC	CGGGAGCGGA	TTTGAACGTT	GCGAAGCAAC
3361	GGCCCGGAGG	GTGGCGGGCA	GGACGCCCGC	CATAAACTGC	CAGGCATCAA	ATTAAGCAGA
3421	AGGCCATCCT	GACGGATGGC	CTTTTTGCGT	TTCTACAAAC	TCTTTTTGTT	TATTTTCTA
	AATACATTCA					
3541	TTGAAAAAGG	AAGAGTATGA	GTATTCAACA	TTTCCGTGTC	GCCCTTATTC	CCTTTTTTGC
3601	${\tt GGCATTTTGC}$	CTTCCTGTTT	TTGCTCACCC	AGAAACGCTG	GTGAAAGTAA	AAGATGCTGA
3661	AGATCAGTTG	GGTGCACGAG	TGGGTTACAT	CGAACTGGAT	CTCAACAGCG	GTAAGATCCT
	${\tt TGAGAGTTTT}$					
3781	TGGCGCGGTA	TTATCCCGTG	TTGACGCCGG	GCAAGAGCAA	CTCGGTCGCC	GCATACACTA
3841	TTCTCAGAAT	GACTTGGTTG	AGTACTCACC	AGTCACAGAA	AAGCATCTTA	CGGATGGCAT
3901	GACAGTAAGA	GAATTATGCA	GTGCTGCCAT	AACCATGAGT	GATAACACTG	CGGCCAACTT
3961	ACTTCTGACA	ACGATCGGAG	GACCGAAGGA	GCTAACCGCT	TTTTTGCACA	ACATGGGGGA
4021	TCATGTAACT	CGCCTTGATC	GTTGGGAACC	GGAGCTGAAT	GAAGCCATAC	CAAACGACGA
4081	GCGTGACACC	ACGATGCCTA	CAGCAATGGC	AACAACGTTG	CCCAAACTAT	TAACTCCCCA
4141	ACTACTTACT	CTAGCTTCCC	GGCAACAATT	AATAGACTGG	ATGGAGGCGG	ATANAGTTCC
4201	AGGACCACTT	CTGCGCTCGG	CCCTTCCGGC	TGGCTGGTTT	ATTGCTGATA	AATCTGGAGC
4261	CGGTGAGCGT	GGGTCTCGCG	GTATCATTGC	AGCACTGGGG	CCAGATGGTA	AGCCCTCCCG
4321				GGCAACTATG		
4381	CGCTGAGATA	GGTGCCTCAC	TGATTAAGCA	TTGGTAACTG	TCAGACCAAG	TTTACTCATA
4441	TATACTTTAG	ATTGATTTAA	AACTTCATTT	TTAATTTAAA	AGGATCTAGG	TGAAGATCCT
4501	TTTTGATAAT	CTCATGACCA	AAATCCCTTA	ACGTGAGTTT	TCGTTCCACT	GAGCGTCAGA
4561	CCCCGTAGAA	AAGATCAAAG	GATCTTCTTG	AGATCCTTTT	TTTCTGCGCG	TAATCTCCTC
4621	CTTGCAAACA	AAAAAACCAC	CGCTACCAGC	GGTGGTTTGT	TTGCCGGATC	AAGAGCTACC
4681	AACTCTTTTT	CCGAAGGTAA	CTGGCTTCAG	CAGAGCGCAG	ATACCAAATA	CTCTCCTTCT
4741	AGTGTAGCCG	TAGTTAGGCC	ACCACTTCAA	GAACTCTGTA	GCACCGCCTA	CATACCTCC
4801	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	CAGTGGCGAT	AAGTCGTGTC	TTACCCCCTT
4861	GGACTCAAGA	CGATAGTTAC	CGGATAAGGC	GCAGCGGTCG	GGCTGAACGG	GCCCTTCCTC
4921	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	CACCGAACTG	AGATACCTAC	ACCCTCACCT
4981	ATGAGAAAGC	GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	ACCTATCCGC	TARGUGUAGU
5041	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	TCCAGGGGGA	AACGCCTGGT	ATCTTTATAC
5101	TCCTGTCGGG	TTTCGCCACC	TCTGACTTGA	GCGTCGATTT	TTCTCATCCT	CCTCACCCCC
5161	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	GGCCTTTTTTA	CCCTTCCTCC	CCTTTTTCCTC
	GCCTTTTGCT					
5281	CGCCTTTGAG	TGAGCTGATA	CCGCTCGCCG	CAGCCCAACC	ACCCACCCCA	CCCACTCACT
5341	GAGCGAGGAA	GCGGAAGAGC	GCCTGATGCG	CTATTTTCTC	CTTACCCATC	TCTCCCCTAT
5401	TTCACACCGC	ATAATTTTGT	TAAAATTCGC	GTTTANATTTT	TCTTAAATCA	CCTCATCTTCT
5461	TAACCAATAG	GCCGAAATCG	GCAAAATCCC	TTATAAATII	AAACAATCA	CCCACATATA
5521	GTTGAGTGTT	GTTCCAGTTT	GGAACAAGAG	TCCACTACTA	AAAGAATAGA	ACTOCA ACCT
5581	CAAAGGGCGA	AAAACCGTCT	ATCAGGGCCGA	TGGCCCNCTN	CCTCVVCCIOC	CACCCENAGE
5641	AAGTTTTTTG	GGGTCGAGGT	GCCGTAAAGC	ACTANATOCC	ANCCCTANA	CONCCCCAAIC
5701	ATTTAGAGCT	TGACGGGGAA	AGCCGGCGAA	CCTCAATCGG	AUCCINAMO	ACAAACCCAA
5761	AGGAGCGGGC	GCTAGGGCGC	TGGCAAGTGT	ACCCCTCACC	CTCCCCCTA	CCACCACACA
5821	CGCCGCGCTT	AATGCGCCGC	TACAGGGCGC	GTCCCATTCC	CIGCGCGIAA	TCCTATCCTC
5881	CACTCTCAGT	ACAATCTGCT	CTGATGCCGC	ATACTTAACC	CACTATACAC	TCCCCTATGGTG
5941	CTACGTGACT	GGGTCATGGC	TGCGCCCCGA	UTUGITANGC	CAGINIMONC	CCCCCCCCCC
6001	CGGGCTTGTC	TGCTCCCGGC	ATCCGCTTAC	ACACACCCAA	TCACCCGCIGA	CGCGCCCTGA
				ON CANGE I G	.unccurcic	COGGRAGE TOC-

FIGURE 22C

6061 ATGTGTCAGA	GGTTTTCACC	GTCATCACCG	AAACGCGCGA	GGCAGCAGAT	CAATTCGCGC
6121 GCGAAGGCGA	AGCGGCATGC	ATTTACGTTG	ACACCATCGA	ATGGTGCAAA	ACCTTTCGCG
6181 GTATGGCATG	ATAGCGCCCG	${\tt GAAGAGAGTC}$	AATTCAGGGT	GGTGAATGTG	AAACCAGTAA
6241 CGTTATACGA	TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	CGCGTGGTGA
6301 ACCAGGCCAG	CCACGTTTCT	GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	ATGGCGGAGC
6361 TGAATTACAT	TCCCAACCGC	GTGGCACAAC	AACTGGCGGG	CAAACAGTCG	TTGCTGATTG
6421 GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA	AATTGTCGCG	GCGATTAAAT
6481 CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTCGAT	GGTAGAACGA	AGCGGCGTCG
6541 AAGCCTGTAA	AGC				

Figure 23A: PDEST3

#### GST fusions in E. coli

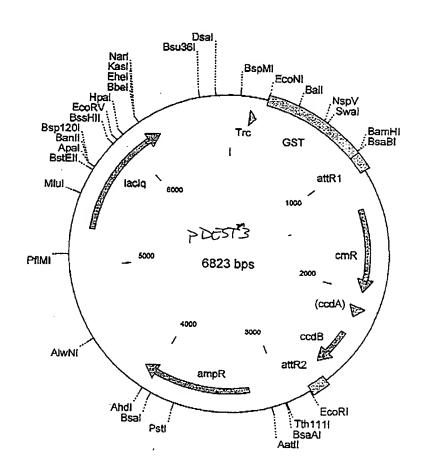
cgg ttc tgg caa ata ttc tga aat gag ctg ttg aca att aat cat cgg ctc gcc aag acc gtt tat aag act tta ctc gac aac tgt taa tta gta gcc gag

205 gta taa dgt gtg gaa ttg tga gcg gat aac aat ttc aca cag gaa aca gta cat att aca cac ctt aac act cgc cta ttg tta aag tgt gtc ctt tgt cat

256 ttc atg tcc cct ata cta ggt tat tgg aaa att aag gge ctt gtg caa ccc aag gaa tat gat cca ata acc ttt taa ttc ccg gaa cac gtt ggg

919 ctg gtt ccg cgt gga tct cgt cgt gca tct gtt gga tcc cca tca aca agt gac caa ggc gca cct aga gca gca cgt aga caa cct agg ggt agt tgt tca

970 ttg zac aaz aza get gaa cga gaa acg taa aat gat ata aat azc aat ata aac atg ttt ttt cga czt gcz czt tgc att tta cta tat tta tag tta tat



### pDEST3 6823 bp

Location (Base Nos.)	Gene Encoded
150200	Trc
1087963	attR1
13371996	CmR
21162200	inactivated ccdA
23382643	ccdB
26842808	attR2
32314091	ampR
52956254	lacIq

				_		
1	ACGTTATCGA	CTGCACGGTG	CACCAATGCT	TCTGGCGTCA	GGCAGCCATC	GGAAGCTGTG
61	GTATGGCTGT	GCAGGTCGTA	AATCACTGCA	TAATTCGTGT	CGCTCAAGGC	GCACTCCCGT
121	TCTGGATAAT	GTTTTTTGCG	CCGACATCAT	AACGGTTCTG	GCAAATATTC	TGAAATGAGC
181	TGTTGACAAT	TAATCATCGG	CTCGTATAAT	GTGTGGAATT	GTĠAGCGGAT	AACAATTTCA
241	CACAGGAAAC	AGTATTCATG	TCCCCTATAC	TAGGTTATTG	GAAAATTAAG	GGCCTTGTGC
301	AACCCACTCG	ACTTCTTTTG	GAATATCTTG	AAGAAAAATA	TGAAGAGCAT	TTGTATGAGC
361	${\tt GCGATGAAGG}$	TGATAAATGG	CGAAACAAAA	AGTTTGAATT	GGGTTTGGAG	TTTCCCAATC
421	TTCCTTATTA	TATTGATGGT	GATGTTAAAT	TAACACAGTC	TATGGCCATC	ATACGTTATA
481	TAGCTGACAA	GCACAACATG	${\tt TTGGGTGGTT}$	GTCCAAAAGA	GCGTGCAGAG	ATTTCAATGC
541	${\tt TTGAAGGAGC}$	GGTTTTGGAT	ATTAGATACG	GTGTTTCGAG	AATTGCATAT	AGTAAAGACT
601	TTGAAACTCT	CAAAGTTGAT	TTTCTTAGCA	AGCTACCTGA	AATGCTGAAA	ATGTTCGAAG
661	ATCGTTTATG	TCATAAAACA	TATTTAAATG	GTGATCATGT	AACCCATCCT	GACTTCATGT
721	TGTATGACGC	TCTTGATGTT	GTTTTATACA	TGGACCCAAT	GTGCCTGGAT	GCGTTCCCAA
781	AATTAGTTTG	TTTTAAAAAA	CGTATTGAAG	CTATCCCACA	AATTGATAAG	TACTTGAAAT
841	CCAGCAAGTA	TATAGCATGG	CCTTTGCAGG	GCTGGCAAGC	CACGTTTGGT	GGTGGCGACC
901	ATCCTCCAAA	ATCGGATCTG	GTTCCGCGTG	GATCTCGTCG	TGCATCTGTT	GGATCCCCAT
961	CAACAAGTTT	GTACAAAAAA	GCTGAACGAG	AAACGTAAAA	TGATATAAAT	ATCAATATAT
1021	TAAATTAGAT	TTTGCATAAA	AAACAGACTA	CATAATACTG	TAAAACACAA	CATATCCAGT
1081	CACTATGGCG	GCCGCTAAGT	TGGCAGCATC	ACCCGACGCA	CTTTGCGCCG	AATAAATACC
1141	TGTGACGGAA	GATCACTTCG	CAGAATAAAT	AAATCCTGGT	GTCCCTGTTG	ATACCGGGAA
1201	GCCCTGGGCC	AACTTTTGGC	GAAAATGAGA	CGTTGATCGG	CACGTAAGAG	GTTCCAACTT
1261	TCACCATAAT	GAAATAAGAT	CACTACCGGG	CGTATTTTTT	GAGTTATCGA	GATTTTCAGG
1321	AGCTAAGGAA	GCTAAAATGG	AGAAAAAAAT	CACTGGATAT	ACCACCGTTG	ATATATCCCA
1381	ATGGCATCGT	AAAGAACATT	TTGAGGCATT	TCAGTCAGTT	GCTCAATGTA	CCTATAACCA
					AAGAAAAATA	
					GCTCATCCGG	
					CACCCTTGTT	
					TACCACGACG	
					GAAAACCTGG	
				· -	CCCTGGGTGA	
					CCCGTTTTCA	
					ATTCAGGTTC	
					CAACAGTACT	
					GCCAGATAAC	
					ATGTATACCC	
					TTGACAGCGA	
					AAGCACAACC	
					TCAGGAAGGG	
					GAACAGGGAC	
					GTCTGTTTGT	
					CCCTGGCCAG	
					ATATCGGGGA	
					TTATCGGGGA	
		ACCGCGAAAA				CTGGGGAATA
2641	TAAATGTCAG	GUTUUUTTAT	ACACAGCCAG	TCTGCAGGTC	GACCATAGTG	ACTGGATATG-

FIGURE 23B

2701 TTGTGTTTTA CAGTATTATG TAGTCTGTTT TTTATGCAAA ATCTAATTTA ATATATTGAT 2761 ATTTATATCA TTTTACGTTT CTCGTTCAGC TTTCTTGTAC AAAGTGGTTG ATGGGAATTC 2821 ATCGTGACTG ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC 2881 ACATGCAGCT CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG 2941 CCCGTCAGGG CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC 3001 GTAGCGATAG CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT 3061 TATAGGTTAA TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA 3121 ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA 3181 TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC 3241 AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC 3301 ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT 3361 ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT 3421 TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG 3481 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT 3541 CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG 3601 CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA 3661 AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG 3721 AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 3781 TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC 3841 AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC 3901 CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA 3961 TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA 4021 GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 4081 AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT TTAAAACTTC 4141 ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC 4201 CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT 4261 CTTGAGATCC TTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC 4321 CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT 4381 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT 4441 TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG 4501 CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA 4561 AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA 4621 CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG 4681 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG 4741 AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC 4801 TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGGGGAG CCTATGGAAA AACGCCAGCA 4861 ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG 4921 CGTTATCCCC TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC 4981 GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GAGCGCCTGA 5041 TGCGGTATTT TCTCCTTACG CATCTGTGCG GTATTTCACA CCGCATAAAT TCCGACACCA 5101 TCGAATGGTG CAAAACCTTT CGCGGTATGG CATGATAGCG CCCGGAAGAG AGTCAATTCA 5161 GGGTGGTGAA TGTGAAACCA GTAACGTTAT ACGATGTCGC AGAGTATGCC GGTGTCTCTT 5221 ATCAGACCGT TTCCCGCGTG GTGAACCAGG CCAGCCACGT TTCTGCGAAA ACGCGGGAAA 5281 AAGTGGAAGC GGCGATGGCG GAGCTGAATT ACATTCCCAA CCGCGTGGCA CAACAACTGG 5341 CGGGCAAACA GTCGTTGCTG ATTGGCGTTG CCACCTCCAG TCTGGCCCTG CACGCGCCGT 5401 CGCAAATTGT CGCGGCGATT AAATCTCGCG CCGATCAACT GGGTGCCAGC GTGGTGGTGT 5461 CGATGGTAGA ACGAAGCGGC GTCGAAGCCT GTAAAGCGGC GGTGCACAAT CTTCTCGCGC 5521 AACGCGTCAG TGGGCTGATC ATTAACTATC CGCTGGATGA CCAGGATGCC ATTGCTGTGG 5581 AAGCTGCCTG CACTAATGTT CCGGCGTTAT TTCTTGATGT CTCTGACCAG ACACCCATCA 5641 ACAGTATTAT TTTCTCCCAT GAAGACGGTA CGCGACTGGG CGTGGAGCAT CTGGTCGCAT 5701 TGGGTCACCA GCAAATCGCG CTGTTAGCGG GCCCATTAAG TTCTGTCTCG GCGCGTCTGC 5761 GTCTGGCTGG CTGGCATAAA TATCTCACTC GCAATCAAAT TCAGCCGATA GCGGAACGGG 5821 AAGGCGACTG GAGTGCCATG TCCGGTTTTC AACAAACCAT GCAAATGCTG AATGAGGGCA 5881 TCGTTCCCAC TGCGATGCTG GTTGCCAACG ATCAGATGGC GCTGGGCGCA ATGCGCGCCA 5941 TTACCGAGTC CGGGCTGCGC GTTGGTGCGG ATATCTCGGT AGTGGGATAC GACGATACCG 6001 AAGACAGCTC ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT CGCCTGCTGG 6061 GGCAAACCAG CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG AAGGGCAATC 6121 AGCTGTTGCC CGTCTCACTG GTGAAAAGAA AAACCACCCT GGCGCCCAAT ACGCAAACCG-

FIGURE 23C

6181	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	ACGACAGGTT	TCCCGACTGG
6241	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCCAG
6301	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGCGG	ATAACAATTT
6361	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GGATTCACTG	GCCGTCGTTT	TACAACGTCG
6421	TGACTGGGAA	AACCCTGGCG	TTACCCAACT	TAATCGCCTT	GCAGCACATC	CCCCTTTCGC
6481	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	TGCGCAGCCT
6541	GAATGGCGAA	TGGCGCTTTG	CCTGGTTTCC	GGCACCAGAA	GCGGTGCCGG	AAAGCTGGCT
6601	GGAGTGCGAT	CTTCCTGAGG	CCGATACTGT	CGTCGTCCCC	TCAAACTGGC	AGATGCACGG
6661	TTACGATGCG	CCCATCTACA	CCAACGTAAC	CTATCCCATT	ACGGTCAATC	CGCCGTTTGT
6721	TCCCACGGAG	AATCCGACGG	GTTGTTACTC	GCTCACATTT	AATGTTGATG	AAAGCTGGCT
6781	ACAGGAAGGC	CAGACGCGAA	TTATTTTTGA	TGGCGTTGGA	ATT	

FIGURE 23D

Figure 24A: PDEST4

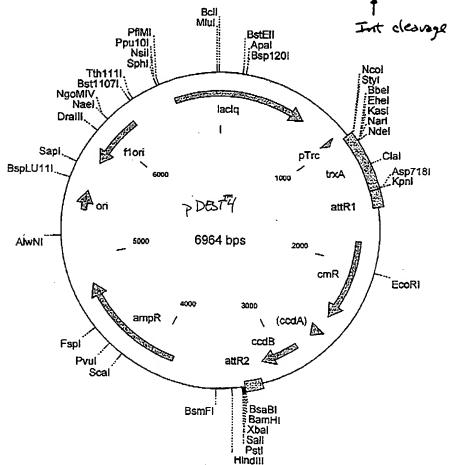
### His6-thioredoxin fusions in E. coli

- 919 gca aat att ctg aas tgs gct gtt gat sat taa tca tcc ggt ccg tat aat cgt tta taa gac ttt act cgs cas ctg tta att agt agg cca ggc ata tta
- 978 ctg tgg last tgt gag egg ata aca att tca cac agg ass cag acc atg ggt gac acc tta aca ctc gcc tat tgt tas agt gtg tcc ttt gtc tgg tac cca

TEV protease Thioredoxin - (~150 amine deles)

1072 tet cag gge gec cat atg age gat has att att cae etg act gge gat agt
ana gec eeg egg gea tae teg eta tet taa taa geg gae tga eeg eeg eeg tea

1429 fat gat gat gat and gta ccc atc atc age the red and set gas coa cta ctg cta ctg ttc cat ggg tag tgt tca aac arg ret tet gga get get



### pDEST4 6964 bp

Location (Base Nos.)			Gene Encoded			
9641003			Trc			
		157714	53	attR1		
		182724	86	CmR		
		260626	90	inactivated ccdA		
	28283133			ccdB		
		317432	98	attR2		
		387247	77	ampR		
		537855	38	ori		
		577862	15	flori	(fl interge	nic region)
		658770	)4	lacIq	_	_
				-		
1	CTATCCGCTG	GATGACCAGG	ATGCCATTGC	TGTGGAAGCT	GCCTGCACTA	ATGTTCCGGC
61	GTTATTTCTT	GATGTCTCTG	ACCAGACACC	CATCAACAGT	ATTATTTTCT	CCCATGAAGA
121	CGGTACGCGA	CTGGGCGTGG	AGCATCTGGT	CGCATTGGGT	CACCAGCAAA	TCGCGCTGTT
181	AGCGGGCCCA	TTAAGTTCTG	TCTCGGCGCG	TCTGCGTCTG	GCTGGCTGGC	ATAAATATCT
241	CACTCGCAAT	CAAATTCAGC	CGATAGCGGA	ACGGGAAGGC	GACTGGAGTG	CCATGTCCGG
301	TTTTCAACAA	ACCATGCAAA	TGCTGAATGA	GGGCATCGTT	CCCACTGCGA	TGCTGGTTGC
361	CAACGATCAG	ATGGCGCTGG	GCGCAATGCG	CGCCATTACC	GAGTCCGGGC	TGCGCGTTGG
421	TGCGGATATC	TCGGTAGTGG	GATACGACGA	TACCGAAGAC	AGCTCATGTT	ATATCCCGCC
481	GTCAACCACC	ATCAAACAGG	ATTTTCGCCT	GCTGGGGCAA	ACCAGCGTGG	ACCGCTTGCT
541	GCAACTCTCT	CAGGGCCAGG	${\tt CGGTGAAGGG}$	CAATCAGCTG	TTGCCCGTCT	CACTGGTGAA
601	AAGAAAAACC	ACCCTGGCAC	CCAATACGCA	AACCGCCTCT	CCCCGCGCGT	TGGCCGATTC
661	ATTAATGCAG	CTGGCACGAC	AGGTTTCCCG	ACTGGAAAGC	GGGCAGTGAG	CGCAACGCAA
721	TTAATGTGAG	TTAGCGCGAA	TTGATCTGGT	TTGACAGCTT	ATCATCGACT	GCACGGTGCA
781	CCAATGCTTC	TGGCGTCAGG	CAGCCATCGG	AAGCTGTGGT	ATGGCTGTGC	AGGTCGTAAA
841	TCACTGCATA	ATTCGTGTCG	CTCAAGGCGC	ACTCCCGTTC	TGGATAATGT	TTTTTGCGCC
901	GACATCATAA	CGGTTCTGGC	AAATATTCTG	AAATGAGCTG	TTGACAATTA	ATCATCCGGT
961	CCGTATAATC	TGTGGAATTG	TGAGCGGATA	ACAATTTCAC	ACAGGAAACA	GACCATGGGT
1021	CATCATCATC	ATCATCACGA	TTACGATATC	CCAACGACCG	AAAACCTGTA	TTTTCAGGGC
1081	GCCCATATGA	GCGATAAAAT	TATTCACCTG	ACTGACGACA	GTTTTGACAC	GGATGTACTC
1141	AAAGCGGACG	GGGCGATCCT	CGTCGATTTC	TGGGCAGAGT	GGTGCGGTCC	GTGCAAAATG
1201	ATCGCCCCGA	TTCTGGATGA	AATCGCTGAC	GAATATCAGG	GCAAACTGAC	CGTTGCAAAA
1261	CTGAACATCG	ATCAAAACCC	TGGCACTGCG	CCGAAATATG	GCATCCGTGG	TATCCCGACT
1321	CTGCTGCTGT	TCAAAAACGG	TGAAGTGGCG	GCAACCAAAG	TGGGTGCACT	GTCTAAAGGT
1381	CAGTTGAAAG	AGTTCCTCGA	CGCTAACCTG	GCCGGTTCTG	${\tt GTTCTGGTGA}$	TGACGATGAC
1441	AAGGTACCCA	TCACAAGTTT	GTACAAAAAA	GCTGAACGAG	AAACGTAAAA	TGATATAAAT
1501	ATCAATATAT	TAAATTAGAT	TTTGCATAAA	AAACAGACTA	CATAATACTG	TAAAACACAA
1561	CATATCCAGT	CACTATGGCG	GCCGCTAAGT	TGGCAGCATC	ACCCGACGCA	CTTTGCGCCG
	AATAAATACC					
1681	ATACCGGGAA	GCCCTGGGCC	AACTTTTGGC	GAAAATGAGA	CGTTGATCGG	CACGTAAGAG
1741	GTTCCAACTT	TCACCATAAT	GAAATAAGAT	CACTACCGGG	CGTATTTTTT	GAGTTATCGA
1801	GATTTTCAGG	AGCTAAGGAA	GCTAAAATGG	AGAAAAAAAT	CACTGGATAT	ACCACCGTTG
1861	ATATATCCCA	ATGGCATCGT	AAAGAACATT	TTGAGGCATT	TCAGTCAGTT	GCTCAATGTA
1921	CCTATAACCA	GACCGTTCAG	CTGGATATTA	CGGCCTTTTT	AAAGACCGTA	AAGAAAATA
	AGCACAAGTT					
2041	· AATTCCGTAT	GGCAATGAAA	GACGGTGAGC	TGGTGATATG	GGATAGTGTT	CACCCTTGTT
	ACACCGTTTT					
	ATTTCCGGCA					
	CCTATTTCCC					
	GTTTCACCAG					
2341	CCATGGGCAA	ATATTATACG	CAAGGCGACA	AGGTGCTGAT	GCCGCTGGCG	ATTCAGGTTC
2401	ATCATGCCGT	CTGTGATGGC	TTCCATGTCG	GCAGAATGCT	TAATGAATTA	CAACAGTACT
2461	GCGATGAGTG	GCAGGGCGGG	GCGTAAACGC	GTGGATCCGG	CTTACTAAAA	GCCAGATAAC
2521	AGTATGCGTA	TTTGCGCGCT	GATTTTTGCG	GTATAAGAAT	ATATACTGAT	ATGTATACCC-
					•	

FIGURE 24B

2501	CAACTATICTIC	333330300	amaan.			
2501	CAAGIAIGIC	AAAAAGAGGT	GIGCTATGAA	GCAGCGTATT	ACAGTGACAG	TTGACAGCGA
2041	CAGCTATCAG	TIGCTCAAGG	CATATATGAT	GTCAATATCT	CCGGTCTGGT	AAGCACAACC
2701	ATGCAGAATG	AAGCCCGTCG	TCTGCGTGCC	GAACGCTGGA	AAGCGGAAAA	TCAGGAAGGG
2/01	ATGGCTGAGG	TUGUUUGIT	TATTGAAATG	AACGGCTCTT	TTGCTGACGA	GAACAGGGAC
2821	TGGTGAAATG	CAGTTTAAGG	TITACACCTA	TAAAAGAGAG	AGCCGTTATC	GTCTGTTTGT
2881	GGATGTACAG	AGTGATATTA	TTGACACGCC	CGGGCGACGG	ATGGTGATCC	CCCTGGCCAG
2941	TGCACGTCTG	CTGTCAGATA	AAGTCTCCCG	TGAACTTTAC	CCGGTGGTGC	ATATCGGGGA
3001	TGAAAGCTGG	CGCATGATGA	CCACCGATAT	GGCCAGTGTG	CCGGTCTCCG	TTATCGGGGA
3061	AGAAGTGGCT	GATCTCAGCC	ACCGCGAAAA	TGACATCAAA	AACGCCATTA	ACCTGATGTT
3121	CTGGGGAATA	TAAATGTCAG	GCTCCCTTAT	ACACAGCCAG	TCTGCAGGTC	GACCATAGTG
3181	ACTGGATATG	TTGTGTTTTA	CAGTATTATG	TAGTCTGTTT	TTTATGCAAA	ATCTAATTTA
3241	ATATATTGAT	ATTTATATCA	TTTTACGTTT	CTCGTTCAGC	TTTCTTGTAC	AAAGTGGTGA
3301	TGGGGATCCT	CTAGAGTCGA	CCTGCAGTAA	TCGTACAGGG	TAGTACAAAT	AAAAAAGGCA
3361	CGTCAGATGA	CGTGCCTTTT	TTCTTGTGAG	CAGTAAGCTT	GGCTGTTTTG	GCGGATGAGA
3421	GAAGATTTTC	AGCCTGATAC	AGATTAAATC	AGAACGCAGA	AGCGGTCTGA	TAAAACAGAA
3481	TTTGCCTGGC	GGCAGTAGCG	CGGTGGTCCC	ACCTGACCCC	ATGCCGAACT	CAGAAGTGAA
3541	ACGCCGTAGC	GCCGATGGTA	GTGTGGGGTC	TCCCCATGCG	AGAGTAGGGA	ACTGCCAGGC
3601	ATCAAATAAA	ACGAAAGGCT	CAGTCGAAAG	ACTGGGCCTT	TCGTTTTATC	TGTTGTTTGT
3661	CGGTGAACGC	TCTCCTGAGT	AGGACAAATC	CGCCGGGAGC	<b>GGATTTGAAC</b>	GTTGCGAAGC
3721	AACGGCCCGG	AGGGTGGCGG	GCAGGACGCC	CGCCATAAAC	TGCCAGGCAT	CAAATTAAGC
3781	AGAAGGCCAT	CCTGACGGAT	GGCCTTTTTG	CGTTTCTACA	AACTCTTTTT	GTTTATTTTT
3841	CTAAATACAT	TCAAATATGT	ATCCGCTCAT	GAGACAATAA	CCCTGATAAA	TGCTTCAATA
3901	ATATTGAAAA	AGGAAGAGTA	TGAGTATTCA	ACATTTCCGT	GTCGCCCTTA	Talahalahalahalah
3961	TGCGGCATTT	TGCCTTCCTG	TTTTTGCTCA	CCCAGAAACG	CTGGTGAAAG	TAAAAGATGC
4021	TGAAGATCAG	TTGGGTGCAC	GAGTGGGTTA	CATCGAACTG	GATCTCAACA	GCGGTAAGAT
4081	CCTTGAGAGT	TTTCGCCCCG	AAGAACGTTT	TCCAATGATG	<b>AGCACTTTTA</b>	AAGTTCTGCT
4141	ATGTGGCGCG	GTATTATCCC	GTGTTGACGC	CGGGCAAGAG	CAACTCGGTC	GCCGCATACA
4201	CTATTCTCAG	AATGACTTGG	TTGAGTACTC	ACCAGTCACA	GAAAAGCATC	TTACGGATGG
4261	CATGACAGTA	AGAGAATTAT	GCAGTGCTGC	CATAACCATG	AGTGATAACA	CTGCGGCCAA
4321	CTTACTTCTG	ACAACGATCG	GAGGACCGAA	GGAGCTAACC	GCTTTTTTGC	ACAACATGGG
4381	GGATCATGTA	ACTCGCCTTG	ATCGTTGGGA	ACCGGAGCTG	AATGAAGCCA	TACCAAACGA
4441	CGAGCGTGAC	ACCACGATGC	CTACAGCAAT	GGCAACAACG	TTGCGCAAAC	TATTAACTGG
4501	CGAACTACTT	ACTCTAGCTT	CCCGGCAACA	ATTAATAGAC	TGGATGGAGG	CGGATAAAGT
4561	TGCAGGACCA	CTTCTGCGCT	CGGCCCTTCC	GGCTGGCTGG	TTTATTGCTG	ATAAATCTGG
4621	AGCCGGTGAG	CGTGGGTCTC	GCGGTATCAT	TGCAGCACTG	GGGCCAGATG	GTAAGCCCTC
4681	CCGTATCGTA	GTTATCTACA	CGACGGGGAG	TCAGGCAACT	ATGGATGAAC	GAAATAGACA
4741	GATCGCTGAG	ATAGGTGCCT	CACTGATTAA	GCATTGGTAA	CTGTCAGACC	AAGTTTACTC
4801	ATATATACTT	TAGATTGATT	TAAAACTTCA	TTTTTAATTT	AAAAGGATCT	AGGTGAAGAT
4861	CCTTTTTGAT	AATCTCATGA	CCAAAATCCC	TTAACGTGAG	TTTTCGTTCC	ACTGAGCGTC
4921	AGACCCCGTA	GAAAAGATCA	AAGGATCTTC	TTGAGATCCT	TTTTTTCTGC	GCGTAATCTG
4981	CTGCTTGCAA	ACAAAAAAAC	CACCGCTACC	AGCGGTGGTT	TGTTTGCCGG	ATCAAGAGCT
5041	ACCAACTCTT	TTTCCGAAGG	TAACTGGCTT	CAGCAGAGCG	CAGATACCAA	ATACTGTCCT
5101	TCTAGTGTAG	CCGTAGTTAG	GCCACCACTT	CAAGAACTCT	GTAGCACCGC	СТАСАТАССТ
5161	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	TGCCAGTGGC	GATAAGTCGT	GTCTTACCCC
5221	GTTGGACTCA	AGACGATAGT	TACCGGATAA	GGCGCAGCGG	TCGGGCTGAA	CGGGGGGGTTC
5281	GTGCACACAG	CCCAGCTTGG	AGCGAACGAC	CTACACCGAA	CTGAGATACC	TACAGCGTGA
5341	GCTATGAGAA	AGCGCCACGC	TTCCCGAAGG	GAGAAAGGCG	GACAGGTATC	CGGTAAGCGG
5401	CAGGGTCGGA	ACAGGAGAGC	GCACGAGGGA	GCTTCCAGGG	GGAAACGCCT	GGTATCTTTA
5461:	TAGTCCTGTC	GGGTTTCGCC	ACCTCTGACT	TGAGCGTCGA	TTTTTGTGAT	GCTCGTCAGG
5521	GGGGCGGAGC	CTATGGAAAA	ACGCCAGCAA	CGCGGCCTTT	TTACGGTTCC	TGGCCTTTTTC
5581	CTGGCCTTTT	GCTCACATGT	TCTTTCCTGC	GTTATCCCCT	GATTCTGTGG	ATAACCGTAT
5641	TACCGCCTTT	GAGTGAGCTG	ATACCGCTCG	CCGCAGCCGA	ACGACCGAGC	GCAGCGAGTC
5701	AGTGAGCGAG	GAAGCGGAAG	AGCGCCTGAT	GCGGTATTTT	CTCCTTACGC	ATCTGTGCGG
5761	TATTTCACAC	CGCATAATTT	TGTTAAAATT	CGCGTTAAAT	TTTTGTTAAA	TCACCTCATT
5821	TTTTAACCAA	TAGGCCGAAA	TCGGCAAAAT	CCCTTATAAA	TCAAAAGAAT	AGACCGAGAT
5881	AGGGTTGAGT	GTTGTTCCAG	TTTGGAACAA	GAGTCCACTA	TTAAAGAACG	TGGACTCCAA
5941	CGTCAAAGGG	CGAAAAACCG	TCTATCAGGG	CGATGGCCCA	CTACGTGAAC	CATCACCCTA
6001	ATCAAGTTTT	TTGGGGTCGA	GGTGCCGTAA	AGCACTAAAT	CGGAACCCTA	AAGGGAGCCC-
				·		

FRURE 24C

6061 CCGATTTAGA GCTTGACGGG GAAAGCCGGC GAACGTGGCG AGAAAGGAAG GGAAGAAAGC 6121 GAAAGGAGCG GGCGCTAGGG CGCTGGCAAG TGTAGCGGTC ACGCTGCGCG TAACCACCAC 6181 ACCCGCCGCG CTTAATGCGC CGCTACAGGG CGCGTCCATT CGCCATTCAG GCTGCTATGG 6241 TGCACTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA GCCAGTATAC ACTCCGCTAT 6301 CGCTACGTGA CTGGGTCATG GCTGCGCCCC GACACCCGCC AACACCCGCT GACGCGCCT 6361 GACGGGCTTG TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT 6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGCA ACACCTGCG 6901 CGAAGCCTGT AAAGCGGCG TGCCACAATCT TCTCGCGCAA CGCGCTCAGTN GGGCTGATCA 6961 TTAA							
6181 ACCCGCCGCG CTTAATGCGC CGCTACAGGG CGCGTCCATT CGCCATTCAG GCTGCTATGG 6241 TGCACTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA GCCAGTATAC ACTCCGCTAT 6301 CGCTACGTGA CTGGGTCATG GCTGCGCCC GACACCCGCC ACCACCCGCT GACGCCCCT 6361 GACGGGCTTG TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT 6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGCCA CGCGTCAGTN GGGCTGATCA	6061	CCGATTTAGA	GCTTGACGGG				
6241 TGCACTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA GCCAGTATAC ACTCCGCTAT 6301 CGCTACGTGA CTGGGTCATG GCTGCGCCCC GACACCCGCC AACACCCGCT GACGCGCCCT 6361 GACGGGCTTG TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT 6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGCCA CGCGTCAGTN GGGCTGATCA	6121	GAAAGGAGCG	GGCGCTAGGG	CGCTGGCAAG	TGTAGCGGTC	ACGCTGCGCG	TAACCACCAC
6301 CGCTACGTGA CTGGGTCATG GCTGCGCCCC GACACCCGCC AACACCCGCT GACGCGCCCT 6361 GACGGGCTTG TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT 6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGCCG ATGGTAGAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6181	ACCCGCCGCG	CTTAATGCGC	CGCTACAGGG	CGCGTCCATT	CGCCATTCAG	GCTGCTATGG
6361 GACGGGCTTG TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT 6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTG GTGCCAGCGT GGTGGTGCC ACGCTCAGTN GGGCTGATCA	6241	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	GCCAGTATAC	ACTCCGCTAT
6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6301	CGCTACGTGA	CTGGGTCATG	GCTGCGCCCC	GACACCCGCC	AACACCCGCT	GACGCGCCCT
6421 GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCAG ATCAATTCGC 6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGAG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6361	GACGGGCTTG	TCTGCTCCCG	GCATCCGCTT	ACAGACAAGC	TGTGACCGTC	TCCGGGAGCT
6481 GCGCGAAGGC GAAGCGGCAT GCATTTACGT TGACACCATC GAATGGTGCA AAACCTTTCG 6541 CGGTATGGCA TGATAGCGCC CGGAAGAGG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6421						
6541 CGGTATGGCA TGATAGCGCC CGGAAGAGG TCAATTCAGG GTGGTGAATG TGAAACCAGT 6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6481						
6601 AACGTTATAC GATGTCGCAG AGTATGCCGG TGTCTCTTAT CAGACCGTTT CCCGCGTGGT 6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA							
6661 GAACCAGGCC AGCCACGTTT CTGCGAAAAC GCGGGAAAAA GTGGAAGCGG CGATGGCGGA 6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA							
6721 GCTGAATTAC ATTCCCAACC GCGTGGCACA ACAACTGGCG GGCAAACAGT CGTTGCTGAT 6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	000-						CGATGGCGGA
6781 TGGCGTTGCC ACCTCCAGTC TGGCCCTGCA CGCGCCGTCG CAAATTGTCG CGGCGATTAA 6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	PPPI						
6841 ATCTCGCGCC GATCAACTGG GTGCCAGCGT GGTGGTGTCG ATGGTAGAAC GAAGCGGCGT 6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6721	GCTGAATTAC	ATTCCCAACC				
6901 CGAAGCCTGT AAAGCGGCGG TGCACAATCT TCTCGCGCAA CGCGTCAGTN GGGCTGATCA	6781	TGGCGTTGCC	ACCTCCAGTC	TGGCCCTGCA	CGCGCCGTCG	CAAATTGTCG	CGGCGATTAA
	6841	ATCTCGCGCC	GATCAACTGG	GTGCCAGCGT	GGTGGTGTCG	ATGGTAGAAC	GAAGCGGCGT
	6901		-	TGCACAATCT	TCTCGCGCAA	CGCGTCAGTN	GGGCTGATCA
6961 TTAA		••					
	6961	T-TAA					

Figure 241)

. . <u>A</u>

Figure 25A PDESTS

## pSPORT '+' (for sequencing, probes, phagemid)

- 1 agg cac ccc agg ctt tac act tta tgc ttc cgg ctc gta tgt tgt gtg gaa tcc gtg ggg tcc gaa atg tga aat acg aag gcc gag cat aca aca cac ctt
- ttg tga gcg gat aac aat ttc aca cag gaa aca gct atg acc atg att acg aac act cgc cta ttg tta aag tgt gtc ctt tgt cga tac tgg tac taa tgc
- 103 cca age tet aat aeg aet cae tat agg gaa age tgg tae gee tge agg tae]
  ggt teg aga tta tge tga gtg ata tee ett teg ace atg egg aeg tee atg
- 154 cgg tec gga att cec ggg teg acg atc aca agt ttg xac ara sha get gaa gec agg cet taa ggg cee age tge tag tgt tea aac atg ttt ttx cga get

Gene

- Int Str 2 Spe

  1990 tir acg tit ctc oft cag ctr tet tot aca aag tog tog tea cta oft oge

  aaa tog asa gas caa otc sas aga aca togt tit acc act agt gat cag ccg
- Not Xha Bam Hmd3 Mlu Sph

  2041 bgc cgc tct aga gga tcc abg ctt acg tac gcg tgc atglega cgt cat agc

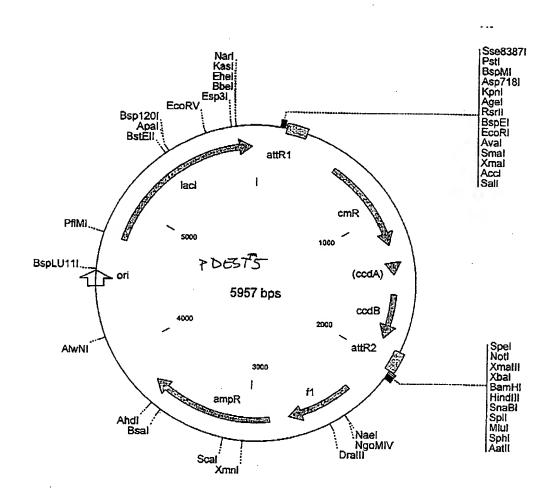
  ccg gcg aga tct cct agg ttc gaa tgc atg cgc acg tac gct gca gta tcg
- 2092 tot tot ata gree to act and the ant ten ere gee gree gree that can egrage aga tat can agr gga tot and the agr gan egg can and gree gea gray sequences.

  "forward sequences."
- cgt gac tgg gaa aac cct ggc gtt acc caa ctt aat cgc ctt gca gca cat gca ctg acc ctt ttg gga ccg caa tgg gtt gaa tta gcg gaa cgt cgt gta

Figure 45B

7 DOSTS

(cont'd)



### pDEST5 5957 bp

	Loc	cation (Base	Nos.)	Gene I	Encoded		
		305181		attR1	<u> </u>		
	5551214			CmR			
	13341418			inactivated ccdA			
		155618		ccdB	evacca ccar		
		190220		attR2			
		227827			l intergenio	region)	
		286537		ampR	· ····cergeiii	icgion,	
		537855		ori			
		475659		lacI			
1	AGGCACCCCA	GGCTTTACAC	TTTATGCTTC	CGGCTCGTAT	GTTGTGTGGA	ATTGTGAGCG	
	GATAACAATT						
	CACTATAGGG						
	ACAAGTTTGT						
	AATTAGATTT						
	CTATGGCGGC						
	TGACGGAAGA						
421	CCTGGGCCAA	CTTTTGGCGA	AAATGAGACG	TTGATCGGCA	CGTAAGAGGT	TCCAACTTTC	
	ACCATAATGA						
	CTAAGGAAGC						
	GGCATCGTAA						
	CCGTTCAGCT						
	ATCCGGCCTT						
	CAATGAAAGA						
	ATGAGCAAAC						
	TTCTACACAT						
	AAGGGTTTAT						
	TTGATTTAAA						
	ATTATACGCA						
	GTGATGGCTT						
1201	AGGGCGGGC	GTAAACGCGT	GGATCCGGCT	TACTAAAAGC	CAGATAACAG	TATGCGTATT	
1261	TGCGCGCTGA	TTTTTGCGGT	ATAAGAATAT	TATACTCATAT	GTATACCCGA	AGTATCTCAA	
1321	AAAGAGGTGT	GCTATGAAGC	AGCGTATTAC	AGTGACAGTT	GACAGCGACA	GCTATCAGTT	
	GCTCAAGGCA						
	GCCCGTCGTC						
1501	GCCCGGTTTA	TTGAAATGAA	CGGCTCTTTT	GCTGACGAGA	ACAGGGACTG	GTGAAATGCA	
1561	GTTTAAGGTT	TACACCTATA	AAAGAGAGAG	CCGTTATCGT	CTGTTTGTGG	ATGTACAGAG	
1621	TGATATTATT	GACACGCCCG	GGCGACGGAT	GGTGATCCCC	CTGGCCAGTG	CACGTCTGCT	
	GTCAGATAAA						
1741	CATGATGACC	ACCGATATGG	CCAGTGTGCC	GGTCTCCGTT	ATCGGGGAAG	AAGTGGCTGA	
1801	TCTCAGCCAC	CGCGAAAATG	ACATCAAAAA	CGCCATTAAC	CTGATGTTCT	GGGGAATATA	
1861	AATGTCAGGC	TCCCTTATAC	ACAGCCAGTC	TGCAGGTCGA	CCATAGTGAC	TGGATATGTT	
1921	GTGTTTTACA	GTATTATGTA	GTCTGTTTTT	TATGCAAAAT	CTAATTTAAT	ברבת המדרכם ב	
	TTATATCATT						
2041	GGCCGCTCTA	GAGGATCCAA	GCTTACGTAC	GCGTGCATGC	GACGTCATAG	CTCTTCTTATA	
2101	GTGTCACCTA	AATTCAATTC	ACTGGCCGTC	GTTTTACAAC	GTCGTGACTG	CCANANCCCT	
2161	GGCGTTACCC	AACTTAATCG	CCTTGCAGCA	CATCCCCCTT	TCGCCAGCTG	CCCTAATACC	
2221	GAAGAGGCCC	GCACCGATCG	CCCTTCCCAA	CARTECCCCIT	GCCTGAATGG	CCAATCCACC	
2281	CGCCCTGTAG	CGGCGCATTA	AGCGCGGCGG	CAGIIGCGCA	TACGCGCAGC	COMMIGGACG	
2341	CACTTGCCAG	CGCCCTAGCG	CCCCCCCCC	TOTO TOTO TOTO	CCCAALCCAGC	CTCGCCACCO	
2401	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	GGGGGGTTCTT	TTTTACCTT	CICGCCACGI	
2461	CTTTACGGCA	CCTCGACCCC	סדיסומממממ	ATTACCCTCA	TITAGGGIIC	ACTCCCCCA	
2521	CGCCCTGATA	GACGGTTTTT	CGCCCALACT	CCTTCCACTC	TOGITCACGI	AGIGGGCCAT	
2581	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	CTATCTCCC	CACGIICIII	CATTOLICAC	
O I	ICIIGIICCA	. ACTOUNACA	ACACTCAACC	CIAICICGGI	CIAITCITT	GATTTATAAG	

FIGURE 25C

					a. mmm a	>>>mmm>> cc
2641	GGATTTTGCC	GATTTCGGCC	TATTGGTTAA	AAAATGAGCT	GATTTAACAA	AAATTTAACG
2701	CGAATTTTAA	CAAAATATTA	ACGTTTACAA	TTTCAGGTGG	CACTTTTCGG	GGAAATGTGC
2761	GCGGAACCCC	TATTTGTTTA	TTTTTCTAAA	TACATTCAAA	TATGTATCCG	CTCATGAGAC
2821	AATAACCCTG	ATAAATGCTT	CAATAATATT	GAAAAAGGAA	GAGTATGAGT	ATTCAACATT
2881	TCCGTGTCGC	CCTTATTCCC	TTTTTTGCGG	CATTTTGCCT	TCCTGTTTTT	GCTCACCCAG
2941	AAACGCTGGT	GAAAGTAAAA	GATGCTGAAG	ATCAGTTGGG	TGCACGAGTG	GGTTACATCG
3001	AACTGGATCT	CAACAGCGGT	AAGATCCTTG	AGAGTTTTCG	CCCCGAAGAA	CGTTTTCCAA
3061	TGATGAGCAC	TTTTAAAGTT	CTGCTATGTG	GCGCGGTATT	ATCCCGTATT	GACGCCGGGC
3121	AAGAGCAACT	CGGTCGCCGC	ATACACTATT	CTCAGAATGA	CTTGGTTGAG	TACTCACCAG
2181	TCACAGAAAA	GCATCTTACG	GATGGCATGA	CAGTAAGAGA	ATTATGCAGT	GCTGCCATAA
3241	CCATGAGTGA	TAACACTGCG	GCCAACTTAC	TTCTGACAAC	GATCGGAGGA	CCGAAGGAGC
2241	TARCCCCTTT	TTTGCACAAC	ATGGGGGATC	ATGTAACTCG	CCTTGATCGT	TGGGAACCGG
3301	ACCTCAATCA	AGCCATACCA	AACGACGAGC	GTGACACCAC	GATGCCTGTA	GCAATGGCAA
3361	AGC IGAAIGA	CANACTATTA	ACTECCEDAC	TACTTACTCT	AGCTTCCCGG	CAACAATTAA
3421	CAACGIIGCG	CAMACIATIA	AAAGTTGCAG	GACCACTTCT	GCGCTCGGCC	CTTCCGGCTG
3481	TAGACTGGAT	TO COTO ATA A A	TOTOGAGOOG	GTGAGCGTGG	GTCTCGCGGT	ATCATTGCAG
3541	GCTGGTTTAT	TGCTGATAAA	CCCTCCCCTA	TCGTAGTTAT	CTACACGACG	GGGAGTCAGG
3601	CACTGGGGCC	AGATGGTAAG	CCCTCCCGTA	CTGAGATAGG	TCCCTCACTC	ATTAAGCATT
3661	CAACTATGGA	TGAACGAAAT	AGACAGATCG	CIGNONIAGO	TCATTTAAAA	Colonia Deliminator
3721	GGTAACTGTC	AGACCAAGTT	TACTCATATA	TACTTTAGAT	CATCACCAAA	ATCCCTTAAC
3781	AATTTAAAAG	GATCTAGGTG	AAGATCCTTT	TTGATAATCT	CATGACCAAA	TOTTOTO
3841	GTGAGTTTTC	GTTCCACTGA	GCGTCAGACC	CCGTAGAAAA	GATCAAAGGA	CENCENCECC
3901	ATCCTTTTTT	TCTGCGCGTA	ATCTGCTGCT	TGCAAACAAA	AAAACCACCG	CIACCAGCGG
3961	TGGTTTGTTT	GCCGGATCAA	GAGCTACCAA	CTCTTTTTCC	GAAGGTAACT	GGCTTCAGCA
4021	GAGCGCAGAT	ACCAAATACT	GTCCTTCTAG	TGTAGCCGTA	GTTAGGCCAC	CACTTCAAGA
4081	ACTCTGTAGC	ACCGCCTACA	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG	GCTGCTGCCA
4141	GTGGCGATAA	GTCGTGTCTT	ACCGGGTTGG	ACTCAAGACG	ATAGTTACCG	GATAAGGCGC
4201	AGCGGTCGGG	CTGAACGGGG	GGTTCGTGCA	CACAGCCCAG	CTTGGAGCGA	ACGACCTACA
4261	CCGAACTGAG	ATACCTACAG	CGTGAGCATT	GAGAAAGCGC	CACGCTTCCC	GAAGGGAGAA
4321	AGGCGGACAG	GTATCCGGTA	AGCGGCAGGG	TCGGAACAGG	AGAGCGCACG	AGGGAGCTTC
4381	CAGGGGGAAZ	CGCCTGGTAT	CTITATAGTO	CTGTCGGGTT	TCGCCACCTC	TGACTTGAGC
4441	CTTTATA	GTGATGCTCG	TCAGGGGGG	GGAGCCTATG	GAAAAACGCC	AGCAACGCGG
4501		CTTCCTGGCC	TTTTGCTGGC	CTTTTGCTCA	CATGTTCTTT	CCTGCGTTAT
4501	CCCCTCATTC	TGTGGATAAC	CGTATTACCC	CCTTTGAGTG	AGCTGATACC	GCTCGCCGCA
4501	CCCCIGATIO	CONCCECNEC	CACTCACTG	GCGAGGAAGC	GGAAGAGCGC	CCAATACGCA
462	A A COCCOCTO	r ccccccccc	TGGCCGATTC	ATTAATGCAG	AGCTTGCAAT	TCGCGCGCGA
468	AACCGCCIC.	CCATTTACCT	TOGCCGAIIC	GAATGGCGCA	AAACCTTTCG	CGGTATGGCA
4741	AGGCGAAGCG	GCALLIACG	TOACACCAIC	GTGGTGAATG	TGAAACCAGT	AACGTTATAC
480	I TGATAGCGC	CGGAAGAGAG	TCAATICAGO	GIGGIGAAIG	CCCCCCTCCT	GAACCAGGCC
486	L GATGTCGCA	3 AGTATGCCGC	GIGICICITA	CAGACCGTTT	CCCGCGIGGI	CCTCAATTAC
492	l AGCCACGTT	r ctgcgaaaa	GCGGGAAAAA	GTGGAAGCGG	CGAIGGCGGA	TCCCCTTCCC
498	1 ATTCCCAAC	C GCGTGGCACA	ACAACTGGCC	GGCAAACAGT	CGIIGCIGAI	NTCTCCCCCCC
504	1 ACCTCCAGT	C TGGCCCTGC/	A CGCGCCGTC	CAAATTGTCG	CGGCGATTAA	AICICGCGCC
510	1 GATCAACTG	G GTGCCAGCG	r GGTGGTGTC	ATGGTAGAAC	GAAGCGGCGT	CGAAGCCIGI
516	1 AAAGCGGCG	G TGCACAATC	r TCTCGCGCA	A CGGGTCAGTG	GGCTGATCAT	TAACTATCCG
522	1 CTGGATGAC	C AGGATGCCAT	r TGCTGTGGA	A GCTGCCTGCA	CTAATGTTCC	GGCGTTATTT
528	1 CTTGATGTC	T CTGACCAGA	C ACCCATCAA	C AGTATTATTI	TCTCCCATGA	AGACGGTACG
534	1 CGACTGGGC	G TGGAGCATC	r GGTCGCATT	G GGTCACCAGO	AAATCGCGCT	GTTAGCGGGC
540	1 CCATTAAGT	T CTGTCTCGG	C GCGTCTGCG	r ctggctggci	GGCATAAATA	TCTCACTCGC
546	1 AATCAAATT	C AGCCGATAG	C GGAACGGGA	A GGCGACTGGA	GTGCCATGTC	CGGTTTTCAA
552	1. CAAACCATG	C AAATGCTGA	A TGAGGGCAT	C GTTCCCACTC	GATGCTGGT	TGCCAACGAT
558	1 CAGATGGCG	C TGGGCGCAA	T GCGCGCCAT	T ACCGAGTCC	GGCTGCGCG1	TGGTGCGGAT
564	1 ATCTCGGTA	G TGGGATACG	A CGATACCGA	A GACAGCTCAT	GTTATATCC	GCCGTCAACC
570	1 ACCATCANA	C AGGATTTTC	G CCTGCTGGG	G CAAACCAGC	TGGACCGCT	GCTGCAACTC
576	1 TCTCAGGG	C AGGCGGTGA	A GGGCAATCA	G CTGTTGCCC	TCTCACTGGT	GAAAAGAAAA
5/6	1 ACCACCCCC	C CCCCCAATA	C GCAAACCGC	C TCTCCCCCC	CGTTGGCCG	A TTCATTAATG
502	1 CACCACCCIO	C COCCCULIA	C CCGACTGGA	A ACCECECTAC	r GAGCGCAACG	G CAATTAATGT
588	1 GAGCTGGCA	C PUTCHAILII	CCCACIGGA	A AGCGGGCAG		
594	I GAGTTAGCT	.C ACICALI				

FIGURE 25D

Figure 26A PDETG

### pSPORT "-" (opposite strand)

### "forward" sequencing primers

- 1 taa egc cag ggt ttt ccc agt cac gac gtt gta aaa cga cgg cca gtg aat att gcg gtc cca aaa ggg tca gtg ctg caa cat ttt gct gcc ggt cac tta
- 586 pomoter 57h Mlu
  52 tga att tag gtg aca cta tag aag age tat gae gte gea tge acg egt aeg
  act taa ate eae tgt gat ate tte teg ata etg eag egt aeg tge gea tge
- Hud3 Bom Xba Not See HR1 Int

  103 tala get tal ate ede tag agel gge ege get get de tag tgt teg tae
  att ega acc tag gag ate teg eeg geg get gat dae tag tgt tea aac atg
- 154 and data get get cga get acg tax act get at act act act at the dat tet tet cga cit get cit tge att tra cta tat the tax tax tax tax act the

Gene

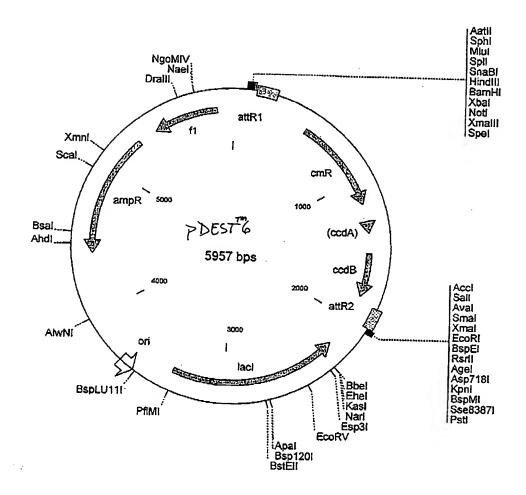
- 1939 tal tto tat pat til acg ett ced gir tag ert tet tgt aca aag tgg ega ata aat ata gta aaa tge aaa gag eaa gte gaa aga aca tgt tte ace abt
- Sal Son Ecoli Kin Bot

  1990 togltog acc dag das tto ogg acc ggt ado tge agg ogt acc ago ttt locc
  ago ago tgg doc ott aag goo tgg doa tgg acg tco goa tgg tog aaa ggg
- 2092 gtg tga aat tgt tat eeg ete aca att eea cae aac ata ega get gga age cae act tta aca ata gge gag tgt taa ggt gtg ttg tat get egg eet teg
- 2143 ata aag tgt aaa gcc tgg ggt gcc taa tga gtg agc taa ctc aca tta att tat ttc aca ttt cgg acc cca cgg att act cac tcg att gag tgt aat taa

Figure 26B

PDEST6

(cont'd)



### pDEST6 5957 bp

Gene Encoded

Location (Base Nos.)

LOCATION (Base NOS.)			Gene Encoded					
	266142			attR1				
	5161175			CmR	CmR			
		129513	79	inacti	inactivated ccdA			
		151718	122	ccdB				
		186319	87	attR2				
		220333	169	lacI				
		440352	260	ampR				
		539258	147	-	intergenio	region)		
				,				
1	TAACGCCAGG	GTTTTCCCAG	TCACGACGTT	GTAAAACGAC	GGCCAGTGAA	TTGAATTTAG		
	GTGACACTAT							
	AGCGGCCGCC							
	GATATAAATA							
	AAAACACAAC							
	TTTGCGCCGA							
	TCCCTGTTGA				_			
	ACGTAAGAGG					_		
	AGTTATCGAG							
	CCACCGTTGA							
	CTCAATGTAC							
	AGAAAAATAA							
	CTCATCCGGA							
781	ACCCTTGTTA	CACCGTTTTC	CATGAGCAAA	CTGAAACGTT	TTCATCGCTC	TGGAGTGAAT		
841	ACCACGACGA	TTTCCGGCAG	TTTCTACACA	TATATTCGCA	AGATGTGGCG	TGTTACGGTG		
901	AAAACCTGGC	CTATTTCCCT	AAAGGGTTTA	TTGAGAATAT	GTTTTTCGTC	TCAGCCAATC		
961	CCTGGGTGAG	TTTCACCAGT	TTTGATTTAA	ACGTGGCCAA	TATGGACAAC	TTCTTCGCCC		
1021	CCGTTTTCAC	CATGGGCAAA	TATTATACGC	AAGGCGACAA	GGTGCTGATG	CCGCTGGCGA		
1081	TTCAGGTTCA	TCATGCCGTC	TGTGATGGCT	TCCATGTCGG	CAGAATGCTT	AATGAATTAC		
	AACAGTACTG							
1201	CCAGATAACA	GTATGCGTAT	TTGCGCGCTG	ATTTTTGCGG	TATAAGAATA	TATACTGATA		
1261	TGTATACCCG	AAGTATGTCA	AAAAGAGGTG	TGCTATGAAG	CAGCGTATTA	CAGTGACAGT		
	TGACAGCGAC							
	AGCACAACCA							
	CAGGAAGGGA							
	AACAGGGACT							
	TCTGTTTGTG							
	CCTGGCCAGT							
	TATCGGGGAT							
	TATCGGGGAA							
	CCTGATGTTC							
	ACCATAGTGA							
1921	TCTAATTTAA	TATATTGATA	TTTATATCAT	TTTACGTTTC	TCGTTCAGCT	TTCTTGTACA		
1981	AAGTGGTGAT	CGTCGACCCG	GGAATTCCGG	ACCGGTACCT	GCAGGCGTAC	CAGCTTTCCC		
2041	TATAGTGAGT	CGTATTAGAG	CTTGGCGTAA	TCATGGTCAT	AGCTGTTTCC	TGTGTGAAAT		
2101	TGTTATCCGC	TCACAATTCC	ACACAACATA	CGAGCCGGAA	GCATAAAGTG	TAAAGCCTGG		
2161	GGTGCCTAAT	GAGTGAGCTA	ACTCACATTA	ATTGCGTTGC	GCTCACTGCC	CGCTTTCCAG		
2221	TCGGGAAACC	TGTCGTGCCA	GCTGCATTAA	TGAATCGGCC	AACGCGCGGG	GAGAGGCGGT		
2281	TTGCGTATTG	GGCGCCAGGG	TGGTTTTTCT	TTTCACCAGT	GAGACGGGCA	ACAGCTGATT		
2341	GCCCTTCACC	GCCTGGCCCT	GAGAGAGTTG	CAGCAAGCGG	TCCACGCTGG	TTTGCCCCAG		
2401	CAGGCGAAAA	TCCTGTTTGA	TGGTGGTTGA	CGGCGGGATA	TAACATGAGC	TGTCTTCGGT		
2461	ATCGTCGTAT	CCCACTACCG	AGATATCCGC	ACCAACGCGC	AGCCCGGACT	CGGTAATGGC		
2521	GCGCATTGCG	CCCAGCGCCA	TCTGATCGTT	GGCAACCAGC	ATCGCAGTGG	GAACGATGCC		
2581	CTCATTCAGC	ATTTGCATGG	TTTGTTGAAA	ACCGGACATG	GCACTCCAGT	CGCCTTCCCC		
2641	TTCCGCTATC	GGCTGAATTT	GATTGCGAGT	GAGATATTTA	TGCCAGCCAG	CCAGACGCAG-		
						- 5		

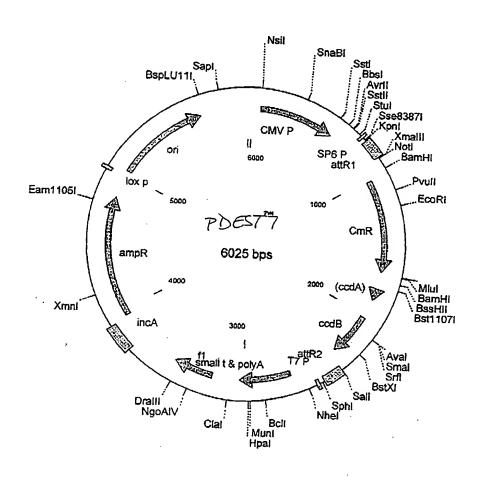
FIGURE 26C

2701	ACGCGCCGAG	ACAGAACTTA	ATGGGCCCGC	TAACAGCGCG	ATTTGCTGGT	GACCCAATGC
2761	GACCAGATGC	TCCACGCCCA	GTCGCGTACC	GTCTTCATGG	GAGAAAATAA	TACTGTTGAT
2821	GGGTGTCTGG	TCAGAGACAT	CAAGAAATAA	CGCCGGAACA	TTAGTGCAGG	CAGCTTCCAC
2881	AGCAATGGCA	TCCTGGTCAT	CCAGCGGATA	GTTAATGATC	AGCCCACTGA	CCCGTTGCGC
2941	GAGAAGATTG	TGCACCGCCG	CTTTACAGGC	TTCGACGCCG	CTTCGTTCTA	CCATCGACAC
3001	CACCACGCTG	GCACCCAGTT	GATCGGCGCG	AGATTTAATC	GCCGCGACAA	TTTGCGACGG
3061	CGCGTGCAGG	GCCAGACTGG	AGGTGGCAAC	GCCAATCAGC	AACGACTGTT	TGCCCGCCAG
3121	TTGTTGTGCC	ACGCGGTTGG	GAATGTAATT	CAGCTCCGCC	ATCGCCGCTT	CCACTTTTTC
3181	CCGCGTTTTC	GCAGAAACGT	GGCTGGCCTG	GTTCACCACG	CGGGAAACGG	TCTGATAAGA
3241	GACACCGGCA	TACTCTGCGA	CATCGTATAA	CGTTACTGGT	TTCACATTCA	CCACCCTGAA
3301	TTGACTCTCT	TCCGGGCGCT	ATCATGCCAT	ACCGCGAAAG	GTTTTGCGCC	ATTCGATGGT
3361	GTCAACGTAA	ATGCCGCTTC	GCCTTCGCGC	GCGAATTGCA	AGCTCTGCAT	TAATGAATCG
3421	GCCAACGCGC	GGGGAGAGGC	GGTTTGCGTA	TTGGGCGCTC	TTCCGCTTCC	TCGCTCACTG
3481	ACTCGCTGCG	CTCGGTCGTT	CGGCTGCGGC	GAGCGGTATC	AGCTCACTCA	AAGGCGGTAA
3541	TACGGTTATC	CACAGAATCA	GGGGATAACG	CAGGAAAGAA	CATGTGAGCA	AAAGGCCAGC
3601	AAAAGGCCAG	GAACCGTAAA	AAGGCCGCGT	TGCTGGCGTT	TTTCCATAGG	CTCCGCCCCC
3661	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA	GTCAGAGGTG	GCGAAACCCG	ACAGGACTAT
3721	AAAGATACCA	GGCGTTTCCC	CCTGGAAGCT	CCCTCGTGCG	CTCTCCTGTT	CCGACCCTGC
3781	CGCTTACCGG	ATACCTGTCC	GCCTTTCTCC	CTTCGGGAAG	CGTGGCGCTT	TCTCAATGCT
3841	CACGCTGTAG	GTATCTCAGT	TCGGTGTAGG	TCGTTCGCTC	CAAGCTGGGC	TGTGTGCACG
3901	AACCCCCCGT	TCAGCCCGAC	CGCTGCGCCT	TATCCGGTAA	CTATCGTCTT	GAGTCCAACC
3961	CGGTAAGACA	CGACTTATCG	CCACTGGCAG	CAGCCACTGG	TAACAGGATT	AGCAGAGCGA
4021	GGTATGTAGG	CGGTGCTACA	GAGTTCTTGA	AGTGGTGGCC	TAACTACGGC	TACACTAGAA
4081	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGTA
4141	GCTCTTGATC	CGGCAAACAA	ACCACCGCTG	GTAGCGGTGG	TTTTTTTTTTT	TGCAAGCAGC
4201	AGATTACGCG	CAGAAAAAAA	GGATCTCAAG	AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG
4261	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	GGATTTTGGT	CATGAGATTA	TCAAAAAGGA
4321	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	GAAGTTTTAA	ATCAATCTAA	AGTATATATG
4381	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	TAATCAGTGA	GGCACCTATC	TCAGCGATCT
4441	GTCTATTTCG	TTCATCCATA	GTTGCCTGAC	TCCCCGTCGT	GTAGATAACT	ACGATACGGG
4501	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	TGATACCGCG	AGACCCACGC	TCACCGGCTC
4561	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	GAAGGGCCGA	GCGCAGAAGT	GGTCCTGCAA
4621	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC
4681	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	TTGCTACAGG	CATCGTGGTG	TCACGCTCGT
4741	CGTTTGGTAT	GGCTTCATTC	AGCTCCGGTT	CCCAACGATC	AAGGCGAGTT	ACATGATCCC
4801	CCATGTTGTG	CAAAAAAGCG	GTTAGCTCCT	TCGGTCCTCC	GATCGTTGTC	AGAAGTAAGT
4861	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	CAGCACTGCA	TAATTCTCTT	ACTGTCATGC
4921	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	AGTACTCAAC	CAAGTCATTC	TGAGAATAGT
		ACCGAGTTGC				
		AAAAGTGCTC				
		GTTGAGATCC				
		TTTCACCAGC				
		AAGGGCGACA				
		TTATCAGGGT				
						GAAATTGTAA
						TTTTTTAACC
						ATAGGGTTGA
						AACGTCAAAG
						TAATCAAGTT
						CCCCGATTTA
						GCGAAAGGAG
						ACACCCGCCG
						ACTGTTGGGA
			CTTCGCTATT	ACGCCAGCTG	GCGAAAGGGG	GATGTGCTGC
5941	AAGGCGATTA	AGTTGGG				

FIGURE 26D

Figure 27A: PDEST 7

### CMV promoter for eukaryotic expression



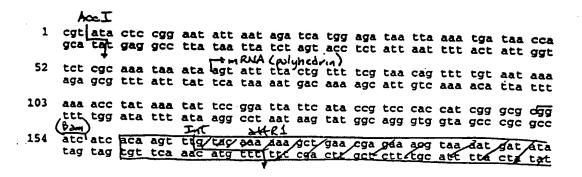
#### pDEST7 6025 bp (rotated to position 2800)

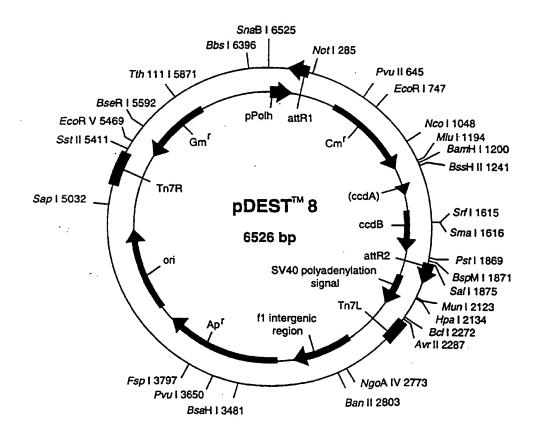
Location (Base Nos.)	Gene Encoded
67589	CMV promoter
906782	attR1
10151674	CmR
17941878	inactivated ccdA
20162321	ccdB
23622486	attR2
26713033	small t & polyA
32273502	£1
39624822	ampR
50225661	ori

```
1 ATTATCATGA CATTAACCTA TAAAAATAGG CGTAGTACGA GGCCCTTTCA CTCATTAGAT
  61 GCATGTCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC TGACCGCCCA ACGACCCCCG
 121 CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG CCAATAGGGA CTTTCCATTG
 181 ACGTCAATGG GTGGAGTATT TACGGTAAAC TGCCCACTTG GCAGTACATC AAGTGTATCA
 241 TATGCCAAGT ACGCCCCCTA TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC
 301 CCAGTACATG ACCTTATGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC
 361 TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC GGTTTGACTC
 421 ACGGGGATTT CCAAGTCTCC ACCCCATTGA CGTCAATGGG AGTTTGTTTT GGCACCAAAA
 481 TCAACGGGAC TTTCCAAAAT GTCGTAACAA CTCCGCCCCA TTGACGCAAA TGGGCGGTAG
 541 GCGTGTACGG TGGGAGGTCT ATATAAGCAG AGCTCGTTTA GTGAACCGTC AGATCGCCTG
 601 GAGACGCCAT CCACGCTGTT TTGACCTCCA TAGAAGACAC CGGGACCGAT CCAGCCTCCG
 661 GACTCTAGCC TAGGCCGCGG AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATT
 721 AGGCCTTTGC AAAAAGCTAT TTAGGTGACA CTATAGAAGG TACGCCTGCA GGTACCGGAT
 781 CACAAGTTTG TACAAAAAAG CTGAACGAGA AACGTAAAAT GATATAAATA TCAATATATT
 841 AAATTAGATT TTGCATAAAA AACAGACTAC ATAATACTGT AAAACACAAC ATATCCAGTC
 901 ACTATGGCGG CCGCATTAGG CACCCCAGGC TTTACACTTT ATGCTTCCGG CTCGTATAAT
 961 GTGTGGATTT TGAGTTAGGA TCCGTCGAGA TTTTCAGGAG CTAAGGAAGC TAAAATGGAG
1021 AAAAAATCA CTGGATATAC CACCGTTGAT ATATCCCAAT GGCATCGTAA AGAACATTTT
1081 GAGGCATTTC AGTCAGTTGC TCAATGTACC TATAACCAGA CCGTTCAGCT GGATATTACG
1141 GCCTTTTTAA AGACCGTAAA GAAAAATAAG CÁCAAGTTTT ATCCGGCCTT TATTCACATT
1201 CTTGCCCGCC TGATGAATGC TCATCCGGAA TTCCGTATGG CAATGAAAGA CGGTGAGCTG
1261 GTGATATGGG ATAGTGTTCA CCCTTGTTAC ACCGTTTTCC ATGAGCAAAC TGAAACGTTT
1321 TCATCGCTCT GGAGTGAATA CCACGACGAT TTCCGGCAGT TTCTACACAT ATATTCGCAA
1381 GATGTGGCGT GTTACGGTGA AAACCTGGCC TATTTCCCTA AAGGGTTTAT TGAGAATATG
1441 TITTTCGTCT CAGCCAATCC CTGGGTGAGT TTCACCAGTT TTGATTTAAA CGTGGCCAAT
1501 ATGGACAACT TCTTCGCCCC CGTTTTCACC ATGGGCAAAT ATTATACGCA AGGCGACAAG
1561 GTGCTGATGC CGCTGGCGAT TCAGGTTCAT CATGCCGTCT GTGATGGCTT CCATGTCGGC
1621 AGAATGCTTA ATGAATTACA ACAGTACTGC GATGAGTGGC AGGGCGGGGC GTAAACGCGT
1681 GGATCCGGCT TACTAAAAGC CAGATAACAG TATGCGTATT TGCGCGCTGA TTTTTGCGGT
1741 ATAAGAATAT ATACTGATAT GTATACCCGA AGTATGTCAA AAAGAGGTGT GCTATGAAGC
1801 AGCGTATTAC AGTGACAGTT GACAGCGACA GCTATCAGTT GCTCAAGGCA TATATGATGT
1861 CAATATCTCC GGTCTGGTAA GCACAACCAT GCAGAATGAA GCCCGTCGTC TGCGTGCCGA
1921 ACGCTGGAAA GCGGAAAATC AGGAAGGGAT GGCTGAGGTC GCCCGGTTTA TTGAAATGAA
1981 CGGCTCTTTT GCTGACGAGA ACAGGGACTG GTGAAATGCA GTTTAAGGTT TACACCTATA
2041 AAAGAGAGAG CCGTTATCGT CTGTTTGTGG ATGTACAGAG TGATATTATT GACACGCCCG
2101 GGCGACGGAT GGTGATCCCC CTGGCCAGTG CACGTCTGCT GTCAGATAAA GTCTCCCGTG
2161 AACTTTACCC GGTGGTGCAT ATCGGGGATG AAAGCTGGCG CATGATGACC ACCGATATGG
2221 CCAGTGTGCC GGTCTCCGTT ATCGGGGAAG AAGTGGCTGA TCTCAGCCAC CGCGAAAATG
2281 ACATCAAAAA CGCCATTAAC CTGATGTTCT GGGGAATATA AATGTCAGGC TCCCTTATAC
2341 ACAGCCAGTC TGCAGGTCGA CCATAGTGAC TGGATATGTT GTGTTTTACA GTATTATGTA
2401 GTCTGTTTTT TATGCAAAAT CTAATTTAAT ATATTGATAT TTATATCATT TTACGTTTCT
2461 CGTTCAGCTT TCTTGTACAA AGTGGTGATC GCGTGCATGC GACGTCATAG CTCTCTCCCT
2521 ATAGTGAGTC GTATTATAAG CTAGGCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA-
```

2501	* * CMCCM* CC	mmaca s mamm	mama saass	COMMA CONTON	CECCECECS C	\m\ \ \ mmaa\ a
	AACTGCTAGC					
	AAACTACCTA					
	GTTAAACTAG					
	AAATATTATA					
	AAGGCTCATT					
	ACATTTGTAG					
	CATAAAATGA					
	TAAAGCAATA					
	GGTTTGTCCA					
	CGGCCAACGC					
	CACCGATCGC					
	CGGCGCATTA					
3301	CGCCCTAGCG	CCCGCTCCTT	TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT
	TCCCCGTCAA					
3421	CCTCGACCCC	AAAAAACTTG	ATTAGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA
	GACGGTTTTT					
3541	AACTGGAACA	ACACTCAACC	CTATCTCGGT	CTATTCTTTT	GATTTATAAG	GGATTTTGCC
3601	GATTTCGGCC	TATTGGTTAA	AAAATGAGCT	GATTTAACAA	AAATTTAACG	CGAATTTTAA
3661	CAAAATATTA	ACGTTTACAA	TTTCAGGTGG	CACTTTTCGG	GGAAATGTGC	GCGGAACCCC
3721	TATTTGTTTA	TTTTTCTAAA	TACATTCAAA	TATGTATCCG	CTCATGCCAG	GTCTTGGACT
3781	GGTGAGAACG	GCTTGCTCGG	CAGCTTCGAT	GTGTGCTGGA	GGGAGAATAA	AGGTCTAAGA
3841	TGTGCGATAG	AGGGAAGTCG	CATTGAATTA	TGTGCTGTGT	AGGGATCGCT	GGTATCAAAT
3901	ATGTGTGCCC	ACCCCTGGCA	TGAGACAATA	ACCCTGATAA	ATGCTTCAAT	AATATTGAAA
	AAGGAAGAGT					
	TTGCCTTCCT					
	GTTGGGTGCA					
	TTTTCGCCCC					
	GGTATTATCC					
4261	GAATGACTTG	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT
	AAGAGAATTA					
	GACAACGATC					
	AACTCGCCTT					
	CACCACGATG					
4561	TACTCTAGCT	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC
	ACTTCTGCGC					
	GCGTGGGTCT					
	AGTTATCTAC					
4801	GATAGGTGCC	TCACTGATTA	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	CATATATACT
	TTAGATTGAT					
	TAATCTCATG					
	CCCTTAACGT					
	TTCTTGAGAT					
	ACCAGCGGTG					
	CTTCAGCAGA					
5221	CTTCAAGAAC	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC
5281	TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA
5341	TAAGGCGCAG	CGGTCGGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC
5401	GACCTACACC	GAACTGAGAT	ACCTACAGCG	TGAGCATTGA	GAAAGCGCCA	CGCTTCCCGA
5461	AGGGAGAAAG	GCGGACAGGT	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG
5521	GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG
5581	ACTTGAGCGT	CGATTTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG
5641	CAACGCGGCC	TTTTTACGGT	TCCTGGCCTT	TTGCTGGCCT	TTTGCTCACA	TGTTCTTTCC
5701	TGCGTTATCC	CCTGATTCTG	TGGATAACCG	TATTACCGCC	TTTGAGTGAG	CTGATACCGC
5761	TCGCCGCAGC	CGAACGACCG	AGCGCAGCGA	GTCAGTGAGC	GAGGAAGCGG	AAGAGCGCCC
5821	AATACGCAAA	CCGCCTCTCC	CCGCGCGTTG	GCCGATTCAT	TAATGCAGAG	CTTCCAATTC
5881	GCGCGTTTTT	CAATATTATT	GAAGCATTTA	TCAGGGTTAT	TGTCTCATGA	GCGGATACAT
5941	ATTTGAATGT	ATTTAGAAAA	ATAAACAAAT	AGGGGTTCCG	CGCACATTTC	CCCGAAAAGT
	GCCACCTGAC					

Figure 78A: pDEST8 Polyhedron Promoter, Baculovirus ...
Transfer Plasmid





### pDEST8 6526 bp

Location (Base Nos.)	Gene Encoded
23152	Ppolh
284160	attR1
5341193	CmR
13131397	inactivated ccdA
15351840	ccdB
18812005	attR2
27663146	f1
32404090	ampR
42894869	ori
55646496	genR

		556464	196	genR		
	CGTATACTCC					
	TAAATAAGTA					
	GGATTATTCA					
	GAACGAGAAA					
	CAGACTACAT					
	CAGCATCACC					
	AAATAAATAA					
	AATGAGACGT					
481	TACCGGGCGT	ATTTTTTGAG	TTATCGAGAT	TTTCAGGAGC	TAAGGAAGCT	AAAATGGAGA
	AAAAAATCAC				+	
601	AGGCATTTCA	GTCAGTTGCT	CAATGTACCT	ATAACCAGAC	CGTTCAGCTG	GATATTACGG
	CCTTTTTAAA					
721	TTGCCCGCCT	GATGAATGCT	CATCCGGAAT	TCCGTATGGC	AATGAAAGAC	GGTGAGCTGG
781	TGATATGGGA	TAGTGTTCAC	CCTTGTTACA	CCGTTTTCCA	TGAGCAAACT	GAAACGTTTT
841	CATCGCTCTG	GAGTGAATAC	CACGACGATT	TCCGGCAGTT	TCTACACATA	TATTCGCAAG
901	ATGTGGCGTG	TTACGGTGAA	AACCTGGCCT	ATTTCCCTAA	AGGGTTTATT	GAGAATATGT
961	TTTTCGTCTC	AGCCAATCCC	TGGGTGAGTT	TCACCAGTTT	TGATTTAAAC	GTGGCCAATA
1021	TGGACAACTT	CTTCGCCCCC	GTTTTCACCA	TGGGCAAATA	TTATACGCAA	GGCGACAAGG
	TGCTGATGCC					
1141	GAATGCTTAA	TGAATTACAA	CAGTACTGCG	ATGAGTGGCA	GGGCGGGGCG	TAAACGCGTG
1201	GATCCGGCTT	ACTAAAAGCC	AGATAACAGT	ATGCGTATTT	GCGCGCTGAT	TTTTGCGGTA
1261	TAAGAATATA	TACTGATATG	TATACCCGAA	GTATGTCAAA	AAGAGGTGTG	CTATGAAGCA
1321	GCGTATTACA	GTGACAGTTG	ACAGCGACAG	CTATCAGTTG	CTCAAGGCAT	ATATGATGTC
1381	AATATCTCCG	GTCTGGTAAG	CACAACCATG	CAGAATGAAG	CCCGTCGTCT	GCGTGCCGAA
1441	CGCTGGAAAG	CGGAAAATCA	GGAAGGGATG	GCTGAGGTCG	CCCGGTTTAT	TGAAATGAAC
1501	GGCTCTTTTG	CTGACGAGAA	CAGGGACTGG	TGAAATGCAG	TTTAAGGTTT	ACACCTATAA
1561	AAGAGAGAGC	CGTTATCGTC	TGTTTGTGGA	TGTACAGAGT	GATATTATTG	ACACGCCCGG
	GCGACGGATG					
1681	ACTTTACCCG	GTGGTGCATA	TCGGGGATGA	AAGCTGGCGC	ATGATGACCA	CCGATATGGC
	CAGTGTGCCG					
,1801	CATCAAAAAC	GCCATTAACC	TGATGTTCTG	GGGAATATAA	ATGTCAGGCT	CCCTTATACA
1861	CAGCCAGTCT	GCAGGTCGAC	CATAGTGACT	GGATATGTTG	TGTTTTACAG	TATTATGTAG
1921	TCTGTTTTTT	ATGCAAAATC	TAATTTAATA	TATTGATATT	TATATCATTT	TACGTTTCTC
	GTTCAGCTTT					
	AGCCATACCA					
2101	AACCTGAAAC	ATAAAATGAA	TGCAATTGTT	GTTGTTAACT	TGTTTATTGC	AGCTTATAAT
	GGTTACAAAT					
2221	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	GTATCTTATC	ATGTCTGGAT	CTGATCACTG
2281	CTTGAGCCTA	GGAGATCCGA	ACCAGATAAG	TGAAATCTAG	TTCCAAACTA	TTTTGTCATT
2341	TTTAATTTTC	GTATTAGCTT	ACGACGCTAC	ACCCAGTTCC	CATCTATTTT	GTCACTCTTC
2401	CCTAAATAAT	CCTTAAAAAC	TCCATTTCCA	CCCCTCCCAG	TTCCCAACTA	TTTTGTCCGC
2461	CCACAGCGGG	GCATTTTTCT	TCCTGTTATG	TITTTAATCA	AACATCCTGC	CAACTCCATG
2521	TGACAAACCG	TCATCTTCGG	CTACTITITC	TCTGTCACAG	AATGAAAATT	TTTCTGTCAT-
				=======================================		

2581	CTCTTCGTTA	TTAATGTTTG	TAATTGACTG	AATATCAACG	CTTATTTGCA (	SCCTGAATGG
2641	CCANTCGACG	CCCCCTGTAG	CGGCGCATTA	AGCGCGGCGG	GTGTGGTGGT :	FACGCGCAGC
2701	CTCACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCGCTCCTT	TCGCTTTCTT	CCCTTCCTTT
2761	CTCCCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	GGGGGCTCCC	I'T'TAGGGTTC
2021	CCATTTACTC	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	ATTAGGGTGA '	TGGTTCACGT
2001	ACTECCCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	CGTTGGAGTC	CACGTTCTTT
20/1	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	CTATCTCGGT	CTATTCTTTT
2001	CATTTATAAG	GGATTTTGCC	GATTTCGGCC	TATTGGTTAA	AAAATGAGCT	GATTTAACAA
3061	ADATTTAACG	CGAATTTTAA	CAAAATATTA	ACGTTTACAA	TTTCAGGTGG	CACTTTTCGG
2121	GCAAATGTGC	GCGGAACCCC	TATTTGTTTA	TTTTTCTAAA	TACATTCAAA	TATGTATCCG
2191	CTCATGAGAC	AATAACCCTG	ATAAATGCTT	CAATAATATT	GAAAAAGGAA	GAGTATGAGT
3241	ATTCAACATT	TCCGTGTCGC	CCTTATTCCC	TTTTTTGCGG	CATTTTGCCT	TCCTGTTTTT
3301	CCTCACCCAG	AAACGCTGGT	GAAAGTAAAA	GATGCTGAAG	ATCAGTTGGG	TGCACGAGTG
2261	CCTTACATCG	AACTGGATCT	CAACAGCGGT	AAGATCCTTG	AGAGTTTTCG	CCCCGAAGAA
2421	CCTTTTCCAA	TGATGAGCAC	TTTTAAAGTT	CTGCTATGTG	GCGCGGTATT	ATCCCGTATT
2/01	GACGCCGGGC	AAGAGCAACT	CGGTCGCCGC	ATACACTATT	CTCAGAATGA	CTTGGTTGAG
25/1	TACTCACCAG	TCACAGAAAA	GCATCTTACG	GATGGCATGA	CAGTAAGAGA	ATTATGCAGT
3541	CCTCCCATAA	CCATGAGTGA	TAACACTGCG	GCCAACTTAC	TTCTGACAAC	GATCGGAGGA
3661	CCCAAGGAGC	TAACCGCTTT	TTTGCACAAC	ATGGGGGATC	ATGTAACTCG	CCTTGATCGT
3001	TCCCAAGGAGC	AGCTGAATGA	AGCCATACCA	AACGACGAGC	GTGACACCAC	GATGCCTGTA
3721	CCAATCCCAA	CAACGTTGCG	CAAACTATTA	ACTGGCGAAC	TACTTACTCT	AGCTTCCCGG
3/81	CAMIGGCAA	TAGACTGGAT	GGAGGCGGAT	AAAGTTGCAG	GACCACTTCT	GCGCTCGGCC
3841	CAACAATTAA	GCTGGTTTAT	TGCTGATAAA	TCTGGAGCCG	GTGAGCGTGG	GTCTCGCGGT
3901	CITCCGGCIG	CACTGGGGCC	AGATGGTAAG	CCCTCCCGTA	TCGTAGTTAT	CTACACGACG
3961	ATCATIGCAG	CAACTATGGA	TGAACGAAAT	AGACAGATCG	CTGAGATAGG	TGCCTCACTG
4021	A CONTRACTOR	GGTAACTGTC	AGACCAAGTT	TACTCATATA	TACTTTAGAT	TGATTTAAAA
4081	ATTAAGCATT	AATTTAAAAG	CATCTAGGTG	AAGATCCTTT	TTGATAATCT	CATGACCAAA
4141	CITCATITI	GTGAGTTTTC	CTTCCACTGA	GCGTCAGACC	CCGTAGAAAA	GATCAAAGGA
4201	MCCCCTTAAC	ATCCTTTTTT	TOTGCGCGTA	ATCTGCTGCT	TGCAAACAAA	AAAACCACCG
4261	TCTTCTTGAG	TGGTTTGTTT	CCCCCATCAA	GAGCTACCAA	CTCTTTTTCC	GAAGGTAACT
4321	CTACCAGCGG	GAGCGCAGAT	ACCA A ATACT	י מתכנותיכים:	TGTAGCCGTA	GTTAGGCCAC
4381	GGCTTCAGCA	ACTCTGTAGC	ACCCCCCTACA	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG
4441	CACTTCAAGA	GTGGCGATAA	CTCCTCTCTT	ACCCCCTTCC	ACTCAAGACG	ATAGTTACCG
4501	. GCTGCTGCCA	AGCGGTCGGG	CTCAACCCC	CCTTCCTCCA	CACAGCCCAG	CTTGGAGCGA
4561	GATAAGGCGC	CCGAACTGAG	ATTACCTACAC	CGTGAGCATT	GAGAAAGCGC	CACGCTTCCC
4621	L ACGACCTACA	A CCGAACIGAG A AGGCGGACAG	CONTOCCCCT	ACCCCCACCA	TCGGAACAGG	AGAGCGCACG
4681	L GAAGGGAGAA	CAGGGGGAAA	GIAICCGGIA	TOPPORTATION	CTCTCGGGTT	TCGCCACCTC
4741	L AGGGAGCTTC	CAGGGGGAAA C GTCGATTTTT	COCCIGGIAI	TONCOCCOC	CRACCCTATG	GAAAAACGCC
4803	L TGACTTGAGG	CCTTTTTACG	GIGAIGCIC	TCAGGGGGGC	CTTTTCCTCA	CATGTTCTTT
4861	L AGCAACGCGC	CCCCTGATTC	CONTRACTOR	. IIIIGCIGGC	CTTTTGACTG	AGCTGATACC
492	1 CCTGCGTTA:	A GCCGAACGAC	. IGIGGAIAAG	COLATIACCO	GCGAGGAAGC	GGAAGAGCGC
498	1 GCTCGCCGCA	COCCAACGAC COCCTTTTCTCT	TACCCATCT	TOCCOUNTET	CACACCGCAG	ACCAGCCGCG
504	1 CTGATGCGG	A AAATCGGTTA	CCCTTCACT	ATANATCAT	CACACCCCTA	AGCGGGTGTG
510:	1 TAACCTGGC	A AAATCGGTTA F AAAGTCTTAA	CGGIIGAGIA	ATAMATOGAT	ACTATGACAA	TANAGTCTTA
516	1 GGCGGACAA	r AAAGTCTTAA 3 AATAGTTGTA	ACIGAACAA	A AIAGAICIAA A ACTOCACTTA	TOCTOTONA	AAGCATACTG
522	1 AACTAGACA	G AATAGTTGTA	AACTGAAAT	AGICCAGIIA	CTCCAAATTC	CCCGTCGTAT
528	1 GACTTTTGT	r Arggeraaac	CAAACTCII	L AIIIICIGAA	CCCCCCCCTTC	TGACAATTTA
534	1 TAAAGAGGG	G CGTGGCCAAC	GGCATGGTA	A AGACIAIAII	CGCGGCGIIG	CCTCCCCCCTA
540	1 CCGAACAAC	T CCGCGGCCGC	GAAGCCGAT	TCGGCTTGAA	A CGAALIGILA	GGTGGCGGTA
546	1 CTTGGGTCG	A TATCAAAGTO	CATCACTTC	r recediance	CAACITIGI	ATAGAGAGCC
552	1 ACTGCGGGA	T CGTCACCGT	A ATCTGCTTG	AUGTAGATCA	A CATAAGCACC	AAGCGCGTTG
558	1 GCCTCATGC	T TGAGGAGAT	r GATGAGCGC	G GTGGCAATGC		GTGCTCGCCG
564	1 GAGACTGCG	A GATCATAGAT	r atagatete	A CTACGCGGC	r GCTCAAACCT	GGGCAGAACG
570	1 TAAGCCGCG	A GAGCGCCAAG	C AACCGCTTC	T TGGTCGAAGO	CAGCAAGCGC	GATGAATGTC
576	1 TTACTACGG	A GCAAGTTCC	C GAGGTAATC	G GAGTCCGGC	r GATGTTGGGA	GTAGGTGGCT
582	1 ACGTCTCCG	A ACTCACGAC	C GAAAAGATC	A AGAGCAGCC	GCATGGATTI	GACTTGGTCA
588	1 GGGCCGAGC	C TACATGTGC	G AATGATGCC	C ATACTTGAG	CACCTAACTI	TGTTTTAGGG
594	1 CGACTGCCC	T GCTGCGTAA	C ATCGTTGCT	G CTGCGTAAC	A TCGTTGCTGC	TCCATAACAT
600	1 CAAACATCG	A CCCACGGCG	T AACGCGCTT	G CTGCTTGGA	r gcccgaggca	A TAGACTGTAC-

6061	AAAAAACAG	TCATAACAAG	CCATGAAAAC	CGCCACTGCG	CCGTTACCAC	CGCTGCGTTC
6121	GGTCAAGGTT	CTGGACCAGT	TGCGTGAGCG	CATACGCTAC	TTGCATTACA	GTTTACGAAC
6181	CGAACAGGCT	TATGTCAACT	GGGTTCGTGC	CTTCATCCGT	TTCCACGGTG	TGCGTCACCC
	GGCAACCTTG					
						ACGGCAAGGT
	GCTGTGCACG					
6421	GCCGGTGGTG	CTGACCCCGG	ATGAAGTGGT	TCGCATCCTC	GGTTTTCTGG	AAGGCGAGCA
6481	TCGTTTGTTC	GCCCAGGACT	CTAGCTATAG	TTCTAGTGGT	TGGCTA	

FIGURE 28D

Figure 29A: PDCST9

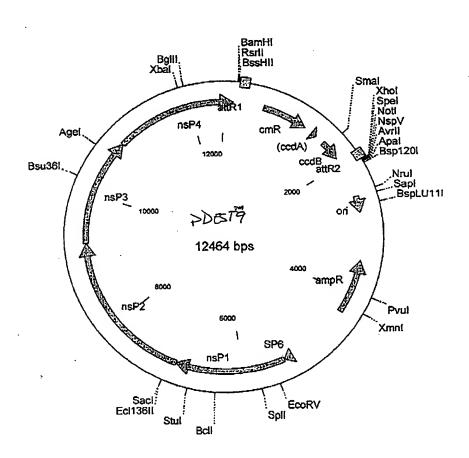
Semliki Forest Virus vector

ttg gcg agg gac att aag gcg ttt aag aaa ttg aga gga cct gtt ata cac
aac cgc tcc ctg taa tte cgc aaa tte ttt aac tct cct gga caa tat gtg

245 aomsky 245 kMA

154 ctc tac gge ggt cct aga ttg gtg cgt taa tac aca gaa tte tga ttg gat
gag atg ccg cca gga tct aac cac gca att atg tgt ctt aag act aac cta

205 ccc ggt ccg aag cgc gct ttc cca tca aca aga ttg tgt tct aag act aac cta
ggg cca ggc ttc gcg cga aag ggt agt tgt tca aac atg ttt ttr cga ctr



### pDEST9 12464 bp

				•			
	Loca	ation (Base	Nos.)	Gene E	ncoded		
		355232		attR1			
		605126	4	CmR			
		138414	68	inacti	vated ccdA		
		160619	11	ccdB			
		195220	78	attR2			
		253227	82	ori			
		348242	82	ampR			
		523253	65	SP6 pr	omoter		
		536569	65	nsP1:n	on-structur	al protein	1
		696592	65	nsP2:n	on-structur	al protein	2
		926510	865	nsP3:n	on-structur	al protein	3
		108651	.61	nsP4:n	on-structur	al protein	4
1	AGCAAGTGGT	TCCGGACAGG	CTTGGGGGCC	GAACTGGAGG	TGGCACTAAC	ATCTAGGTAT	
	GAGGTAGAGG						
	GCGTTTAAGA						
	TAATACACAG						
	ACAAAAAAGC						
	TGCATAAAAA						
	CGCTAAGTTG						
	TCACTTCGCA						
	CTTTTGGCGA						
	AATAAGATCA						
	TAAAATGGAG						
661	AGAACATTTT	GAGGCATTTC	AGTCAGTTGC	TCAATGTACC	TATAACCAGA	CCGTTCAGCT	
	GGATATTACG						
	TATTCACATT						
	CGGTGAGCTG						
	TGAAACGTTT						
961	ATATTCGCAA	GATGTGGCGT	GTTACGGTGA	AAACCTGGCC	TATTTCCCTA	AAGGGTTTAT	
1021	TGAGAATATG	${\tt TTTTTCGTCT}$	CAGCCAATCC	CTGGGTGAGT	TTCACCAGTT	TTGATTTAAA	
	CGTGGCCAAT						
	AGGCGACAAG						
	CCATGTCGGC						
	GTAAAGATCT						
	TTTTTGCGGT						
	GCTATGAAGC						
	TATATGATGT						
	TGCGTGCCGA						
	TTGAAATGAA						
	TACACCTATA						
,1681	GACACGCCCG	GGCGACGGAT	GGTGATCCCC	CTGGCCAGTG	CACGTCTGCT	GTCAGATAAA	
	GTCTCCCGTG						
	ACCGATATGG						
	CGCGAAAATG						
	TCCCTTATAC						
	GTATTATGTA						
	TTTTACGTTT						
	TCGATCCCGC						
	AATTACATCC						
	CCTTGGCCGT						
	ATGCAGCAAC					= : :	
	GCTAGGAGCT						
2401	TATTTCCAAA	AAAAAAAA	AAAAAAAAA	AAAAAAAAA	AAAAAAAA	AAAAAAAAA	٠-

FIGURE 29B

2461 AAAAAAAAA AAAAAAACTA GAAATCGCGA TTTCTAGTCT GCATTAATGA ATCGGCCAAC 2521 GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC 2581 TGCGCTCGGT CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT 2641 TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG 2701 CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCTGACG 2761 AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT 2821 ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA 2881 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCGCGCT 2941 GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC 3001 CCGTTCAGCC CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA 3061 GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG 3121 TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG 3181 TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT 3241 GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA 3301 CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC 3361 AGTGGAACGA AAACTCACGT TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA 3421 CCTAGATCCT TITAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA 3481 CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT 3541 TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT 3601 TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT 3661 TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT 3721 CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA 3781 ATAGTTTGCG CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG 3841 GTATGGCTTC ATTCAGCTCC GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT 3901 TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTCAGAAGT AAGTTGGCCG 3961 CAGTGTTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG 4021 TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC 4081 GGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA 4141 CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC 4201 CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT 4261 TTACTTTCAC CAGCGTTTCT GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG 4321 GAATAAGGGC GACACGGAAA TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA 4381 GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA 4441 AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC TAAGAAACCA 4501 TTATTATCAT GACATTAACC TATAAAAATA GGCGTATCAC GAGGCCCTTT CGTCTCGCGC 4561 GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT CCCGGAGACG GTCACAGCTT 4621 CTGTCTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG CGCGTCAGCG GGTGTTGGCG 4681 GGTGTCGGGG CTGGCTTAAC TATGCGGCAT CAGAGCAGAT TGTACTGAGA GTGCACCATA 4741 TCGACGCTCT CCCTTATGCG ACTCCTGCAT TAGGAAGCAG CCCAGTACTA GGTTGAGGCC 4801 GTTGAGCACC GCCGCCGCAA GGAATGGTGC ATGCAAGGAG ATGGCGCCCA ACAGTCCCCC 4861 GGCCACGGG CCTGCCACCA TACCCACGCC GAAACAAGCG CTCATGAGCC CGAAGTGGCG 4921 AGCCCGATCT TCCCCATCGG TGATGTCGGC GATATAGGCG CCAGCAACCG CACCTGTGGC 4981 GCCGGTGATG CCGGCCACGA TGCGTCCGGC GTAGAGGATC TGGCTAGCGA TGACCCTGCT 5041 GATTGGTTCG CTGACCATTT CCGGGGTGCG GAACGGCGTT ACCAGAAACT CAGAAGGTTC 5101 GTCCAACCAA ACCGACTCTG ACGGCAGTTT ACGAGAGAGA TGATAGGGTC TGCTTCAGTA 5161 AGCCAGATGC TACACAATTA GGCTTGTACA TATTGTCGTT AGAACGCGGC TACAATTAAT 5221 ACATAACCTT ATGTATCATA CACATACGAT TTAGGTGACA CTATAGATGG CGGATGTGTG 5281 ACATACACGA CGCCAAAAGA TTTTGTTCCA GCTCCTGCCA CCTCCGCTAC GCGAGAGATT 5341 AACCACCCAC GATGGCCGCC AAAGTGCATG TTGATATTGA GGCTGACAGC CCATTCATCA 5401 AGTCTTTGCA GAAGGCATTT CCGTCGTTCG AGGTGGAGTC ATTGCAGGTC ACACCAAATG 5461 ACCATGCAAA TGCCAGAGCA TTTTCGCACC TGGCTACCAA ATTGATCGAG CAGGAGACTG 5521 ACAAAGACAC ACTCATCTTG GATATCGGCA GTGCGCCTTC CAGGAGAATG ATGTCTACGC 5581 ACAAATACCA CTGCGTATGC CCTATGCGCA GCGCAGAAGA CCCCGAAAGG CTCGATAGCT 5641 ACGCAAAGAA ACTGGCAGCG GCCTCCGGGA AGGTGCTGGA TAGAGAGATC GCAGGAAAAA 5701 TCACCGACCT GCAGACCGTC ATGGCTACGC CAGACGCTGA ATCTCCTACC TTTTGCCTGC 5761 ATACAGACGT CACGTGTCGT ACGGCAGCCG AAGTGGCCGT ATACCAGGAC GTGTATGCTG 5821 TACATGCACC AACATCGCTG TACCATCAGG CGATGAAAGG TGTCAGAACG GCGTATTGGA 5881 TTGGGTTTGA CACCACCCCG TTTATGTTTG ACGCGCTAGC AGGCGCGTAT CCAACCTACG-

FIGURE Z9C

	CCACAAACTG					
	CCTTGACTGA					
	GCGACACAGT					
	GGAGCTGGCA					
	GCGATACCAT					<del>-</del>
	TGTACGGTAA					
	AGACCACAGA					
	CAACCATCTG					
	AGAAGTTGTT					
	CTAACACGAT					
	GGGAATACAA					
	CTTGCTGCTG					
	ACACCCAGAC					
	GGTCTACAGG					
6781	CCAAGCGAGA	GTTAATACCT	GTTCTCGACG	CGTCGTCAGC	CAGGGATGCT	GAACAAGAGG
	AGAAGGAGAG					-
	CGCCGGCGGA					
	CAGGGGTCGT					
	TACTAGGAAA					
7081	CCGTGCACCC	TCTAGCAGAG	CAGGTGAAAA	TAATAACACA	TAACGGGAGG	GCCGGCGGTT
7141	ACCAGGTCGA	CGGATATGAC	GGCAGGGTCC	TACTACCATG	TGGATCGGCC	ATTCCGGTCC
7201	CTGAGTTTCA	GGCTTTGAGC	GAGAGCGCCA	CTATGGTGTA	CAACGAAAGG	GAGTTCGTCA
7261	ACAGGAAACT	ATACCATATT	GCCGTTCACG	GACCCTCGCT	GAACACCGAC	GAGGAGAACT
7321	ACGAGAAAGT	CAGAGCTGAA	AGAACTGACG	CCGAGTACGT	GTTCGACGTA	GATAAAAAAT
	GCTGCGTCAA					
	CGTTCCATGA					
	CAGTAGTAGG					
	TGACCAAACA					
	ACGTGAAGAA					
	ACGGGTGTCG					
	GTACTCTGCT					
	ACCCCAAGCA					
	TCTGCACTGA					
	TCGTGTCTAC					
	TAATCATAGA					
	TCCGAGGCTG					
	CAGCATCTCA					
	ATCCCTTGTA					
	GGCTGGTGTG					
	AGGGTAACTT					
8341	TGATTGAAGG	ACCGGCTGCG	CCTGTGGACG	CCTTCCACAA	CARACCARA	CTCTCTTTCC
	CGAAAAGCCT					
	GCACCATAAT					
8521	AAATTTGCAC	CAAGTACTAT	GGAGTTGACC	TEGACACTEC	CCTCTTTTTCT	CCCCCCAACC
8581	TGTCCCTGTA	TTACCACAAC	AACCACTGGG	ATTACACACC	TCCTCCAACC	ATCONTOCANO
8641	TCAATGCCGC	AACAGCTGCC	ACCOTOCAAC	CTACACAGACC	CTTCCTCAAGG	AIGTAIGGAT
0701	ATACCCCCAA	CCACCCACTT	AUGCIGGAAG	CIAGACATAC	AGGGGGGGGGGGGGG	GTGCTGGACA
0761	ATACGGGCAA	TATCAACCCC	ACCOMOCOCO	GAAAAATCCA	ACCGCTTTCT	GTGCTGGACA
0/01	AIGIAAIICC	CCTTCACCCC	AGGCTGCCGC	ACGCCCTGGT	GGCTGAGTAC	AAGACGGTTA
0021	CTCACTACA	CCTCCCTTCC	CIGGICAATA	AAGTAAGAGG	GTACCACGTC	CTGCTGGTGA
0041	GTGAGTACAA	TACCECCE TELG	CCTCGACGCA	GGGTCACTTG	GITGTCACCG	CTGAATGTCA
0741	CAGGCGCCGA	TAGGIGCIAC	GACCTAAGTT	TAGGACTGCC	GGCTGACGCC	GGCAGGTTCG
9001	ACTTGGTCTT	TGTGAACATT	CACACGGAAT	TCAGAATCCA	CCACTACCAG	CAGTGTGTCG
9061	ACCACGCCAT	GAAGCTGCAG	ATGCTTGGGG	GAGATGCGCT	ACGACTGCTA	AAACCCGGCG
9121	GCATCTTGAT	GAGAGCTTAC	GGATACGCCG	ATAAAATCAG	CGAAGCCGTT	GTTTCCTCCT
9181	TAAGCAGAAA	GTTCTCGTCT	GCAAGAGTGT	TGCGCCCGGA	TTGTGTCACC	AGCAATACAG
9241	AAGTGTTCTT	GCTGTTCTCC	AACTTTGACA	ACGGAAAGAG	ACCCTCTACG	CTACACCAGA
9301	TGAATACCAA	GCTGAGTGCC	GTGTATGCCG	GAGAAGCCAT	GCACACGGCC	GGGTGTGCAC
9361	CATCCTACAG	AGTTAAGAGA	GCAGACATAG	CCACGTGCAC	AGAAGCGGCT	GTGGTTAACG-

FIGURE 29D

	CAGCTAACGC					
	CGTCAGCCTT					
	CGTACCCCGT					
	ACCGCGAATT					
	GCAGCGTAGC					
	AGCAATCCCT					
	ACTGCAGAGA					
	TGGAGTTGCT					
	GCAGCCTGGT					
9961	AAGGTACGAA	ATTCAACCAG	GCTGCTATTG	ATATGGCAGA	GATACTGACG	TTGTGGCCCA
10021	GACTGCAAGA	GGCAAACGAA	CAGATATGCC	TATACGCGCT	GGGCGAAACA	ATGGACAACA
	TCAGATCCAA					
10141	GCCTGTGCCG	CTACGCAATG	ACAGCAGAAC	GGATCGCCCG	CCTTAGGTCA	CACCAAGTTA
10201	AAAGCATGGT	GGTTTGCTCA	TCTTTTCCCC	TCCCGAAATA	CCATGTAGAT	GGGGTGCAGA
10261	AGGTAAAGTG	CGAGAAGGTT	CTCCTGTTCG	ACCCGACGGT	ACCTTCAGTG	GTTAGTCCGC
10321	GGAAGTATGC	CGCATCTACG	ACGGACCACT	CAGATCGGTC	GTTACGAGGG	TTTGACTTGG
10381	ACTGGACCAC	CGACTCGTCT	TCCACTGCCA	GCGATACCAT	GTCGCTACCC	AGTTTGCAGT
	CGTGTGACAT					
	ACCCTGAACC					
	ATGTGGACCT					
	CCCGCGCGGC					
	CGTTTAGGAA					
	TGGCCTCCGG					
	CATATATTTT					
	ACAATCTCCA					
	TGGATACTGA					
	ATAAGAGTCG					
	TCACATCGGG					
	TTCGGTACCC					
	TAGCAATCGC					
	AGATAACAGA					
	ACAGAGCGAC					
	AGCCGACTGT					
11401	CGGCTGCCAC	CAAGAGAAAC	TGCAACGTCA	CGCAAATGCG	AGAACTACCC	ACCATGGACT
11461	CGGCAGTGTT	CAACGTGGAG	TGCTTCAAGC	GCTATGCCTG	CTCCGGAGAA	TATTCCCAAC
	AATATGCTAA					
	TGAAAGGCCC					
11641	AGGTTCCCAT	GGACAGATTC	ACGGTCGACA	TCADACCACA	TCTCAAACTC	ACTCCACCCA
11701	CGAAACACAC	AGAGGAAAGA	CCCAAAGTCC	ACCTA ATTCA	ACCACACAC	CCATTCCCCA
	CCGCTTACCT					
	CTAACGTGCA					
	ACTTCCACCC					
11941	ACGACTCCTT	GGCTCTTACA	CCTTTNATCA	TCCTCCAACA	TOTACCOCTO	CATCACTACC
12001	TGCTGGACTT	GATCGAGGCA	GCCTTTCCCC	AAATATCCAC	CTCTCACCTA	CCAACTCCCA
12061	CGCGCTTCAA	GTTCGGAGCT	ATCATCADAT	CCCCC ATCTT	TCTCACCIA	TTTATTATTA
12121	CTGTTTTGAA	CATCACCATA	GCAAGCAGGG	TACTCCACCA	CACACTOR	TITATIANCA
12181	GTGCGGCCTT	CATCGGCGAC	CARGCAGGG	THE IGGAGEA	CATCTCCCACT	AACCTCACCT
12241	CGGAGAGGTG	CGCGTCGTGG	CTCAACATCC	T I CACGGAGT	CATCICCGAC	CTCATCCCCC
12301	AAAAACCCCC	ATATTTTTCT	GGGGGATTCA	TACTURATION	CALIGACGCI	GICAIGGGG
12361	GCCGTGTTTC	ACACCCACTOT ACACT	AAGCCCCTCTC	TAGITITIGA	TA ACCCCCTA	ACACCUCCT
12401	ACAAGCAGGA	CCAACACACTI	CCACCACCAC	TCACTCACC	COTT	ACAGC TGAAG
16161	AUUAUUA	COMMONCAGO	COACGAGCAC	1GAG1GACGA	GGII .	

FIGURE 29E

Figure 30A: pDEST10 Polyhedron Promoter with N-His6,
Baculovirus Transfer Plasmid

mRNA from polyhedrin promoter

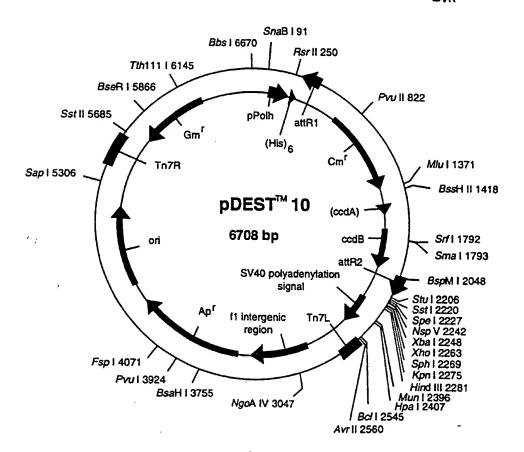
154 aaa taa gta ttt tac tgt ttt cgt aac agt ttt gta ata aaa aaa cct ata
ttt att cat aaa atg aca aaa gca ttg tca aaa cat tat ttt ttt gga tat

205 aat att ceg gat tat tea tae egt eee aee ate ggg ege gga tet egg tee tta taa gge eta ata agt atg gea ggg tgg tag eee geg eet aga gee agg

Met Ser Tyr Tyr His His His His His His Ase Tyr Ase Tie & ctt tgg tac age atg gta gtg gta gtg gta gtg cta atg cta tag ggt

TEV professe

307 Ter Thr Glu Ash Leu Tur Phe Gint Glu Die The Ser Leu Tur Lus Lus acg acc gaa aac ctg tat ttt cag ggc atc aca agt ttg/tec adr aaa gct tgc tgg ctt ttg gac ata aaa gtc ccg tag tgt tca aac atg ttt ttt oga att Ri

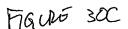


### pDEST10 6708 bp

Location (Base Nos.)	Gene Encoded
23152	Ppolh
461337	attRl
7111370	CmR
14901574	inactivated ccdA
17122017	ccdB
20582182	attR2
33944369	ampR
45105164	ori
565862	genR

1	CCCCGGATGA	AGTGGTTCGC	ATCCTCGGTT	TTCTGGAAGG	CGAGCATCGT	TTGTTCGCCC
61	AGGACTCTAG	CTATAGTTCT	AGTGGTTGGC	TACGTATACT	CCGGAATATT	AATAGATCAT
121	GGAGATAATT	AAAATGATAA	CCATCTCGCA	AATAAATAAG	TATTTTACTG	TTTTCGTAAC
181	AGTTTTGTAA	TAAAAAAACC	TATAAATATT	CCGGATTATT	CATACCGTCC	CACCATCGGG
241	CGCGGATCTC	GGTCCGAAAC	CATGTCGTAC	TACCATCACC	ATCACCATCA	CGATTACGAT
301	ATCCCAACGA	CCGAAAACCT	GTATTTTCAG	GGCATCACAA	GTTTGTACAA	AAAAGCTGAA
361	CGAGAAACGT	AAAATGATAT	AAATATCAAT	ATATTAAATT	AGATTTTGCA	TAAAAAACAG
	ACTACATAAT					
481	CATCACCCGA	CGCACTTTGC	GCCGAATAAA	TACCTGTGAC	GGAAGATCAC	TTCGCAGAAT
541	AAATAAATCC	TGGTGTCCCT	GTTGATACCG	GGAAGCCCTG	GGCCAACTTT	TGGCGAAAAT
	GAGACGTTGA					
661	CGGGCGTATT	TTTTGAGTTA	TCGAGATTTT	CAGGAGCTAA	GGAAGCTAAA	ATGGAGAAAA
	AAATCACTGG					
781	CATTTCAGTC	AGTTGCTCAA	TGTACCTATA	ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT
841	TTTTAAAGAC	CGTAAAGAAA	AATAAGCACA	AGTTTTATCC	GGCCTTTATT	CACATTCTTG
901	CCCGCCTGAT	GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA
	TATGGGATAG					
1021	CGCTCTGGAG	TGAATACCAC	GACGATTTCC	GGCAGTTTCT	ACACATATAT	TCGCAAGATG
1081	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	TCCCTAAAGG	GTTTATTGAG	AATATGTTTT
	TCGTCTCAGC					
	ACAACTTCTT					
	TGATGCCGCT					
	TGCTTAATGA					
1381	CCGGCTTACT	AAAAGCCAGA	TAACAGTATG	CGTATTTGCG	CGCTGATTTT	TGCGGTATAA
1441	GAATATATAC	TGATATGTAT	ACCCGAAGTA	TGTCAAAAAG	${\tt AGGTGTGCTA}$	TGAAGCAGCG
	TATTACAGTG					
	ATCTCCGGTC					
	TGGAAAGCGG					
1681	TCTTTTGCTG	ACGAGAACAG	GGACTGGTGA	AATGCAGTTT	AAGGTTTACA	CCTATAAAAG
1741	AGAGAGCCGT	TATCGTCTGT	TTGTGGATGT	ACAGAGTGAT	ATTATTGACA	CGCCCGGGCG
1801	ACGGATGGTG	ATCCCCCTGG	CCAGTGCACG	TCTGCTGTCA	GATAAAGTCT	CCCGTGAACT
1861	TTACCCGGTG	GTGCATATCG	GGGATGAAAG	CTGGCGCATG	ATGACCACCG	ATATGGCCAG
1921	TGTGCCGGTC	TCCGTTATCG	GGGAAGAAGT	GGCTGATCTC	AGCCACCGCG	AAAATGACAT
1981	CAAAAACGCC	ATTAACCTGA	TGTTCTGGGG	AATATAAATG	TCAGGCTCCC	TTATACACAG
2041	CCAGTCTGCA	GGTCGACCAT	AGTGACTGGA	TATGTTGTGT	TTTACAGTAT	TATGTAGTCT
2101	GTTTTTTATG	CAAAATCTAA	TTTAATATAT	TGATATTTAT	ATCATTTTAC	GTTTCTCGTT
2161	CAGCTTTCTT	GTACAAAGTG	GTGATGCCAT	GGATCCGGAA	TTCAAAGGCC	TACGTCGACG
2221	AGCTCAACTA	GTGCGGCCGC	TTTCGAATCT	AGAGCCTGCA	GTCTCGAGGC	ATGCGGTACC
2281	AAGCTTGTCG	AGAAGTACTA	GAGGATCATA	ATCAGCCATA	CCACATTTGT	AGAGGTTTTA
2341	CTTGCTTTAA	AAAACCTCCC	ACACCTCCCC	CTGAACCTGA	AACATAAAAT	GAATGCAATT
2401	GTTGTTGTTA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA	TAGCATCACA
2461	AATTTCACAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	GTGGTTTGTC	CAAACTCATC
2521	AATGTATCTT	ATCATGTCTG	GATCTGATCA	CTGCTTGAGC	CTAGGAGATC	CGAACCAGAT
2581	AAGTGAAATC	TAGTTCCAAA	CTATTTTGTC	ATTTTTAATT	TTCGTATTAG	CTTACGACGC-

2641 TACACCCAGT TCCCATCTAT TTTGTCACTC TTCCCTAAAT AATCCTTAAA AACTCCATTT 2701 CCACCCCTCC CAGTTCCCAA CTATTTTGTC CGCCCACAGC GGGGCATTTT TCTTCCTGTT 2761 ATGTTTTTAA TCAAACATCC TGCCAACTCC ATGTGACAAA CCGTCATCTT CGGCTACTTT 2821 TTCTCTGTCA CAGAATGAAA ATTTTTCTGT CATCTCTTCG TTATTAATGT TTGTAATTGA 2881 CTGAATATCA ACGCTTATTT GCAGCCTGAA TGGCGAATGG GACGCGCCCT GTAGCGGCGC 2941 ATTAAGCGCG GCGGGTGTGG TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT 3001 AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG 3061 TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC GGCACCTCGA 3121 CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG CCATCGCCCT GATAGACGGT 3181 TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTCTTGT TCCAAACTGG 3241 AACAACACTC AACCCTATCT CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTC 3301 GGCCTATTGG TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT TTAACAAAAT 3361 ATTAACGTTT ACAATTTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTTG 3421 TITATTITC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT 3481 GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCGTG TCGCCCTTAT 3541 TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT 3601 AAAAGATGCT GAAGATCAGT TGGGTGCACG AGTGGGTTAC ATCGAACTGG ATCTCAACAG 3661 CGGTAAGATC CTTGAGAGTT TTCGCCCCGA AGAACGTTTT CCAATGATGA GCACTTTTAA 3721 AGTTCTGCTA TGTGGCGCGG TATTATCCCG TATTGACGCC GGGCAAGAGC AACTCGGTCG 3781 CCGCATACAC TATTCTCAGA ATGACTTGGT TGAGTACTCA CCAGTCACAG AAAAGCATCT 3841 TACGGATGGC ATGACAGTAA GAGAATTATG CAGTGCTGCC ATAACCATGA GTGATAACAC 3901 TGCGGCCAAC TTACTTCTGA CAACGATCGG AGGACCGAAG GAGCTAACCG CTTTTTTGCA 3961 CAACATGGGG GATCATGTAA CTCGCCTTGA TCGTTGGGAA CCGGAGCTGA ATGAAGCCAT 4021 ACCAAACGAC GAGCGTGACA CCACGATGCC TGTAGCAATG GCAACAACGT TGCGCAAACT 4081 ATTAACTGGC GAACTACTTA CTCTAGCTTC CCGGCAACAA TTAATAGACT GGATGGAGGC 4141 GGATAAAGTT GCAGGACCAC TTCTGCGCTC GGCCCTTCCG GCTGGCTGGT TTATTGCTGA 4201 TAAATCTGGA GCCGGTGAGC GTGGGTCTCG CGGTATCATT GCAGCACTGG GGCCAGATGG 4261 TAAGCCCTCC.CGTATCGTAG TTATCTACAC GACGGGGAGT CAGGCAACTA TGGATGAACG 4321 AAATAGACAG ATCGCTGAGA TAGGTGCCTC ACTGATTAAG CATTGGTAAC TGTCAGACCA 4381 AGTTTACTCA TATATACTTT AGATTGATTT AAAACTTCAT TTTTAATTTA AAAGGATCTA 4441 GGTGAAGATC CTTTTTGATA ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTCGTTCCA 4501 CTGAGCGTCA GACCCCGTAG AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTTCTGCG 4561 CGTAATCTGC TGCTTGCAAA CAAAAAAACC ACCGCTACCA GCGGTGGTTT GTTTGCCGGA 4621 TCAAGAGCTA CCAACTCTTT TTCCGAAGGT AACTGGCTTC AGCAGAGCGC AGATACCAAA 4681 TACTGTCCTT CTAGTGTAGC CGTAGTTAGG CCACCACTTC AAGAACTCTG TAGCACCGCC 4741 TACATACCTC GCTCTGCTAA TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG 4801 TCTTACCGGG TTGGACTCAA GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC 4861 GGGGGGTTCG TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT 4921 ACAGCGTGAG CATTGAGAAA GCGCCACGCT TCCCGAAGGG AGAAAGGCGG ACAGGTATCC 4981 GGTAAGCGGC AGGGTCGGAA CAGGAGAGCG CACGAGGGAG CTTCCAGGGG GAAACGCCTG 5041 GTATCTTTAT AGTCCTGTCG GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG 5101 CTCGTCAGGG GGGCGGAGCC TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT 5161 GGCCTTTTGC TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG ATTCTGTGGA 5221 TAACCGTATT ACCGCCTTTG AGTGAGCTGA TACCGCTCGC CGCAGCCGAA CGACCGAGCG 5281 CAGCGAGTCA GTGAGCGAGG AAGCGGAAGA GCGCCTGATG CGGTATTTTC TCCTTACGCA 5341 TCTGTGCGGT ATTTCACACC GCAGACCAGC CGCGTAACCT GGCAAAATCG GTTACGGTTG 5401 AGTAATAAAT GGATGCCCTG CGTAAGCGGG TGTGGGCCGGA CAATAAAGTC TTAAACTGAA 5461 CAAAATAGAT CTAAACTATG ACAATAAAGT CTTAAACTAG ACAGAATAGT TGTAAACTGA 5521 AATCAGTCCA GTTATGCTGT GAAAAAGCAT ACTGGACTTT TGTTATGGCT AAAGCAAACT 5581 CTTCATTTTC TGAAGTGCAA ATTGCCCGTC GTATTAAAGA GGGGCGTGGC CAAGGGCATG 5641 GTAAAGACTA TATTCGCGGC GTTGTGACAA TTTACCGAAC AACTCCGCGG CCGGGAAGCC 5701 GATCTCGGCT TGAACGAATT GTTAGGTGGC GGTACTTGGG TCGATATCAA AGTGCATCAC 5761 TTCTTCCCGT ATGCCCAACT TTGTATAGAG AGCCACTGCG GGATCGTCAC CGTAATCTGC 5821 TTGCACGTAG ATCACATAAG CACCAAGCGC GTTGGCCTCA TGCTTGAGGA GATTGATGAG 5881 CGCGGTGGCA ATGCCCTGCC TCCGGTGCTC GCCGGAGACT GCGAGATCAT AGATATAGAT 5941 CTCACTACGC GGCTGCTCAA ACCTGGGCAG AACGTAAGCC GCGAGAGCGC CAACAACCGC 6001 TTCTTGGTCG AAGGCAGCAA GCGCGATGAA TGTCTTACTA CGGAGCAAGT TCCCGAGGTA 6061 ATCGGAGTCC GGCTGATGTT GGGAGTAGGT GGCTACGTCT CCGAACTCAC GACCGAAAAG-



6121	ATCAAGAGCA	GCCCGCATGG	ATTTGACTTG	GTCAGGGCCG	AGCCTACATG	TGCGAATGAT	
6181	${\tt GCCCATACTT}$	GAGCCACCTA	ACTITGTTTT	AGGGCGACTG	CCCTGCTGCG	TAACATCGTT	
6241	GCTGCTGCGT	AACATCGTTG	CTGCTCCATA	ACATCAAACA	TCGACCCACG	GCGTAACGCG	
6301	CTTGCTGCTT	GGATGCCCGA	GGCATAGACT	GTACAAAAA	ACAGTCATAA	CAAGCCATGA	
6361	AAACCGCCAC	TGCGCCGTTA	CCACCGCTGC	${\tt GTTCGGTCAA}$	${\tt GGTTCTGGAC}$	CAGTTGCGTG	
6421	AGCGCATACG	CTACTTGCAT	TACAGTTTAC	GAACCGAACA	GGCTTATGTC	AACTGGGTTC	
6481	GTGCCTTCAT	CCGTTTCCAC	GGTGTGCGTC	ACCCGGCAAC	CTTGGGCAGC	AGCGAAGTCG	
6541	AGGCATTTCT	GTCCTGGCTG	GCGAACGAGC	GCAAGGTTTC	${\tt GGTCTCCACG}$	CATCGTCAGG	
6601	CATTGGCGGC	CTTGCTGTTC	TTCTACGGCA	AGGTGCTGTG	CACGGATCTG	CCCTGGCTTC	
6661	AGGAGATCGG	AAGACCTCGG	CCGTCGCGGC	GCTTGCCGGT	GGTGCTGA		

Figure 31A:

DEST 11

Tet-regulated eukaryotic expression

ate act tgg cag tet age gat cea gee tee ggg gge ceg aat teg age teg tat etg age teg tat etg tag age teg eag tee etg egg tag gtg ega caa aac tgg agg

409 ata gaa gac ace ggg ace gat eea gee tee geg gee eeg gge tta age teg age

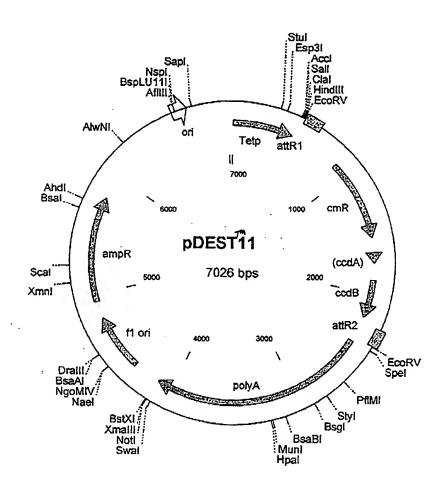
tat ett etg tgg eee tgg eta ggt egg agg ege egg gge tta age teg age

460 gta eee ggg gat eet eta gag teg agg teg aeg gta teg ata age teg age

cat ggg eee eta gga gat ete age tee age tge eat age tat teg ata age

The the 1

511 tea aca agt ttg tag aar aaa get gar egg gaa aeg taa dat gat ata agt tgt tea aac atg tttl tet ega ett tge att tta eta tat tta



### pDEST11 7026 bp

Location (Base Nos.)			Gene Encoded					
	4479			Tetp ((Tet operator)7 and min				
		33/2						
		638514		attR1	hCMV promoter)			
		888154		CmR				
				_	vated ccdA			
		166717		ccdB	vateu ccua			
		188921		"				
		223523		attR2				
		240241		polyA				
		434748 494057		fl ori				
		.494037	31	ampR				
1	CGAGTTTACC	ACTCCCTATC	AGTGATAGAG	AAAAGTGAAA	GTCGAGTTTA	CCACTCCCTA		
61	TCAGTGATAG	AGAAAAGTGA	AAGTCGAGTT	TACCACTCCC	TATCAGTGAT	AGAGAAAAGT		
121	GAAAGTCGAG	TTTACCACTC	CCTATCAGTG	ATAGAGAAAA	GTGAAAGTCG	AGTTTACCAC		
	TCCCTATCAG							
241	AAAAGTGAAA	GTCGAGTTTA	CCACTCCCTA	TCAGTGATAG	AGAAAAGTGA	AAGTCGAGCT		
301	CGGTACCCGG	GTCGAGTAGG	CGTGTACGGT	GGGAGGCCTA	TATAAGCAGA	GCTCGTTTAG		
361	TGAACCGTCA	GATCGCCTGG	AGACGCCATC	CACGCTGTTT	TGACCTCCAT	AGAAGACACC		
421	GGGACCGATC	CAGCCTCCGC	GGCCCCGAAT	TCGAGCTCGG	TACCCGGGGA	TCCTCTAGAG		
	TCGAGGTCGA			-				
	GAAACGTAAA							
	ACATAATACT							
661	CACCCGACGC	ACTTTGCGCC	GAATAAATAC	CTGTGACGGA	AGATCACTTC	GCAGAATAAA		
721	TAAATCCTGG	TGTCCCTGTT	GATACCGGGA	AGCCCTGGGC	CAACTTTTGG	CGAAAATGAG		
781	ACGTTGATCG	GCACGTAAGA	GGTTCCAACT	TTCACCATAA	TGAAATAAGA	TCACTACCGG		
841	GCGTATTTTT	TGAGTTATCG	AGATTTTCAG	GAGCTAAGGA	AGCTAAAATG	GAGAAAAAA		
	TCACTGGATA							
961	TTCAGTCAGT	TGCTCAATGT	ACCTATAACC	AGACCGTTCA	GCTGGATATT	ACGGCCTTTT		
	TAAAGACCGT			-				
1081	GCCTGATGAA	TGCTCATCCG	GAATTCCGTA	TGGCAATGAA	AGACGGTGAG	CTGGTGATAT		
1141	GGGATAGTGT	TCACCCTTGT	TACACCGTTT	TCCATGAGCA	AACTGAAACG	TTTTCATCGC		
	TCTGGAGTGA							
1261	CGTGTTACGG	TGAAAACCTG	GCCTATTTCC	CTAAAGGGTT	TATTGAGAAT	ATGTTTTTCG		
	TCTCAGCCAA							
	ACTTCTTCGC							
	TGCCGCTGGC							
	TTAATGAATT							
	GCTTACTAAA							
	TATATACTGA							
	TACAGTGACA							
	TCCGGTCTGG							
	AAAGCGGAAA							
	TTTGCTGACG							
	GAGCCGTTAT							
	GATGGTGATC							
	CCCGGTGGTG							
	GCCGGTCTCC							
	AAACGCCATT							
	GTCTGCAGGT							
	TTTTATGCAA							
	CTTTCTTGTA							
	GAGCACTGCG							
	TAAACGCCTG							
2521	CGGATCTTTG	TGAAGGAACC	TTACTTCTGT	GGTGTGACAT	AATTGGACAA	ACTACCTACA-		

2501	A1 ~1 mmm1 1 1					
		GCTCTAAGGT				
		TTTGTGTATT				
		TTAATGAGGA				
		CTGACTCTCA				
		TTCCTTCAGA				
		GCTTTGCTAT				
		AATATTCTGT				
3001	CTGTTTTTTC	TTACTCCACA	CAGGCATAGA	GTGTCTGCTA	TTAATAACTA	TGCTCAAAAA
3061	TTGTGTACCT	TTAGCTTTTT	AATTTGTAAA	GGGGTTAATA	AGGAATATTT	GATGTATAGT
3121	GCCTTGACTA	GAGATCATAA	TCAGCCATAC	CACATTTGTA	GAGGTTTTAC	TTGCTTTAAA
3181	AAACCTCCCA	CACCTCCCCC	TGAACCTGAA	ACATAAAATG	AATGCAATTG	TTGTTGTTAA
		GCAGCTTATA				
		TTTTCACTGC				
		ATCCCCAGGA				
		TCCAATCATA				
		AAAGGAAATT				
		GGGAAGTCCC				
		AGCAGAAACA				
		CACTGTGGTT				
		GGTTCCAAAA				
		ATAAGCATTA				
2001	TTCCTA A CA C	TGTAGCATTT	TOGGGTTA	CAGTTTGAGC	AGGATATTTG	GTCCTGTAGT
		ACCCTGCAGC				
		GGGTTTTCCA				
		AGTTACCCCA				
		GGTTAAGTCC				
		GAGCTCCAAT				
		ACGTCGTGAC				
		TTTCGCCAGC				
		CAGCCTGAAT				
4381	CGGGTGTGGT	GGTTACGCGC	AGCGTGACCG	CTACACTTGC	CAGCGCCCTA	GCGCCCGCTC
4441	CTTTCGCTTT	CTTCCCTTCC	TTTCTCGCCA	CGTTCGCCGG	CTTTCCCCGT	CAAGCTCTAA
4501	ATCGGGGGCT	CCCTTTAGGG	TTCCGATTTA	GTGCTTTACG	GCACCTCGAC	CCCAAAAAAC
4561	TTGATTAGGG	TGATGGTTCA	CGTAGTGGGC	CATCGCCCTG	ATAGACGGTT	TTTCGCCCTT
4621	TGACGTTGGA	GTCCACGTTC	TTTAATAGTG	GACTCTTGTT	CCAAACTGGA	ACAACACTCA
4681	ACCCTATCTC	GGTCTATTCT	TTTGATTTAT	AAGGGATTTT	GCCGATTTCG	GCCTATTGGT
		GCTGATTTAA				
		GGCACTTTTC				
		AATATGTATC				
		AAGAGTATGA				
		CTTCCTGTTT				
		GGTGCACGAG				
5101	TGAGAGTTTT	CGCCCGAAG	AACCTTTTCC	AATGATGAGC	ACTTTTAAAC	TTCTCCTATC
		TTATCCCGTA				
5221	TTCTCAGAAT	GACTTGGTTG	AGTACTCACC	ACTUACACAA	AACCATCTTA	CCGATCCCAT
5281	GACAGTAAGA	GAATTATGCA	GTGCTGCCAT	AGICACAGAA	CATAACACTC	CCCCCAACTT
5341	ACTICICACA	ACGATCGGAG	CACCGAACCA	CCTA A CCCCT	GATAACACTG	AGARGGGGGA
5401	TCATCTAACT	CGCCTTGATC	CTTCCCAAGGA	GCIAACCGCI	CARCOCACA	ACAIGGGGGA
5461	CCATCIANCI	ACGATGCCTG	GIIGGGAACC	A A CA A COMMO	GAAGCCATAC	CAAACGACGA
2201	ACCIDACACE.	CTACCTTCCCTC	TUCCHAIGE	AACAACGTTG	LUCAAACTAT	AACTGGCGA
2261	ACIACITACI	CTAGCTTCCC	CCCTTTCCCC	AATAGACTGG	ATGGAGGCGG	ATAAAGTTGC
5501	AGGACCACTT	CTGCGCTCGG	CCCTTCCGGC	TGGCTGGTTT	ATTGCTGATA	AATCTGGAGC
2041	TATOOTT CTT	GGGTCTCGCG	GIATCATIGC	AGCACTGGGG	CCAGATGGTA	AGCCCTCCCG
5/01	TATUGTAGTT	ATCTACACGA	CGGGGAGTCA	GGCAACTATG	GATGAACGAA	ATAGACAGAT
5/61	CGCTGAGATA	GGTGCCTCAC	TGATTAAGCA	TIGGTAACTG	TCAGACCAAG	TTTACTCATA
5821	TATACTTTAG	ATTGATTTAA	AACTTCATTT	TTAATTTAAA	AGGATCTAGG	TGAAGATCCT
5881	TTTTGATAAT	CTCATGACCA	AAATCCCTTA	ACGTGAGTTT	TCGTTCCACT	GAGCGTCAGA
5941	CCCCGTAGAA	AAGATCAAAG	GATCTTCTTG	AGATCCTTTT	TTTCTGCGCG	TAATCTGCTG
6001	CTTGCAAACA	AAAAAACCAC	CGCTACCAGC	GGTGGTTTGT	TTGCCGGATC	AAGAGCTACC-

6061	AACTCTTTTT	CCGAAGGTAA	CTGGCTTCAG	CAGAGCGCAG	ATACCAAATA	CTGTCCTTCT
6121	AGTGTAGCCG	TAGTTAGGCC	ACCACTTCAA	GAACTCTGTA	GCACCGCCTA	CATACCTCGC
6181	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	CAGTGGCGAT	AAGTCGTGTC	TTACCGGGTT
6241	GGACTCAAGA	CGATAGTTAC	CGGATAAGGC	GCAGCGGTCG	GGCTGAACGG	GGGGTTCGTG
6301	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	CACCGAACTG	AGATACCTAC	AGCGTGAGCT
6361	ATGAGAAAGC	GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	TAAGCGGCAG
6421	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG
6481	TCCTGTCGGG	TTTCGCCACC	TCTGACTTGA	GCGTCGATTT	TTGTGATGCT	CGTCAGGGGG
6541	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	GGCCTTTTTA	CGGTTCCTGG	CCTTTTGCTG
6601	GCCTTTTGCT	CACATGTTCT	TTCCTGCGTT	ATCCCCTGAT	TCTGTGGATA	ACCGTATTAC
6661	CGCCTTTGAG	TGAGCTGATA	CCGCTCGCCG	CAGCCGAACG	ACCGAGCGCA	GCGAGTCAGT
6721	GAGCGAGGAA	GCGGAAGAGC	GCCCAATACG	CAAACCGCCT	CTCCCCGCGC	GTTGGCCGAT
6781	TCATTAATGC	AGCTGGCACG	ACAGGTTTCC	CGACTGGAAA	GCGGGCAGTG	AGCGCAACGC
6841	AATTAATGTG	AGTTAGCTCA	CTCATTAGGC	ACCCCAGGCT	TTACACTTTA	TGCTTCCGGC
6901	TCGTATGTTG	TGTGGAATTG	TGAGCGGATA	ACAATTTCAC	ACAGGAAACA	GCTATGACCA
6961	TGATTACGCC	AAGCGCGCAA	TTAACCCTCA	CTAAAGGGAA	CAAAAGCTGG	GTACCGGGCC
7021	CCCCCT					

FIGURE 31)

Figure 32-A: pDEST12.2 CMV Promoter for Eukaryotic Expression, SV40 Promoter/ori for G418 Resistance

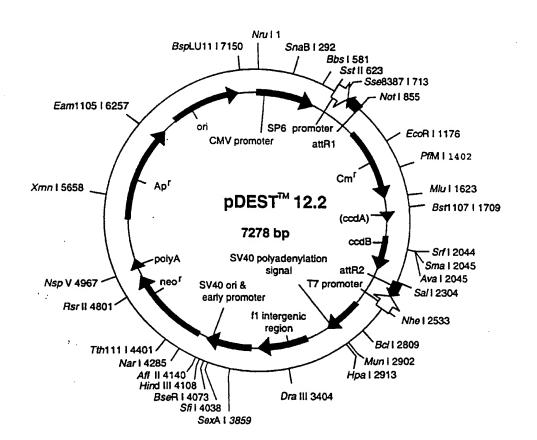
acc gcc aga tcg cct gga gac gcc atc cac gct gtt ttg acc tcc ata gaa tgg cag tct agc gga gac gcc atc cac gct gtt ttg acc tcc ata gaa tgg cag tct agc gga gcc cct ctg cgg tag gtg cga caa aac tgg agg tat ctt

358 gac acc ggg acc gat cca gcc tcc gga ctc tag cct agg ccg cgg agc gga ctg tgg ccc tgg cct tcg cct

409 taa caa ttt cac aca gga aac agc tat gac cat tag gcc ttt gca aaa agc att gtt aaa gtg tgt cct ttg tcg ata ctg gta atc cgg aaa cgt ttt tcg

460 tat tta ggt gac act ata gaa ggt acg cct gca ggt acc ggt ccg gaa ttc ata aat cca ctg tga tat ctt cca tgc gga cgt cca tgg cch ggc ctt aag

511 cca tca aca agt ttg tao ada aaa gct gaa cga gaa acg taa aat gat ata ggt agt tgt tca aac atg ttt ttt cga ctt tgc act tta cat ata gaa ggt agt gcc ctt tgc att tta cta cta acc act gtg tao ada gaa gct gaa cga gaa acg taa aat gat ata ggt agt tgt tca aac atg ttt ttt cga ctt gct ctt tgc act tta cta cta tat cta ca acc act gcd cta acc act gcd cta acc act gcd gcd cct aag



# pDEST12.2 7278 bp (rotated to position 3900)

Location (Base Nos.) 86..136 Gene Encoded

		90130		OLI		
		220742		CMV pr	omoter	
		105993	5	attRl		
		116818	27	CmR		
		194720	31	inacti	vated ccdA	
		216924	74	ccdB		
		251526	39	attR2		
		282431	.86	small	t & polyA	
		331033	78	lac		
		436351	.57	neo		
		568065		ampR		
				-		
1	GGGGGGCGGA	GCCTATGGAA	AAACGCCAGC	AACGCGGCCT	TTTTACGGTT	CCTGGCCTTT
61	TGCTGGCCTT	TTGCTCACAT	GTTCTTTCCT	GCGTTATCCC	CTGATTCTGT	GGATAACCGT
121	ATTACCGCCT	TTGAGTGAGC	TGATACCGCT	CGCCGCAGCC	GAACGACCGA	GCGCAGCGAG
181	TCAGTGAGCG	AGGAAGCGGA	AGAGCTCGCG	AATGCATGTC	GTTACATAAC	TTACGGTAAA
				CCGCCCATTG		
				TTGACGTCAA		
				TCATATGCCA		
				TGCCCAGTAC		
				CGCTATTACC		
				CTCACGGGGA		
				AAATCAACGG		
				TAGGCGTGTA		
				CTGGAGACGC		
				CCGGACTCTA		
				ATTAGGCCTT		
				GATCACAAGT		
				ATTAAATTAG		
				GTCACTATGG		
				AATGTGTGGA		
				GAGAAAAAA		
				TTTGAGGCAT		
				ACGGCCTTTT		
				ATTCTTGCCC		
				CTGGTGATAT		
				TTTTCATCGC		
				CAAGATGTGG		
				ATGTTTTTCG		
				AATATGGACA		
				AAGGTGCTGA		
				GGCAGAATGC		
						AGCCAGATAA
				GGTATAAGAA		
						GTTGACAGCG
						TAAGCACAAC
						ATCAGGAAGG
						AGAACAGGGA
						CGTCTGTTTG
						CCCCTGGCCA
						CATATCGGGG
						GTTATCGGGG
2401	AAGAAGTGGC	TGATCTCAGC	CACCGCGAAA	ATGACATCAA	AAACGCCATT	· AACCTGATGT

FIGURE 32B

2461 TCTGGGGAAT ATAAATGTCA GGCTCCCTTA TACACAGCCA GTCTGCAGGT CGACCATAGT 2521 GACTGGATAT GTTGTGTTTT ACAGTATTAT GTAGTCTGTT TTTTATGCAA AATCTAATTT 2581 AATATATTGA TATTTATATC ATTTTACGTT TCTCGTTCAG CTTTCTTGTA CAAAGTGGTG 2641 ATCGCGTGCA TGCGACGTCA TAGCTCTCTC CCTATAGTGA GTCGTATTAT AAGCTAGGCA 2701 CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACTGCT AGCTTGGGAT CTTTGTGAAG 2761 GAACCTTACT TCTGTGGTGT GACATAATTG GACAAACTAC CTACAGAGAT TTAAAGCTCT 2821 AAGGTAAATA TAAAATTTTT AAGTGTATAA TGTGTTAAAC TAGCTGCATA TGCTTGCTGC 2881 TTGAGAGTTT TGCTTACTGA GTATGATTTA TGAAAATATT ATACACAGGA GCTAGTGATT 2941 CTAATTGTTT GTGTATTTTA GATTCACAGT CCCAAGGCTC ATTTCAGGCC CCTCAGTCCT 3001 CACAGTCTGT TCATGATCAT AATCAGCCAT ACCACATTTG TAGAGGTTTT ACTTGCTTTA 3061 AAAAACCTCC CACACCTCCC CCTGAACCTG AAACATAAAA TGAATGCAAT TGTTGTTGTT 3121 AACTTGTTTA TTGCAGCTTA TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTCACA 3181 AATAAAGCAT TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACTCAT CAATGTATCT 3241 TATCATGTCT GGATCGATCC TGCATTAATG AATCGGCCAA CGCGCGGGGA GAGGCGGTTT 3301 GCGTATTGGC TGGCGTAATA GCGAAGAGGC CCGCACCGAT CGCCCTTCCC AACAGTTGCG 3361 CAGCCTGAAT GGCGAATGGG ACGCGCCCTG TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT 3421 GGTTACGCGC AGCGTGACCG CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT 3481 CTTCCCTTCC TTTCTCGCCA CGTTCGCCGG CTTTCCCCGT CAAGCTCTAA ATCGGGGGGCT 3541 CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC TTGATTAGGG 3601 TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT TTTCGCCCTT TGACGTTGGA 3661 GTCCACGTTC TTTAATAGTG GACTCTTGTT CCAAACTGGA ACAACACTCA ACCCTATCTC 3721 GGTCTATTCT TTTGATTTAT AAGGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA 3781 GCTGATTTAA CAAATATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTCGCC 3841 TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTC ACACCGCATA CGCGGATCTG 3901 CGCAGCACCA TGGCCTGAAA TAACCTCTGA AAGAGGAACT TGGTTAGGTA CCTTCTGAGG 3961 CGGAAAGAAC CAGCTGTGGA ATGTGTGTCA GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC 4021 AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCAGGT GTGGAAAGTC 4081 CCCAGGCTCC CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT 4141 AGTCCCGCC CTAACTCCGC CCATCCCGCC CCTAACTCCG CCCAGTTCCG CCCATTCTCC 4201 GCCCCATGGC TGACTAATTT TTTTTATTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA 4261 GCTATTCCAG AAGTAGTGAG GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGA 4321 TTCTTCTGAC ACAACAGTCT CGAACTTAAG GCTAGAGCCA CCATGATTGA ACAAGATGGA 4381 TTGCACGCAG GTTCTCCGGC CGCTTGGGTG GAGAGGCTAT TCGGCTATGA CTGGGCACAA 4441 CAGACAATCG GCTGCTCTGA TGCCGCCGTG TTCCGGCTGT CAGCGCAGGG GCGCCCGGTT 4501 CTTTTTGTCA AGACCGACCT GTCCGGTGCC CTGAATGAAC TGCAGGACGA GGCAGCGCGG 4561 CTATCGTGGC TGGCCACGAC GGGCGTTCCT TGCGCAGCTG TGCTCGACGT TGTCACTGAA 4621 GCGGGAAGGG ACTGGCTGCT ATTGGGCGAA GTGCCGGGGC AGGATCTCCT GTCATCTCAC 4681 CTTGCTCCTG CCGAGAAAGT ATCCATCATG GCTGATGCAA TGCGGCGGCT GCATACGCTT 4741 GATCCGGCTA CCTGCCCATT CGACCACCAA GCGAAACATC GCATCGAGCG AGCACGTACT 4801 CGGATGGAAG CCGGTCTTGT CGATCAGGAT GATCTGGACG AAGAGCATCA GGGGCTCGCG 4861 CCAGCCGAAC TGTTCGCCAG GCTCAAGGCG CGCATGCCCG ACGGCGAGGA TCTCGTCGTG 4921 ACCCATGGCG ATGCCTGCTT GCCGAATATC ATGGTGGAAA ATGGCCGCTT TTCTGGATTC 4981 ATCGACTGTG GCCGGCTGGG TGTGGCGGAC CGCTATCAGG ACATAGCGTT GGCTACCCGT 5041 GATATTGCTG AAGAGCTTGG CGGCGAATGG GCTGACCGCT TCCTCGTGCT TTACGGTATC 5101 GCCGCTCCCG ATTCGCAGCG CATCGCCTTC TATCGCCTTC TTGACGAGTT CTTCTGAGCG 5161 GGACTCTGGG GTTCGAAATG ACCGACCAAG CGACGCCCAA CCTGCCATCA CGATGGCCGC 5221 AATAAAATAT CTTTATTTTC ATTACATCTG TGTGTTGGTT TTTTGTGTGA ATCGATAGCG 5281 ATAAGGATCC GCGTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC 5341: CAGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGTCT GCTCCCGGCA 5401 TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG GTTTTCACCG 5461 TCATCACCGA AACGCGCGAG ACGAAAGGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT 5521 GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA 5581 ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA 5641 CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT 5701 GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG 5761 CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG 5821 GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG 5881 AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG





5941	CAACTCGGTC	GCCGCATACA	CTATTCTCAG	AATGACTTGG	TTGAGTACTC	ACCAGTCACA	
6001	GAAAAGCATC	TTACGGATGG	CATGACAGTA	AGAGAATTAT	GCAGTGCTGC	CATAACCATG	
6061	AGTGATAACA	CTGCGGCCAA	CTTACTTCTG	ACAACGATCG	GAGGACCGAA	GGAGCTAACC	
6121	GCTTTTTTGC	ACAACATGGG	GGATCATGTA	ACTCGCCTTG	ATCGTTGGGA	ACCGGAGCTG	
6181	AATGAAGCCA	TACCAAACGA	CGAGCGTGAC	ACCACGATGC	CTGTAGCAAT	GGCAACAACG	
6241	TTGCGCAAAC	TATTAACTGG	CGAACTACTT	ACTCTAGCTT	CCCGGCAACA	ATTAATAGAC	
6301	TGGATGGAGG	CGGATAAAGT	TGCAGGACCA	CTTCTGCGCT	CGGCCCTTCC	GGCTGGCTGG	
6361	TTTATTGCTG	ATAAATCTGG	AGCCGGTGAG	CGTGGGTCTC	GCGGTATCAT	TGCAGCACTG	
6421	GGGCCAGATG	GTAAGCCCTC	CCGTATCGTA	GTTATCTACA	CGACGGGGAG	TCAGGCAACT	
6481	ATGGATGAAC	GAAATAGACA	GATCGCTGAG	ATAGGTGCCT	CACTGATTAA	GCATTGGTAA	
6541	CTGTCAGACC	AAGTTTACTC	ATATATACTT	TAGATTGATT	TAAAACTTCA	TTTTTAATTT	
6601	AAAAGGATCT	AGGTGAAGAT	CCTTTTTGAT	AATCTCATGA	CCAAAATCCC	TTAACGTGAG	
6661	TTTTCGTTCC	ACTGAGCGTC	AGACCCCGTA	GAAAAGATCA	AAGGATCTTC	TTGAGATCCT	
6721	TTTTTTCTGC	GCGTAATCTG	CTGCTTGCAA	ACAAAAAAAC	CACCGCTACC	AGCGGTGGTT	
6781	TGTTTGCCGG	ATCAAGAGCT	ACCAACTCTT	TTTCCGAAGG	TAACTGGCTT	CAGCAGAGCG	
6841	CAGATACCAA	ATACTGTCCT	TCTAGTGTAG	CCGTAGTTAG	GCCACCACTT	CAAGAACTCT	
6901	GTAGCACCGC	CTACATACCT	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	TGCCAGTGGC	
6961	GATAAGTCGT	GTCTTACCGG	GTTGGACTCA	AGACGATAGT	TACCGGATAA	GGCGCAGCGG	
7021	TCGGGCTGAA	CGGGGGGTTC	GTGCACACAG	CCCAGCTTGG	AGCGAACGAC	CTACACCGAA	
7081	CTGAGATACC	TACAGCGTGA	GCATTGAGAA	AGCGCCACGC	TTCCCGAAGG	GAGAAAGGCG	
7141	GACAGGTATC	CGGTAAGCGG	CAGGGTCGGA	ACAGGAGAGC	GCACGAGGGA	GCTTCCAGGG	
7201	GGAAACGCCT	GGTATCTTTA	TAGTCCTGTC	GGGTTTCGCC	ACCTCTGACT	TGAGCGTCGA	
7261	TTTTTGTGAT	GCTCGTCA					

FIGURE 32D

Figure 33A;

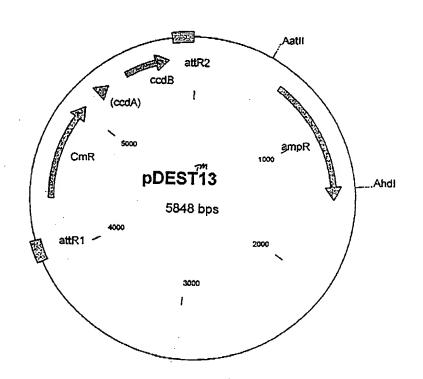
PIRTIS

Native protein in E. coli: λPL promoter

tgggcaaacc aagacagcta aagatetete acctaceaaa caatgeeee etgcaaaaaa accegtttgg ttetgtegat ttetagagag tggatggtt gttacggggg gacgttttt

3781 taaatteata taaaaaacat acagataacc atetgeggtg ataaattate tetggeggtg attaaagtat atttttgta tgtetattgg tagacgeeac tattaatag agacegeeac tagacaacaa acceptattt atggtgacg ggtgatactg agcacateag caggaegeac tgaccaccat acceptattt atggtgaceg ceactatgac teggtgtagte gteetgegtg actggtggta etggtgate gagaagggea gcatteaaag cagaaggett ettecaetge gagaatttt aateeggae ttetteeegt egtaagttte gtetteegaa

3961 tggggtgtgt gatacgaaac gaagcattgg gateatcaca agtttgtaca aaaaagetga accecacaa ctatgetttg ettegtaacc etagtagtgt teaaacatgt Effttegact,



#### pDEST13 5848 bp

Location (Base Nos.)	<u>Gene Encoded</u>
5991458	ampR
41233998	attR1
43725031	CmR
51515235	inactivated ccdA
53735678	ccdB
57195843	attR2

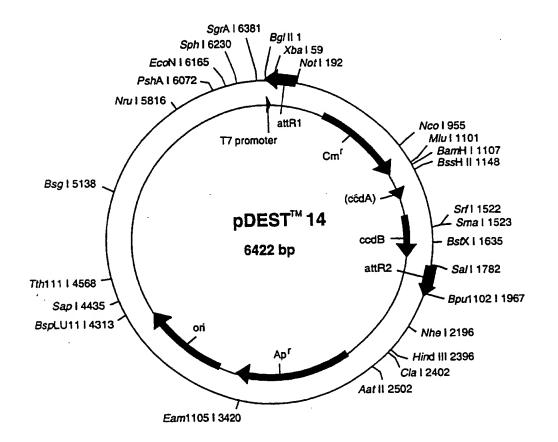
1 TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA 61 TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG CCCGCACCGA 121 TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCCTGATGC GGTATTTTCT 181 CCTTACGCAT CTGTGCGGTA TTTCACACCG CATATGGTGC ACTCTCAGTA CAATCTGCTC 241 TGATGCCGCA TAGTTAAGCC AGCCCCGACA CCCGCCAACA CCCGCTGACG CGCCCTGACG 301 GGCTTGTCTG CTCCCGGCAT CCGCTTACAG ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT 361 GTGTCAGAGG TTTTCACCGT CATCACCGAA ACGCGCGAGA CGAAAGGGCC TCGTGATACG 421 CCTATTTTA TAGGTTAATG TCATGATAAT AATGGTTTCT TAGACGTCAG GTGGCACTTT 481 TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA 541 TCCGCTCATG AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT 601 GAGTATTCAA CATTTCCGTG TCGCCCTTAT TCCCTTTTTT GCGGCATTTT GCCTTCCTGT 661 TTTTGCTCAC CCAGAAACGC TGGTGAAAGT AAAAGATGCT GAAGATCAGT TGGGTGCACG 721 AGTGGGTTAC ATCGAACTGG ATCTCAACAG CGGTAAGATC CTTGAGAGTT TTCGCCCCGA 781 AGAACGTTTT CCAATGATGA GCACTTTTAA AGTTCTGCTA TGTGGCGCGG TATTATCCCG 841 TATTGACGCC GGGCAAGAGC AACTCGGTCG CCGCATACAC TATTCTCAGA ATGACTTGGT 901 TGAGTACTCA CCAGTCACAG AAAAGCATCT TACGGATGGC ATGACAGTAA GAGAATTATG 961 CAGTGCTGCC ATAACCATGA GTGATAACAC TGCGGCCAAC TTACTTCTGA CAACGATCGG 1021 AGGACCGAAG GAGCTAACCG CTTTTTTGCA CAACATGGGG GATCATGTAA CTCGCCTTGA 1081 TCGTTGGGAA CCGGAGCTGA ATGAAGCCAT ACCAAACGAC GAGCGTGACA CCACGATGCC 1141 TGTAGCAATG GCAACAACGT TGCGCAAACT ATTAACTGGC GAACTACTTA CTCTAGCTTC 1201 CCGGCAACAA TTAATAGACT GGATGGAGGC GGATAAAGTT GCAGGACCAC TTCTGCGCTC 1261 GGCCCTTCCG GCTGGCTGGT TTATTGCTGA TAAATCTGGA GCCGGTGAGC GTGGGTCTCG 1321 CGGTATCATT GCAGCACTGG GGCCAGATGG TAAGCCCTCC CGTATCGTAG TTATCTACAC 1381 GACGGGGAGT CAGGCAACTA TGGATGAACG AAATAGACAG ATCGCTGAGA TAGGTGCCTC 1441 ACTGATTAAG CATTGGTAAC TGTCAGACCA AGTTTACTCA TATATACTTT AGATTGATTT 1501 AAAACTTCAT TTTTAATTTA AAAGGATCTA GGTGAAGATC CTTTTTGATA ATCTCATGAC 1561 CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGAGCGTCA GACCCCGTAG AAAAGATCAA 1621 AGGATCTTCT TGAGATCCTT TTTTTCTGCG CGTAATCTGC TGCTTGCAAA CAAAAAAACC 1681 ACCGCTACCA GCGGTGGTTT GTTTGCCGGA TCAAGAGCTA CCAACTCTTT TTCCGAAGGT 1741 AACTGGCTTC AGCAGAGCGC AGATACCAAA TACTGTTCTT CTAGTGTAGC CGTAGTTAGG 1801 CCACCACTTC AAGAACTCTG TAGCACCGCC TACATACCTC GCTCTGCTAA TCCTGTTACC 1861 AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG TTGGACTCAA GACGATAGTT 1921 ACCGGATAAG GCGCAGCGGT CGGGCTGAAC GGGGGGTTCG TGCACACAGC CCAGCTTGGA 1981 GCGAACGACC TACACCGAAC TGAGATACCT ACAGCGTGAG CATTGAGAAA GCGCCACGCT 2041 TCCCGAAGGG AGAAAGGCGG ACAGGTATCC GGTAAGCGGC AGGGTCGGAA CAGGAGAGCG 2101 CACGAGGGAG CTTCCAGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTCG GGTTTCGCCA 2161 CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG GGGCGGAGCC TATGGAAAAA 2221 CGCCAGCAAC GCGGCCTTTT TACGGTTCCT GGCCTTTTGC TGGCCTTTTG CTCACATGTT 2281 CTTTCCTGCG TTATCCCCTG ATTCTGTGGA TAACCGTATT ACCGCCTTTG AGTGAGCTGA 2341 TACCGCTCGC CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG AAGCGGAAGA 2401 GCGCCCAATA CGCAAACCGC CTCTCCCCGC GCGTTGGCCG ATTCATTAAT GCAGCTGGCA 2461 CGACAGGTTT CCCGACTGGA AAGCGGGCAG TGAGCGCAAC GCAATTAATG TGAGTTAGCT 2521 CACTCATTAG GCACCCCAGG CTTTACACTT TATGCTTCCG GCTCGTATGT TGTGTGGAAT 2581 TGTGAGCGGA TAACAATTTC ACACAGGAAA CAGCTATGAC CATGATTACG CCAAGCTTGG 2641 CTGCAGGTGA TGATTATCAG CCAGCAGAGA TTAAGGAAAA CAGACAGGTT TATTGAGCGC 2701 TTATCTTTCC CTTTATTTTT GCTGCGGTAA GTCGCATAAA AACCATTCTT CATAATTCAA-



2761	TCCATTTACT	ATGTTATGTT	CTGAGGGGAG	TGAAAATTCC	CCTAATTCGA	TGAAGATTCT
2821	TGCTCAATTG	TTATCAGCTA	TGCGCCGACC	AGAACACCTT	GCCGATCAGC	CAAACGTCTC
2881	TTCAGGCCAC	TGACTAGCGA	TAACTTTCCC	CACAACGGAA	CAACTCTCAT	TGCATGGGAT
2941	CATTGGGTAC	TGTGGGTTTA	GTGGTTGTAA	AAACACCTGA	CCGCTATCCC	TGATCAGTTT
3001	CTTGAAGGTA	AACTCATCAC	CCCCAAGTCT	GGCTATGCAG	AAATCACCTG	GCTCAACAGC
3061	CTGCTCAGGG	TCAACGAGAA	TTAACATTCC	GTCAGGAAAG	CTTGGCTTGG	AGCCTGTTGG
3121	TGCGGTCATG	GAATTACCTT	CAACCTCAAG	CCAGAATGCA	GAATCACTGG	CTTTTTTGGT
3181	TGTGCTTACC	CATCTCTCCG	CATCACCTIT	GGTAAAGGTT	CTAAGCTTAG	GTGAGAACAT
3241	CCCTGCCTGA	ACATGAGAAA	AAACAGGGTA	CTCATACTCA	CTTCTAAGTG	ACGGCTGCAT
3301	ACTAACCGCT	TCATACATCT	CGTAGATTTC	TCTGGCGATT	GAAGGGCTAA	ATTCTTCAAC
3361	GCTAACTTTG	AGAATTTTTG	CAAGCAATGC	GGCGTTATAA	GCATTTAATG	CATTGATGCC
3421	ATTAAATAAA	GCACCAACGC	CTGACTGCCC	CATCCCCATC	TTGTCTGCGA	CAGATTCCTG
3481	GGATAAGCCA	AGTTCATTTT	${\tt TCTTTTTTC}$	ATAAATTGCT	TTAAGGCGAC	GTGCGTCCTC
3541	AAGCTGCTCT	TGTGTTAATG	GTTTCTTTTT	TGTGCTCATA	CGTTAAATCT	ATCACCGCAA
3601	GGGATAAATA	TCTAACACCG	TGCGTGTTGA	CTATTTTACC	TCTGGCGGTG	ATAATGGTTG
3661	CATGTACTAA	GGAGGTTGTA	TGGAACAACG	CATAACCCTG	AAAGATTATG	CAATGCGCTT
3721	TGGGCAAACC	AAGACAGCTA	<b>AAGATCTCTC</b>	ACCTACCAAA	CAATGCCCCC	CTGCAAAAAA
3781	TAAATTCATA	TAAAAAACAT	ACAGATAACC	ATCTGCGGTG	ATAAATTATC	TCTGGCGGTG
3841	TTGACATAAA	TACCACTGGC	GGTGATACTG	AGCACATCAG	CAGGACGCAC	TGACCACCAT
3901	GAAGGTGACG	CTCTTAAAAA	TTAAGCCCTG	AAGAAGGGCA	GCATTCAAAG	CAGAAGGCTT
3961	TGGGGTGTGT	GATACGAAAC	GAAGCATTGG	GATCATCACA	AGTTTGTACA	AAAAAGCTGA
4021	ACGAGAAACG	TAAAATGATA	TAAATATCAA	TATATTAAAT	TAGATTTTGC	ATAAAAAAACA
4081	GACTACATAA	TACTGTAAAA	CACAACATAT	CCAGTCACTA	TGGCGGCCGC	TAAGTTGGCA
4141	GCATCACCCG	ACGCACTTTG	CGCCGAATAA	ATACCTGTGA	CGGAAGATCA	CTTCGCAGAA
4201	TAAATAAATC	CTGGTGTCCC	TGTTGATACC	GGGAAGCCCT	GGGCCAACTT	TTGGCGAAAA
4261	TGAGACGTTG	ATCGGCACGT	AAGAGGTTCC	AACTTTCACC	ATAATGAAAT	AAGATCACTA
4321	CCGGGCGTAT	TTTTTGAGTT	ATCGAGATTT	TCAGGAGCTA	AGGAAGCTAA	AATGGAGAAA
4381	AAAATCACTG	GATATACCAC	CGTTGATATA	TCCCAATGGC	ATCGTAAAGA	ACATTTTGAG
4441	GCATTTCAGT	CAGTTGCTCA	ATGTACCTAT	AACCAGACCG	TTCAGCTGGA	TATTACGGCC
4501	TTTTTAAAGA	CCGTAAAGAA	AAATAAGCAC	AAGTTTTATC	CGGCCTTTAT	TCACATTCTT
4561	GCCCGCCTGA	TGAATGCTCA	TCCGGAATTC	CGTATGGCAA	TGAAAGACGG	TGAGCTGGTG
4621	ATATGGGATA	GTGTTCACCC	TTGTTACACC	GTTTTCCATG	AGCAAACTGA	AACGTTTTCA
4681	TCGCTCTGGA	GTGAATACCA	CGACGATTTC	CGGCAGTTTC	TACACATATA	TTCGCAAGAT
4741	GTGGCGTGTT	ACGGTGAAAA	CCTGGCCTAT	TTCCCTAAAG	GGTTTATTGA	GAATATGTTT
4801	TTCGTCTCAC	CCAATCCCTG	GGTGAGTTTC	ACCAGTTTTG	ATTTAAACGT	GGCCAATATG
4861	GACAACTTCT	TCGCCCCCGT	TTTCACCATO	GGCAAATATT	ATACGCAAGG	CGACAAGGTG
4921	CTGATGCCGC	TGGCGATTCA	GGTTCATCAT	GCCGTCTGTG	ATGGCTTCCA	TGTCGGCAGA
4981	ATGCTTAATC	AATTACAACA	GTACTGCGAT	GAGTGGCAGG	GCGGGGCGTA	AACGCGTGGA
5041	TCCGGCTTAC	TAAAAGCCAG	ATAACAGTAT	r- GCGTATTTGC	GCGCTGATTT	TTGCGGTATA
5101	AGAATATATA	CTGATATGTA	TACCCGAAGT	r ATGTCAAAAA	GAGGTGTGCT	ATGAAGCAGC
5161	GTATTACAG	C GACAGTTGAC	AGCGACAGCT	T ATCAGTTGCT	CAAGGCATAT	ATGATGTCAA
522	TATCTCCGG	r CTGGTAAGC	CAACCATGC	A GAATGAAGCC	CGTCGTCTGC	GTGCCGAACG
528	CTGGAAAGC	GAAAATCAG	AAGGGATGG	TGAGGTCGCC	CGGTTTATTG	AAATGAACGG
534	CTCGTTTTGC	r gacgagaaca	GGGACTGGT	AAATGCAGTT	TAAGGTTTAC	ACCTATAAAA
540	GAGAGAGCCC	TTATCGTCTC	TTTGTGGAT	TACAGAGTGA	TATTATTGAC	ACGCCCGGGC
546	GACGGATGG	r GATCCCCCTC	GCCAGTGCAG	C GTCTGCTGTC	AGATAAAGTO	TCCCGTGAAC
550	. האכפפאופפ זיייין ארררפני	r GGTGCATATO	GGGGATGAA	A GCTGGCGCAT	GATGACCACC	GATATGGCCA
550	ו התהתההההה	T CTCCGTTATO	GGGGAAGAA	G TGGCTGATCT	CAGCCACCGC	GAAAATGACA
564	יטטעעעעטטדי. ו	C CATTAACCT	ATGTTCTGG	GAATATAAA1	GTCAGGCTCC	GTTATACACA
570		C AGGTCGACC	TAGTGACTG	G ATATGTTGTG	TTTTACAGTA	TTATGTAGTC
570	T GCCWGICIG	T GCAAATCT	מידיר ביינים ביינים ביינים	A TTGATATTT	TATCATTTA	CGTTTCTCGT
		T TGTACAAAG				
302	I ICAGCIIIC	LIGIACAAAG	L JOIONIAA			

FIGURE 33C

Figure 34. pDEST14 Native Protein Expression in E. coli, T7
Promoter



#### pDEST14 6422 bp (rotated to position 4000)

Location (Base Nos.)	Gene Encoded
18561	attR1
4351094	CmR
12141298	inactivated ccdA
14361741	ccdB
17821906	attR2
26323489	ampR

1 CGATCCCGCG AAATTAATAC GACTCACTAT AGGGAGACCA CAACGGTTTC CCTCTAGATC 61 ACAAGTTTGT ACAAAAAAGC TGAACGAGAA ACGTAAAATG ATATAAATAT CAATATTTA 121 AATTAGATTT TGCATAAAAA ACAGACTACA TAATACTGTA AAACACAACA TATCCAGTCA 181 CTATGGCGGC CGCTAAGTTG GCAGCATCAC CCGACGCACT TTGCGCCGAA TAAATACCTG 241 TGACGGAAGA TCACTTCGCA GAATAAATAA ATCCTGGTGT CCCTGTTGAT ACCGGGAAGC 301 CCTGGGCCAA CTTTTGGCGA AAATGAGACG TTGATCGGCA CGTAAGAGGT TCCAACTTTC 361 ACCATAATGA AATAAGATCA CTACCGGGCG TATTTTTTGA GTTATCGAGA TTTTCAGGAG 421 CTAAGGAAGC TAAAATGGAG AAAAAATCA CTGGATATAC CACCGTTGAT ATATCCCAAT 481 GGCATCGTAA AGAACATTTT GAGGCATTTC AGTCAGTTGC TCAATGTACC TATAACCAGA 541 CCGTTCAGCT GGATATTACG GCCTTTTTAA AGACCGTAAA GAAAAATAAG CACAAGTTTT 601 ATCCGGCCTT TATTCACATT CTTGCCCGCC TGATGAATGC TCATCCGGAA TTCCGTATGG 661 CAATGAAAGA CGGTGAGCTG GTGATATGGG ATAGTGTTCA CCCTTGTTAC ACCGTTTTCC 721 ATGAGCAAAC TGAAACGTTT TCATCGCTCT GGAGTGAATA CCACGACGAT TTCCGGCAGT 781 TTCTACACAT ATATTCGCAA GATGTGGCGT GTTACGGTGA AAACCTGGCC TATTTCCCTA 841 AAGGGTTTAT TGAGAATATG TTTTTCGTCT CAGCCAATCC CTGGGTGAGT TTCACCAGTT 901 TTGATTTAAA CGTGGCCAAT ATGGACAACT TCTTCGCCCC CGTTTTCACC ATGGGCAAAT 961 ATTATACGCA AGGCGACAAG GTGCTGATGC CGCTGGCGAT TCAGGTTCAT CATGCCGTCT 1021 GTGATGGCTT CCATGTCGGC AGAATGCTTA ATGAATTACA ACAGTACTGC GATGAGTGGC 1081 AGGGCGGGC GTAAACGCGT GGATCCGGCT TACTAAAAGC CAGATAACAG TATGCGTATT 1141 TGCGCGCTGA TTTTTGCGGT ATAAGAATAT ATACTGATAT GTATACCCGA AGTATGTCAA 1201 AAAGAGGTGT GCTATGAAGC AGCGTATTAC AGTGACAGTT GACAGCGACA GCTATCAGTT 1261 GCTCAAGGCA TATATGATGT CAATATCTCC GGTCTGGTAA GCACAACCAT GCAGAATGAA 1321 GCCCGTCGTC TGCGTGCCGA ACGCTGGAAA GCGGAAAATC AGGAAGGGAT GGCTGAGGTC 1381 GCCCGGTTTA TTGAAATGAA CGGCTCTTTT GCTGACGAGA ACAGGGACTG GTGAAATGCA 1441 GTTTAAGGTT TACACCTATA AAAGAGAGAG CCGTTATCGT CTGTTTGTGG ATGTACAGAG 1501 TGATATTATT GACACGCCCG GGCGACGGAT GGTGATCCCC CTGGCCAGTG CACGTCTGCT 1561 GTCAGATAAA GTCTCCCGTG AACTTTACCC GGTGGTGCAT ATCGGGGATG AAAGCTGGCG 1621 CATGATGACC ACCGATATGG CCAGTGTGCC GGTCTCCGTT ATCGGGGAAG AAGTGGCTGA 1681 TCTCAGCCAC CGCGAAAATG ACATCAAAAA CGCCATTAAC CTGATGTTCT GGGGAATATA 1741 AATGTCAGGC TCCCTTATAC ACAGCCAGTC TGCAGGTCGA CCATAGTGAC TGGATATGTT 1801 GTGTTTTACA GTATTATGTA GTCTGTTTTT TATGCAAAAT CTAATTTAAT ATATTGATAT 1861 TTATATCATT TTACGTTTCT CGTTCAGCTT TCTTGTACAA AGTGGTGATG ATCCGGCTGC 1921 TAACAAAGCC CGAAAGGAAG CTGAGTTGGC TGCTGCCACC GCTGAGCAAT AACTAGCATA 1981 ACCCCTTGGG GCCTCTAAAC GGGTCTTGAG GGGTTTTTTG CTGAAAGGAG GAACTATATC 2041 CGGATATCCA CAGGACGGT GTGGTCGCCA TGATCGCGTA GTCGATAGTG GCTCCAAGTA 2101 GCGAAGCGAG CAGGACTGGG CGGCGGCCAA AGCGGTCGGA CAGTGCTCCG AGAACGGGTG 2161 CGCATAGAAA TTGCATCAAC GCATATAGCG CTAGCAGCAC GCCATAGTGA CTGGCGATGC 2221: TGTCGGAATG GACGATATCC CGCAAGAGGC CCGGCAGTAC CGGCATAACC AAGCCTATGC 2281 CTACAGCATC CAGGGTGACG GTGCCGAGGA TGACGATGAG CGCATTGTTA GATTTCATAC 2341 ACGGTGCCTG ACTGCGTTAG CAATTTAACT GTGATAAACT ACCGCATTAA AGCTTATCGA 2401 TGATAAGCTG TCAAACATGA GAATTCTTGA AGACGAAAGG GCCTCGTGAT ACGCCTATTT 2461 TTATAGGTTA ATGTCATGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTCGGGGA 2521 AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC 2581 ATGAGACAAT AACCCTGATA AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT 2641 CAACATTTCC GTGTCGCCCT TATTCCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT 2701 CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT-

Figure 34B

				ATCCTTGAGA		
2821	TTTCCAATGA	TGAGCACTTT	TAAAGTTCTG	CTATGTGGCG	CGGTATTATC	CCGTGTTGAC
2881	GCCGGGCAAG	AGCAACTCGG	TCGCCGCATA	CACTATTCTC	AGAATGACTT	GGTTGAGTAC
2941	TCACCAGTCA	CAGAAAAGCA	TCTTACGGAT	GGCATGACAG	TAAGAGAATT	ATGCAGTGCT
3001	GCCATAACCA	TGAGTGATAA	CACTGCGGCC	AACTTACTTC	TGACAACGAT	CGGAGGACCG
3061	AAGGAGCTAA	CCGCTTTTTT	GCACAACATG	GGGGATCATG	TAACTCGCCT	TGATCGTTGG
3121	GAACCGGAGC	TGAATGAAGC	CATACCAAAC	GACGAGCGTG	ACACCACGAT	GCCTGCAGCA
				GGCGAACTAC		
				GTTGCAGGAC		
				GGAGCCGGTG		*
				TCCCGTATCG		
				CAGATCGCTG		
				TCATATATAC		
				ATCCTTTTTG		
				TCAGACCCCG		
				TGCTGCTTGC		
				CTACCAACTC		
				CTTCTAGTGT		•
-	-			CTCGCTCTGC		
				GGGTTGGACT		
				TCGTGCACAC		
4021	ACCTACACCG	AACTGAGATA	CCTACAGCGT	GAGCTATGAG	AAAGCGCCAC	GCTTCCCGAA
4081	GGGAGAAAGG	CGGACAGGTA	TCCGGTAAGC	GGCAGGGTCG	GAACAGGAGA	GCGCACGAGG
4141	GAGCTTCCAG	GGGGAAACGC	CTGGTATCTT	TATAGTCCTG	TCGGGTTTCG	CCACCTCTGA
4201	CTTGAGCGTC	GATTTTTGTG	ATGCTCGTCA	GGGGGGCGGA	GCCTATGGAA	AAACGCCAGC
4261	AACGCGGCCT	TTTTACGGTT	CCTGGCCTTT	TGCTGGCCTT	TTGCTCACAT	GTTCTTTCCT
4321	GCGTTATCCC	CTGATTCTGT	GGATAACCGT	ATTACCGCCT	TTGAGTGAGC	TGATACCGCT
4381	CGCCGCAGCC	GAACGACCGA	GCGCAGCGAG	TCAGTGAGCG	AGGAAGCGGA	AGAGCGCCTG
4441	ATGCGGTATT	TTCTCCTTAC	GCATCTGTGC	GGTATTTCAC	ACCGCATATA	TGGTGCACTC
				TAAGCCAGTA		
				GCCAACACCC		
				AGCTGTGACC		
				CGCGAGGCAG		
				CTGTTCATCC		
				AAAGCGGGCC		
				GGGATTTCTG		
				GGTTACTGAT		
				ATGGATGCGG		
				AGATGTAGGT		
				GGTGCAGGGC		
				TCATGTTGTT		
				TATCGGTGAT		
				CGACAGGAGC		
						CGGACGCGAT
						ATTGATTGGC
						TCAGGTCGAG
5521	GTGGCCCGGC	TCCATGCACC	GCGACGCAAC	GCGGGGAGGC	AGACAAGGTA	TAGGGCGGCG
5581	. CCTACAATCC	: ATGCCAACCC	GTTCCATGTG	CTCGCCGAGG	CGGCATAAAT	CGCCGTGACG
5641	ATCAGCGGTC	CAGTGATCGA	AGTTAGGCTG	GTAAGAGCCG	CGAGCGATCC	TTGAAGCTGT
5701	CCCTGATGGT	CGTCATCTAC	CTGCCTGGAC	AGCATGGCCT	GCAACGCGGG	CATCCCGATG
5761	. CCGCCGGAAG	CGAGAAGAAT	CATAATGGGG	AAGGCCATCC	AGCCTCGCGT	CGCGAACGCC
5821	AGCAAGACGT	AGCCCAGCGC	GTCGGCCGCC	ATGCCGGCGA	TAATGGCCTG	CTTCTCGCCG
5881	AAACGTTTGG	TGGCGGGACC	AGTGACGAAG	GCTTGAGCGA	GGGCGTGCAA	GATTCCGAAT
5941	ACCGCAAGCG	ACAGGCCGAT	CATCGTCGCG	CTCCAGCGAA	AGCGGTCCTC	GCCGAAAATG
						AGTCATAAGT
						GAAGGCTCTC
						AGCAGCCCAG
						AGGAGATGGC-

FIGURE 34C

6241 GCCCAACAGT CCCCCGGCCA CGGGGCCTGC CACCATACCC ACGCCGAAAC AAGCGCTCAT 6301 GAGCCCGAAG TGGCGAGCCC GATCTTCCCC ATCGGTGATG TCGGCGATAT AGGCGCCAGC 6361 AACCGCACCT GTGGCGCCGG TGATGCCGGC CACGATGCGT CCGGCGTAGA GGATCGAGAT 6421 CT

FIGURE 34D

Figure 357: pDEST15 Glutathione-S-transferase Fusion in E. coli, T7 Promoter

1 nat cga gat ctc gat ccc gcg aaa tta ata cga ctc atc ata ggg aga cca gtt gag ctc ata ggg cgc ttt at tat gct gag tga tat ccc tct ggt

52 caa cgg ttt ccc tct aga aat aat ttt gtt taa ctt taa gaa gga gat ata gtt gcc aaa ggg aga tcj tta tta aaa caa att gaa att ctt cct cta tat

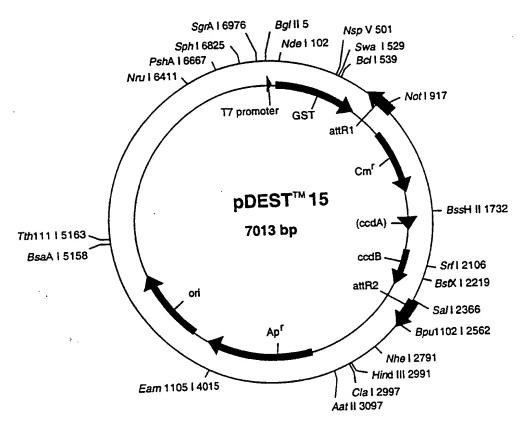
103 cgt atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc gta tat agat caa ata acc ttt taa ttc ccg gaa cac gtt ggg

154 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa at aga gag cat ttg tat tga gct gaa gct gaa gaa aac ctt ata gaa ctt ctt tt ata ctt ctc gta aac ata

715 cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat gtc ccg acc gtt cgg tgc aaa cca cca ccg ccg ctg gta gga ggt ttt agc cta

766 ctg gtt ccg cgt cca tgg tcg aaa cca acc aca acc agt tgg tcg acc agt ttg tat aga gaa acc agt ttg tat caa acc agt ttg tac aaa aaa gct gaa

817 cga gaa acg taa aat gat ata aat atc aat tta aat tta atc taa acc gta



88/240

#### pDEST15 7013 bp

Gene Encoded

Location (Base Nos.)

108..776

		108//	0	GSI			
		916792			attR1		
		10251	537	CmR			
		18041	888	inact	ivated ccdA		
,		20262	331	ccdB			
		237224		attR2			
		323340	093	ampR			
1	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	GACTCACTAT	AGGGAGACCA	CAACGGTTTC	
	CCTCTAGAAA						
	GTTATTGGAA						
181	AAAAATATGA	AGAGCATTTG	TATGAGCGCG	ATGAAGGTGA	TAAATGGCGA	AACAAAAAGT	
	TTGAATTGGG						
301	CACAGTCTAT	GGCCATCATA	CGTTATATAG	CTGACAAGCA	CAACATGTTG	GGTGGTTGTC	
	CAAAAGAGCG						
421	TTTCGAGAAT	TGCATATAGT	AAAGACTTTG	AAACTCTCAA	AGTTGATTTT	CTTAGCAAGC	
481	TACCTGAAAT	GCTGAAAATG	TTCGAAGATC	GTTTATGTCA	TAAAACATAT	TTAAATGGTG	
541	ATCATGTAAC	CCATCCTGAC	TTCATGTTGT	ATGACGCTCT	TGATGTTGTT	TTATACATGG	
601	ACCCAATGTG	CCTGGATGCG	TTCCCAAAAT	TAGTTTGTTT	TAAAAAACGT	ATTGAAGCTA	
661	TCCCACAAAT	TGATAAGTAC	TTGAAATCCA	GCAAGTATAT	AGCATGGCCT	TTGCAGGGCT	
721	GGCAAGCCAC	GTTTGGTGGT	GGCGACCATC	CTCCAAAATC	GGATCTGGTT	CCGCGTCCAT	
781	GGTCGAATCA	AACAAGTTTG	TACAAAAAAG	CTGAACGAGA	AACGTAAAAT	GATATAAATA	
841	TCAATATATT	AAATTAGATT	TTGCATAAAA	AACAGACTAC	ATAATACTGT	AAAACACAAC	
	ATATCCAGTC						
961	CTCGTATAAT	GTGTGGATTT	TGAGTTAGGA	TCCGTCGAGA	TTTTCAGGAG	CTAAGGAAGC	
1021	TAAAATGGAG	AAAAAAATCA	CTGGATATAC	CACCGTTGAT	ATATCCCAAT	GGCATCGTAA	
1081	AGAACATTTT	GAGGCATTTC	AGTCAGTTGC	TCAATGTACC	TATAACCAGA	CCGTTCAGCT	
1141	GGATATTACG	GCCTTTTTAA	AGACCGTAAA	GAAAAATAAG	CACAAGTTTT	ATCCGGCCTT	
1201	TATTCACATT	CTTGCCCGCC	TGATGAATGC	TCATCCGGAA	TTCCGTATGG	CAATGAAAGA	
	CGGTGAGCTG						
1321	TGAAACGTTT	TCATCGCTCT	GGAGTGAATA	CCACGACGAT	TTCCGGCAGT	TTCTACACAT	
1381	ATATTCGCAA	GATGTGGCGT	GTTACGGTGA	AAACCTGGCC	TATTTCCCTA	AAGGGTTTAT	
1441	TGAGAATATG	TTTTTCGTCT	CAGCCAATCC	CTGGGTGAGT	TTCACCAGTT	TTGATTTAAA	
1501	CGTGGCCAAT	ATGGACAACT	TCTTCGCCCC	CGTTTTCACC	ATGGGCAAAT	ATTATACGCA	
1561	AGGCGACAAG	GTGCTGATGC	CGCTGGCGAT	TCAGGTTCAT	CATGCCGTCT	GTGATGGCTT	
1621	CCATGTCGGC	AGAATGCTTA	ATGAATTACA	ACAGTACTGC	GATGAGTGGC	AGGGCGGGC	
1681	GTAATCTAGA	GGATCCGGCT	TACTAAAAGC	CAGATAACAG	TATGCGTATT	TGCGCGCTGA	
1741	TTTTTGCGGT	ATAAGAATAT	ATACTGATAT	${\tt GTATACCCGA}$	${\tt AGTATGTCAA}$	AAAGAGGTGT	
1801	GCTATGAAGC	AGCGTATTAC	AGTGACAGTT	GACAGCGACA	${\tt GCTATCAGTT}$	GCTCAAGGCA	
1861	TATATGATGT	CAATATCTCC	GGTCTGGTAA	GCACAACCAT	GCAGAATGAA	GCCCGTCGTC	
1921	TGCGTGCCGA	ACGCTGGAAA	GCGGAAAATC	AGGAAGGGAT	GGCTGAGGTC	GCCCGGTTTA	
	TTGAAATGAA						
2041	TACACCTATA	AAAGAGAGAG	CCCTTATATCCT	CHCHMMANA	ATTOTA CACAC	CO MEN COMMENCE	

FOURE 35B

2041 TACACCTATA AAAGAGAGAG CCGTTATCGT CTGTTTGTGG ATGTACAGAG TGATATTATT 2101 GACACGCCCG GGCGACGGAT GGTGATCCCC CTGGCCAGTG CACGTCTGCT GTCAGATAAA 2161 GTCTCCCGTG AACTTTACCC GGTGGTGCAT ATCGGGGGATG AAAGCTGGCG CATGATGACC 2221 ACCGATATGG CCAGTGTGCC GGTCTCCGTT ATCGGGGAAG AAGTGGCTGA TCTCAGCCAC 2281 CGCGAAAATG ACATCAAAAA CGCCATTAAC CTGATGTTCT GGGGAATATA AATGTCAGGC 2341 TCCCTTATAC ACAGCCAGTC TGCAGGTCGA CCATAGTGAC TGGATATGTT GTGTTTTACA 2401 GTATTATGTA GTCTGTTTTT TATGCAAAAT CTAATTTAAT ATATTGATAT TTATATCATT 2461 TTACGTTTCT CGTTCAGCTT TCTTGTACAA AGTGGTTTGA TTCGACCCGG GATCCGGCTG 2521 CTAACAAAGC CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT 2581 AACCCCTTGG GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACTATAT 2641 CCGGATATCC ACAGGACGGG TGTGGTCGCC ATGATCGCGT AGTCGATAGT GGCTCCAAGT-

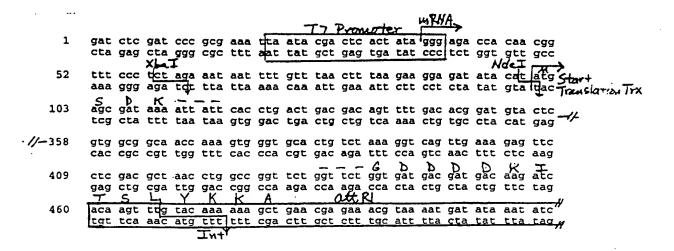
2701 AGCGAAGCGA GCAGGACTGG GCGGCGGCCA AAGCGGTCGG ACAGTGCTCC GAGAACGGGT 2761 GCGCATAGAA ATTGCATCAA CGCATATAGC GCTAGCAGCA CGCCATAGTG ACTGGCGATG 2821 CTGTCGGAAT GGACGATATC CCGCAAGAGG CCCGGCAGTA CCGGCATAAC CAAGCCTATG 2881 CCTACAGCAT CCAGGGTGAC GGTGCCGAGG ATGACGATGA GCGCATTGTT AGATTTCATA 2941 CACGGTGCCT GACTGCGTTA GCAATTTAAC TGTGATAAAC TACCGCATTA AAGCTTATCG 3001 ATGATAAGCT GTCAAACATG AGAATTCTTG AAGACGAAAG GGCCTCGTGA TACGCCTATT 3061 TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG 3121 AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT 3181 CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT 3241 TCAACATTTC CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC 3301 TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG 3361 TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG 3421 TTTTCCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTGTTGA 3481 CGCCGGGCAA GAGCAACTCG GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA 3541 CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 3601 TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC 3661 GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG 3721 GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGCAGC 3781 AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA 3841 ACAATTAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 3901 TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT CTCGCGGTAT 3961 CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG 4021 GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT 4081 TAAGCATTGG TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT 4141 TCATTTTTAA TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 4201 CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC 4261 TTCTTGAGAT CCTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT 4321 ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA AGGTAACTGG 4381 CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA 4441 CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 4501 TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA 4561 TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC 4621 GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCTATGA GAAAGCGCCA CGCTTCCCGA 4681 AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG 4741 GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 4801 ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG 4861 CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC 4921 TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTTGAGTGAG CTGATACCGC 4981 TCGCCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCT 5041 GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT 5101 CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGT ATACACTCCG CTATCGCTAC 5161 GTGACTGGGT CATGGCTGCG CCCCGACACC CGCCAACACC CGCTGACGCG CCCTGACGGG 5221 CTTGTCTGCT CCCGGCATCC GCTTACAGAC AAGCTGTGAC CGTCTCCGGG AGCTGCATGT 5281 GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGGCA GCTGCGGTAA AGCTCATCAG 5341 CGTGGTCGTG AAGCGATTCA CAGATGTCTG CCTGTTCATC CGCGTCCAGC TCGTTGAGTT 5401 TCTCCAGAAG CGTTAATGTC TGGCTTCTGA TAAAGCGGGC CATGTTAAGG GCGGTTTTTT 5461 CCTGTTTGGT CACTGATGCC TCCGTGTAAG GGGGATTTCT GTTCATGGGG GTAATGATAC 5521 CGATGAAACG AGAGAGGATG CTCACGATAC GGGTTACTGA TGATGAACAT GCCCGGTTAC 5581 TGGAACGTTG TGAGGGTAAA CAACTGGCGG TATGGATGCG GCGGGACCAG AGAAAAATCA 5641 CTCAGGGTCA ATGCCAGCGC TTCGTTAATA CAGATGTAGG TGTTCCACAG GGTAGCCAGC 5701 AGCATCCTGC GATGCAGATC CGGAACATAA TGGTGCAGGG CGCTGACTTC CGCGTTTCCA 5761 GACTITACGA AACACGGAAA CCGAAGACCA TTCATGTTGT TGCTCAGGTC GCAGACGTTT 5821 TGCAGCAGCA GTCGCTTCAC GTTCGCTCGC GTATCGGTGA TTCATTCTGC TAACCAGTAA 5881 GGCAACCCCG CCAGCCTAGC CGGGTCCTCA ACGACAGGAG CACGATCATG CGCACCCGTG 5941 GCCAGGACCC AACGCTGCCC GAGATGCGCC GCGTGCGGCT GCTGGAGATG GCGGACGCGA 6001 TGGATATGTT CTGCCAAGGG TTGGTTTGCG CATTCACAGT TCTCCGCAAG AATTGATTGG 6061 CTCCAATTCT TGGAGTGGTG AATCCGTTAG CGAGGTGCCG CCGGCTTCCA TTCAGGTCGA 6121 GGTGGCCCGG CTCCATGCAC CGCGACGCAA CGCGGGGAGG CAGACAAGGT ATAGGGCGGC-

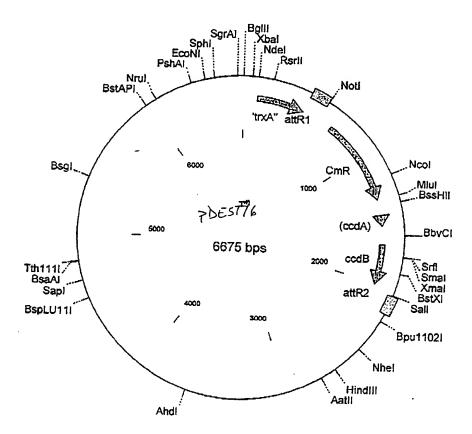
FIGURE 35C

6181	GCCTACAATC	CATGCCAACC	CGTTCCATGT	GCTCGCCGAG	GCGGCATAAA	TCGCCGTGAC
6241	GATCAGCGGT	CCAGTGATCG	AAGTTAGGCT	GGTAAGAGCC	GCGAGCGATC	CTTGAAGCTG
6301	TCCCTGATGG	TCGTCATCTA	CCTGCCTGGA	CAGCATGGCC	TGCAACGCGG	GCATCCCGAT
6361	GCCGCCGGAA	GCGAGAAGAA	TCATAATGGG	GAAGGCCATC	CAGCCTCGCG	TCGCGAACGC
6421	CAGCAAGACG	TAGCCCAGCG	CGTCGGCCGC	CATGCCGGCG	ATAATGGCCT	GCTTCTCGCC
6481	GAAACGTTTG	GTGGCGGGAC	CAGTGACGAA	GGCTTGAGCG	AGGGCGTGCA	AGATTCCGAA
6541	TACCGCAAGC	GACAGGCCGA	TCATCGTCGC	GCTCCAGCGA	AAGCGGTCCT	CGCCGAAAAT
6601	GACCCAGAGC	GCTGCCGGCA	CCTGTCCTAC	GAGTTGCATG	ATAAAGAAGA	CAGTCATAAG
6661	TGCGGCGACG	ATAGTCATGC	CCCGCGCCCA	CCGGAAGGAG	CTGACTGGGT	TGAAGGCTCT
6721	CAAGGGCATC	GGTCGATCGA	CGCTCTCCCT	TATGCGACTC	CTGCATTAGG	AAGCAGCCCA
6781	GTAGTAGGTT	GAGGCCGTTG	AGCACCGCCG	CCGCAAGGAA	TGGTGCATGC	AAGGAGATGG
6841	CGCCCAACAG	TCCCCCGGCC	ACGGGGCCTG	CCACCATACC	CACGCCGAAA	CAAGCGCTCA
6901	TGAGCCCGAA	GTGGCGAGCC	CGATCTTCCC	CATCGGTGAT	GTCGGCGATA	TAGGCGCCAG
6961	CAACCGCACC	TGTGGCGCCG	GTGATGCCGG	CCACGATGCG	TCCGGCGTAG	AGG

Figure 36A: PDEST16

# Thioredoxin N-Fusion Protein in E. coli with T7 Promoter





# pDEST16 6675 bp

Location (Base Nos.)	Gene Encoded
104457	trxA
585461	attR1
6941353	CmR
14731557	inactivated ccdA
16952000	ccdB
20412165	attR2

3	AGATCTCGAT	CCCGCGAAAT	TAATACGACT	CACTATAGG	AGACCACAAC	GGTTTCCCTC
6]	I IAGAAATAAT	' TTTGTTTAAC	TTTAAGAAGG	AGATATACAT	ATGAGCGATZ	እአአጥጥአጥጥርአ
121	L CCTGACTGAC	GACAGTTTTG	ACACGGATGT	' ACTCAAAGCC	GACGGGGGG	TOTOTOTO
181	l TITCTGGGCA	GAGTGGTGCG	GTCCGTGCAA	AATGATCGCC	CCGATTCTGG	ATCANATOCC
241	I TGACGAATAT	' CAGGGCAAAC	TGACCGTTGC	AAAACTGAAC	י אַרירכאַריראַא	ACCCMCCCAA
301	I TGCGCCGAAA	TATGGCATCC	GTGGTATCCC	GACTCTGCTG	מממטדדנדדר	ACCOURGA ACID
361	GGCGGCAACC	AAAGTGGGTG	CACTGTCTAA	AGGTCAGTTC	: AAAGAGTTCC	TOCACCOMA
421	. CCTGGCCGGT	TCTGGTTCTG	GTGATGACGA	TGACAAGATC	' ΑΓΆΔαννναν	* ACAAAAAACC
481	. IGAACGAGAA	. ACGTAAAATG	ATATAAATAT	CAATATATTA	<b>ልልጥጥል</b> ርልጥጥፕ	TOTATION
541	. ACAGACTACA	TAATACTGTA	AAACACAACA	TATCCAGTCA	CTATCCCCCC	CCCATTACCC
601	. ACCCCAGGCT	TTACACTTTA	TGCTTCCGGC	TCGTATAATG	TCTCC אייייייים	Cacmmaccam
661	. CCGGCGAGAT	TTTCAGGAGC	TAAGGAAGCT	AAAATGGAGA	. אססמאתראר	TOOMERTAGE
/21	. ACCGTTGATA	TATCCCAATG	- GCATCGTAAA	GAACATTTTC	ACCCATTTCA	CTCACTTCCT
/81	CAATGTACCT	ATAACCAGAC	CGTTCAGCTG	GATATTACGG	ע ע ע דיידידידידי	CACCCTAAAC
841	AAAAATAAGC	ACAAGTTTA	TCCGGCCTTT	ATTCACATTC	TTGCCCCCC	GATCAATCCT
301	CATCCGGAAT	TCCGTATGGC	AATGAAAGAC	GGTGAGCTGG	TGATATCCCA	TACTOTTO
96 T	CCTTGTTACA	CCGTTTTCCA	TGAGCAAACT	GAAACGTTTT	САТСССТСТС	CACTCAATTAC
TOST	CACGACGATT	TCCGGCAGTT	TCTACACATA	TATTCGCAAG	ATGTGGCGTG	TTACCCTCAA
1081	AACCTGGCCT	ATTTCCCTAA	AGGGTTTATT	GAGAATATGT	<b>Վուհանարարարարարարարարարարարարարարարարարարա</b>	ACCCAATCCC
1141	TGGGTGAGTT	TCACCAGTIT	TGATTTAAAC	GTGGCCAATA	TEGACAACTT	CTTCCCCCCC
1201	GTTTTCACCA	TGGGCAAATA	TTATACGCAA	GGCGACAAGG	TECTEATECE	CCTCCCCAmm
T501	CAGGTTCATC	ATGCCGTCTG	TGATGGCTTC	CATGTCGGCA	GAATCCTTAA	ጥሮ አ አጥጥ አ ር አ አ
1321	CAGTACTGCG	ATGAGTGGCA	GGGCGGGGCG	TAAACGCGTG	CATCCCCCTT	ስርሞስ እ እ አርርርር
1381	AGATAACAGT	ATGCGTATTT	GCGCGCTGAT	TTTTGCGGTA	ТААСААТАТА	<b>ፕልሮ</b> ሞር አጥአጥር
1441	TATACCCGAA	GTATGTCAAA	AAGAGGTGTG	CTATGAAGCA	CCCTATTACA	CTCACACTOR
1501	ACAGCGACAG	CTATCAGTTG	CTCAAGGCAT	ATATGATGTC	AATATCTCCC	CTCTCCTA AC
1201	CACAACCATG	CAGAATGAAG	CCCGTCGTCT	GCGTGCCGAA	CCCTCCAAAC	CCCAAAATCA
1671	GGAAGGGATG	GCTGAGGTCG	CCCGGTTTAT	TGAAATGAAC	CCCTCTTTTC	CTCACCACA
TPST	CAGGGACTGG	TGAAATGCAG	TTTAAGGTTT	ACACCTATAA	AAGAGAGAGC	CCTTATCCTC
1/41	TGTTTGTGGA	TGTACAGAGT	GATATTATTG	ACACGCCCGG	GCGACGGATC	CTCATCCCCC
TOOT	TGGCCAGTGC	ACGTCTGCTG	TCAGATAAAG	TCTCCCGTGA	ACTITALCCC	CTCCTCCAADA
TOOT	ICGGGGAIGA	AAGCTGGCGC	ATGATGACCA	CCGATATGGC	CAGTGTGCCG	CTCTCCCTTC
1321	1 CGGGGAAGA	AGTGGCTGAT	CTCAGCCACC	GCGAAAATGA	CATCANANC	CCCATTAACC
1301	IGATGTTCTG	GGGAATATAA	ATGTCAGGCT	CCCTTATACA	CAGCCAGTCT	CCACCTCCAC
2,041	CATAGTGACT	GGATATGTTG	TGTTTTACAG	TATTATGTAG	ተርተርተተተተተተ	ATCCAAAATC
2101	TAATTTAATA	TATTGATATT	TATATCATTT	TACGTTTCTC	CTTCACCTTT	COMOTAGAAA
2101	GIGGIGATGA	TCCGGCTGCT	AACAAAGCCC	GAAAGGAAGC	TCACTTCCCT	CCTCCCTCTCC
2221	CIGAGCAAIA	ACIAGCATAA	CCCCTTGGGG	<b>ሮሮሞሮሞል ል ልሮሮ</b>	CCTCTTCACC	CCMMmmmaa
2201	JOAAAGGAGG	AACTATATCC	GGATATCCAC	AGGACGGGTG	TECTCECCAT	CATCCCCCTA
2311	CONTROLOG	CICCAMGIAG	CGAAGCGAGC	AGGACTGGGC	CCCCCCCNNN	CCCCCCCCC
2401	MOTOCICCOA	GAACGGGTGC	GCATAGAAAT	TGCATCAACG	CATATACCCC	TRACTACA
2401	CCATAGIGAC	TGGCGATGCT	GTCGGAATGG	እሮርእጥአጥረርር	CCAACACCC	00000
2321	OGCATAACCA	MGCCIAIGCC	TACAGCATCC	AGGGTGACGG	TECCCACCAT	CACCAMOAGO
	CCHILOTING	WITITHIA	CGGTGCCTGA	CTCCCTTACC	ለ አጥጥጥ አ ለጥጥ	TO A TO A A A COMA
2041	CCGCHIIMAM	GULLATUGAL	GATAAGCTCT	<u>ሮል አአሮአሞሮአሮ</u>	A A COUNTY COUNTY A PA	G3 GG3
2,01	CCICGIGMIM	CGCCTATTTT	ממידידים אוראיזי	ערדי עידי אידי אידי אידי אידי	A TO A TO CO COMMO	~
2/01	AGGTGGCACT	TTTCGGGGAA	ATGTGCGCGG	AACCCCTATT	TGTTTATTTT	TCTAAATACA-

2821 TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA 2881 AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 2941 TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA 3001 GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG 3061 TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC 3121 GGTATTATCC CGTGTTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA 3181 GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 3241 AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT 3301 GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT 3361 AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA 3421 CACCACGATG CCTGCAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT 3481 TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 3541 ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA 3601 GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT 3661 AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA 3721 GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT 3781 TTAGATTGAT TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA 3841 TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT 3901 AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA 3961 AACAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT 4021 TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA 4081 GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT 4141 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC 4201 AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA 4261 GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA 4321 AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG 4381 AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT 4441 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG 4501 CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT 4561 TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA TTACCGCCTT 4621 TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA 4681 GGAAGCGGAA GAGCGCCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG GTATTTCACA 4741 CCGCATATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT 4801 ACACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC CCGACACCCCG CCAACACCCG 4861 CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG 4921 TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGC 4981 TGCGGTAAAG CTCATCAGCG TGGTCGTGAA GCGATTCACA GATGTCTGCC TGTTCATCCG 5041 CGTCCAGCTC GTTGAGTTTC TCCAGAAGCG TTAATGTCTG GCTTCTGATA AAGCGGGCCA 5101 TGTTAAGGGC GGTTTTTTCC TGTTTGGTCA CTGATGCCTC CGTGTAAGGG GGATTTCTGT 5161 TCATGGGGGT AATGATACCG ATGAAACGAG AGAGGATGCT CACGATACGG GTTACTGATG 5221 ATGAACATGC CCGGTTACTG GAACGTTGTG AGGGTAAACA ACTGGCGGTA TGGATGCGGC 5281 GGGACCAGAG AAAAATCACT CAGGGTCAAT GCCAGCGCTT CGTTAATACA GATGTAGGTG 5341 TTCCACAGGG TAGCCAGCAG CATCCTGCGA TGCAGATCCG GAACATAATG GTGCAGGGCG 5401 CTGACTTCCG CGTTTCCAGA CTTTACGAAA CACGGAAACC GAAGACCATT CATGTTGTTG 5461 CTCAGGTCGC AGACGTTTTG CAGCAGCAGT CGCTTCACGT TCGCTCGCGT ATCGGTGATT 5521 CATTCTGCTA ACCAGTAAGG CAACCCCGCC AGCCTAGCCG GGTCCTCAAC GACAGGAGCA 5581 CGATCATGCG CACCCGTGGC CAGGACCCAA CGCTGCCCGA GATGCGCCGC GTGCGGCTGC 5641 TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT GGTTTGCGCA TTCACAGTTC 5701, TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA TCCGTTAGCG AGGTGCCGCC 5761 GGCTTCCATT CAGGTCGAGG TGGCCCGGCT CCATGCACCG CGACGCAACG CGGGGAGGCA 5821 GACAAGGTAT AGGGCGGCGC CTACAATCCA TGCCAACCCG TTCCATGTGC TCGCCGAGGC 5881 GGCATAAATC GCCGTGACGA TCAGCGGTCC AGTGATCGAA GTTAGGCTGG TAAGAGCCGC 5941 GAGCGATCCT TGAAGCTGTC CCTGATGGTC GTCATCTACC TGCCTGGACA GCATGGCCTG 6001 CAACGCGGGC ATCCCGATGC CGCCGGAAGC GAGAAGAATC ATAATGGGGA AGGCCATCCA 6061 GCCTCGCGTC GCGAACGCCA GCAAGACGTA GCCCAGCGCG TCGGCCGCCA TGCCGGCGAT 6121 AATGGCCTGC TTCTCGCCGA AACGTTTGGT GGCGGGACCA GTGACGAAGG CTTGAGCGAG 6181 GGCGTGCAAG ATTCCGAATA CCGCAAGCGA CAGGCCGATC ATCGTCGCGC TCCAGCGAAA 6241 GCGGTCCTCG CCGAAAATGA CCCAGAGCGC TGCCGGCACC TGTCCTACGA GTTGCATGAT-

FOURE 36C

6301	AAAGAAGACA	GTCATAAGTG	CGGCGACGAT	AGTCATGCCC	CGCGCCCACC	GGAAGGAGCT
6361	GACTGGGTTG	AACCCTCTCA	AGGGCATCGG	TCGATCGACG	CTCTCCCTTA	TGCGACTCCT
6361	CONTENCON	CCACCCCAGT	AGTAGGTTGA	GGCCGTTGAG	CACCGCCGCC	GCAAGGAATG
6421	GTGCATGCAA	GCAGCCCAGI	CCCAACACTC	CCCCGGCCAC	GGGGCCTGCC	ACCATACCCA
6481	GTGCATGCAA	GGAGATGGCG	CCCAACAGIC	GCCC3GCCAC	ATCTTCCCCA	TCGGTGATGT
6541	CGCCGAAACA	AGCGCTCATG	AGCCCGAAGT	GGCGAGCCCG	ATCTTCCCCA	TCGGTGATGT
6601	CGGCGATATA	GGCGCCAGCA	ACCGCACCTG	TGGCGCCGGT	GATGCCGGCC	ACGATGCGTC
6661	CCCCCTAGAG	GATCG				

gat ccc gcg aaa tta ata cga ctc act ata ggg aga cca caa cgg ttt ccc cta ggg cgc ttt aat tat gct gag tga tat ccc tct ggt gtt gcc aaa ggg

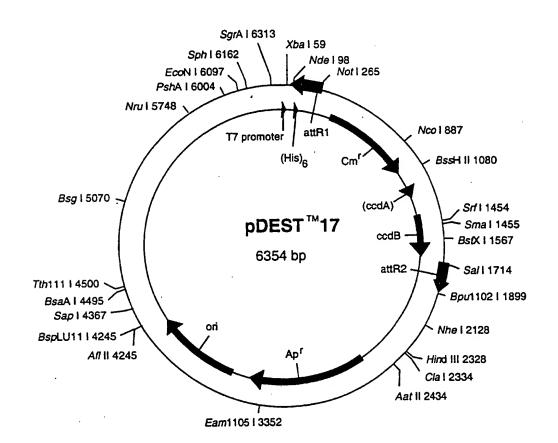
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103 tac cat cac cat cac cat cac ctc gaa tca agt ttg tac aaa aaa gct

104 A H H H H H L E S aca agt ttg tac aaa aaa gct

105 atg gta gtg gta gtg gag ctt agt tca aac atg ttt ttt cga

106 A Tmt



Location (Base Nos.)

258..134

## pDEST17 6354 bp

Gene Encoded

attR1

		250					
		367102	16	CmR	. 0.		
	11461230			inactivated ccdA			
		136816	73	ccdB			
		171418	138	attR2			
		256434	21	ampR			
1	CGATCCCGCG	AAATTAATAC	GACTCACTAT	AGGGAGACCA	CAACGGTTTC	CCTCTAGAAA	
61	TAATTTTGTT	TAACTTTAAG	AAGGAGATAT	ACATATGTCG	TACTACCATC	ACCATCACCA	
121	TCACCTCGAA	TCAACAAGTT	TGTACAAAAA	AGCTGAACGA	GAAACGTAAA	ATGATATAAA	
181	TATCAATATA	TTAAATTAGA	TTTTGCATAA	AAAACAGACT	ACATAATACT	GTAAAACACA	
241	ACATATCCAG	TCACTATGGC	GGCCGCATTA	GGCACCCCAG	GCTTTACACT	TTATGCTTCC	
301	GGCTCGTATA	ATGTGTGGAT	TTTGAGTTAG	GATCCGTCGA	GATTTTCAGG	AGCTAAGGAA	
361	GCTAAAATGG	AGAAAAAAAT	CACTGGATAT	ACCACCGTTG	ATATATCCCA	ATGGCATCGT	
				GCTCAATGTA			
481	CTGGATATTA	CGGCCTTTTT	AAAGACCGTA	AAGAAAAATA	AGCACAAGTT	TTATCCGGCC	
541	TTTATTCACA	TTCTTGCCCG	CCTGATGAAT	GCTCATCCGG	AATTCCGTAT	GGCAATGAAA	
601	GACGGTGAGC	TGGTGATATG	GGATAGTGTT	CACCCTTGTT	ACACCGTTTT	CCATGAGCAA	
661	ACTGAAACGT	TTTCATCGCT	CTGGAGTGAA	TACCACGACG	ATTTCCGGCA	GTTTCTACAC	
721	ATATATTCGC	AAGATGTGGC	GTGTTACGGT	GAAAACCTGG	CCTATTTCCC	TAAAGGGTTT	
781	ATTGAGAATA	TGTTTTTCGT	CTCAGCCAAT	CCCTGGGTGA	GTTTCACCAG	TTTTGATTTA	
				CCCGTTTTCA			
901	CAAGGCGACA	AGGTGCTGAT	GCCGCTGGCG	ATTCAGGTTC	ATCATGCCGT	CTGTGATGGC	
961	TTCCATGTCG	GCAGAATGCT	TAATGAATTA	CAACAGTACT	GCGATGAGTG	GCAGGGCGGG	
				GCCAGATAAC			
				ATGTATACCC			
1141	GTGCTATGAA	GCAGCGTATT	ACAGTGACAG	TTGACAGCGA	CAGCTATCAG	TTGCTCAAGG	
1201	CATATATGAT	GTCAATATCT	CCGGTCTGGT	AAGCACAACC	ATGCAGAATG	AAGCCCGTCG	
1261	TCTGCGTGCC	GAACGCTGGA	AAGCGGAAAA	TCAGGAAGGG	ATGGCTGAGG	TCGCCCGGTT	
1321	TATTGAAATG	AACGGCTCTT	TTGCTGACGA	GAACAGGGAC	TGGTGAAATG	CAGTTTAAGG	
				GTCTGTTTGT			
1441	TTGACACGCC	CGGGCGACGG	ATGGTGATCC	CCCTGGCCAG	TGCACGTCTG	CTGTCAGATA	
1501	AAGTCTCCCG	TGAACTTTAC	CCGGTGGTGC	ATATCGGGGA	TGAAAGCTGG	CGCATGATGA	
1561	CCACCGATAT	GGCCAGTGTG	CCGGTCTCCG	TTATCGGGGA	AGAAGTGGCT	GATCTCAGCC	
1621	ACCGCGAAAA	TGACATCAAA	AACGCCATTA	ACCTGATGTT	CTGGGGAATA	TAAATGTCAG	
1681	GCTCCCTTAT	ACACAGCCAG	TCTGCAGGTC	GACCATAGTG	ACTGGATATG	TTGTGTTTTA	
				ATCTAATTTA			
				AAAGTGGTTG			
				CCGCTGAGCA			
				TGCTGAAAGG			
				TAGTCGATAG			
						TGCGCATAGA	
						GCTGTCGGAA	
						GCCTACAGCA	
				ACCOGCATAA			
2221	TCCAGGGTGA	ACCA ACCORD	CUCUCAUA	CTACCCCATTGI	A A A C C TT A TC	GATGATAAGC	
2281	TGACTGCGTT	AGCAAIIIAA	CIGIGAIAAA	CIACCOCATI	AMAGCITATC	TTTTATAGGT	
						GAAATGTGCG	
						TCATGAGACA	
2521	ATAACCCTGA	TAAATGCTTC	AATAATATTG	AAAAAGGAAG	AGTATGAGTA	TTCAACATTT	
2581	CCGTGTCGCC	CTTATTCCCT	TTTTTGCGGC	ATTTTGCCTT	CCIGITITIG	CTCACCCAGA	
2641	AACGCTGGTG	AAAGTAAAAG	ATGCTGAAGA	TCAGTTGGGT	GCACGAGTGG	GTTACATCGA-	

Figure 373

2701 ACTGGATCTC AACAGCGGTA AGATCCTTGA GAGTTTTCGC CCCGAAGAAC GTTTTCCAAT 2761 GATGAGCACT TTTAAAGTTC TGCTATGTGG CGCGGTATTA TCCCGTGTTG ACGCCGGGCA 2821 AGAGCAACTC GGTCGCCGCA TACACTATTC TCAGAATGAC TTGGTTGAGT ACTCACCAGT 2881 CACAGAAAAG CATCTTACGG ATGGCATGAC AGTAAGAGAA TTATGCAGTG CTGCCATAAC 2941 CATGAGTGAT AACACTGCGG CCAACTTACT TCTGACAACG ATCGGAGGAC CGAAGGAGCT 3001 AACCGCTTTT TTGCACAACA TGGGGGATCA TGTAACTCGC CTTGATCGTT GGGAACCGGA 3061 GCTGAATGAA GCCATACCAA ACGACGAGCG TGACACCACG ATGCCTGCAG CAATGGCAAC 3121 AACGTTGCGC AAACTATTAA CTGGCGAACT ACTTACTCTA GCTTCCCGGC AACAATTAAT 3181 AGACTGGATG GAGGCGGATA AAGTTGCAGG ACCACTTCTG CGCTCGGCCC TTCCGGCTGG 3241 CTGGTTTATT GCTGATAAAT CTGGAGCCGG TGAGCGTGGG TCTCGCGGTA TCATTGCAGC 3301 ACTGGGGCCA GATGGTAAGC CCTCCCGTAT CGTAGTTATC TACACGACGG GGAGTCAGGC 3361 AACTATGGAT GAACGAAATA GACAGATCGC TGAGATAGGT GCCTCACTGA TTAAGCATTG 3421 GTAACTGTCA GACCAAGTTT ACTCATATAT ACTTTAGATT GATTTAAAAC TTCATTTTTA 3481 ATTTAAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG 3541 TGAGTTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA 3601 TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACCACCGC TACCAGCGGT 3661 GGTTTGTTTG CCGGATCAAG AGCTACCAAC TCTTTTTCCG AAGGTAACTG GCTTCAGCAG 3721 AGCGCAGATA CCAAATACTG TCCTTCTAGT GTAGCCGTAG TTAGGCCACC ACTTCAAGAA 3781 CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG CTGCTGCCAG 3841 TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTTACCGG ATAAGGCGCA 3901 GCGGTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA CGACCTACAC 3961 CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA 4021 GGCGGACAGG TATCCGGTAA GCGGCAGGGT CGGAACAGGA GAGCGCACGA GGGAGCTTCC 4081 AGGGGGAAAC GCCTGGTATC TTTATAGTCC TGTCGGGTTT CGCCACCTCT GACTTGAGCG 4141 TCGATTTTTG TGATGCTCGT CAGGGGGGCG GAGCCTATGG AAAAACGCCA GCAACGCGGC 4201 CTTTTTACGG TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTTCTTTC CTGCGTTATC 4261 CCCTGATTCT GTGGATAACC GTATTACCGC CTTTGAGTGA GCTGATACCG CTCGCCGCAG 4321 CCGAACGACC GAGCGCAGCG AGTCAGTGAG CGAGGAAGCG GAAGAGCGCC TGATGCGGTA 4381 TTTTCTCCTT ACGCATCTGT GCGGTATTTC ACACCGCATA TATGGTGCAC TCTCAGTACA 4441 ATCTGCTCTG ATGCCGCATA GTTAAGCCAG TATACACTCC GCTATCGCTA CGTGACTGGG 4501 TCATGGCTGC GCCCCGACAC CCGCCAACAC CCGCTGACGC GCCCTGACGG GCTTGTCTGC 4561 TCCCGGCATC CGCTTACAGA CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT 4621 TTTCACCGTC ATCACCGAAA CGCGCGAGGC AGCTGCGGTA AAGCTCATCA GCGTGGTCGT 4681 GAAGCGATTC ACAGATGTCT GCCTGTTCAT CCGCGTCCAG CTCGTTGAGT TTCTCCAGAA 4741 GCGTTAATGT CTGGCTTCTG ATAAAGCGGG CCATGTTAAG GGCGGTTTTT TCCTGTTTGG 4801 TCACTGATGC CTCCGTGTAA GGGGGATTTC TGTTCATGGG GGTAATGATA CCGATGAAAC 4861 GAGAGAGGAT GCTCACGATA CGGGTTACTG ATGATGAACA TGCCCGGTTA CTGGAACGTT 4921 GTGAGGGTAA ACAACTGGCG GTATGGATGC GGCGGGACCA GAGAAAAATC ACTCAGGGTC 4981 AATGCCAGCG CTTCGTTAAT ACAGATGTAG GTGTTCCACA GGGTAGCCAG CAGCATCCTG 5041 CGATGCAGAT CCGGAACATA ATGGTGCAGG GCGCTGACTT CCGCGTTTCC AGACTTTACG 5101 AAACACGGAA ACCGAAGACC ATTCATGTTG TTGCTCAGGT CGCAGACGTT TTGCAGCAGC 5161 AGTCGCTTCA CGTTCGCTCG CGTATCGGTG ATTCATTCTG CTAACCAGTA AGGCAACCCC 5221 GCCAGCCTAG CCGGGTCCTC AACGACAGGA GCACGATCAT GCGCACCCGT GGCCAGGACC 5281 CAACGCTGCC CGAGATGCGC CGCGTGCGGC TGCTGGAGAT GGCGGACGCG ATGGATATGT 5341 TCTGCCAAGG GTTGGTTTGC GCATTCACAG TTCTCCGCAA GAATTGATTG GCTCCAATTC 5401 TTGGAGTGGT GAATCCGTTA GCGAGGTGCC GCCGGCTTCC ATTCAGGTCG AGGTGGCCCG 5461 GCTCCATGCA CCGCGACGCA ACGCGGGGAG GCAGACAAGG TATAGGGCGG CGCCTACAAT 5521 CCATGCCAAC CCGTTCCATG TGCTCGCCGA GGCGGCATAA ATCGCCGTGA CGATCAGCGG 5581: TCCAGTGATC GAAGTTAGGC TGGTAAGAGC CGCGAGCGAT CCTTGAAGCT GTCCCTGATG 5641 GTCGTCATCT ACCTGCCTGG ACAGCATGGC CTGCAACGCG GGCATCCCGA TGCCGCCGGA 5701 AGCGAGAAGA ATCATAATGG GGAAGGCCAT CCAGCCTCGC GTCGCGAACG CCAGCAAGAC 5761 GTAGCCCAGC GCGTCGGCCG CCATGCCGGC GATAATGGCC TGCTTCTCGC CGAAACGTTT 5821 GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG 5881 CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG 5941 CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC 6001 GATAGTCATG CCCCGCGCCC ACCGGAAGGA GCTGACTGGG TTGAAGGCTC TCAAGGGCAT 6061 CGGTCGATCG ACGCTCTCCC TTATGCGACT CCTGCATTAG GAAGCAGCCC AGTAGTAGGT 6121 TGAGGCCGTT GAGCACCGCC GCCGCAAGGA ATGGTGCATG CAAGGAGATG GCGCCCAACA-

FRURE 37C

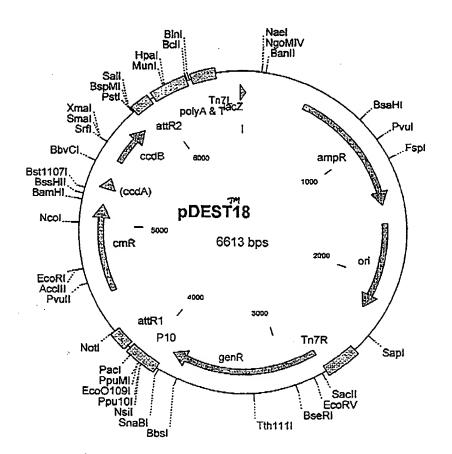
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FIGURE 37D

Figure 38A: PDESTIE

# FastBac Transfer Vector with p10 Baculovirus Promoter

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gaagaceteg geegtegegg egettgeegg tggtgetgae eeeggatgaa gtggttegea
        cttctggage eggeagegee gegaacggee accaegactg gggeetaett caecaagegt
        tecteggttt tetggaagge gageategtt tgttegeeca ggaetetage tatagtteta aggagecaaa agaeetteeg etegtageaa acaagegggt eetgagateg atateaagat
 61
     gtggttgget acgtategag caagaaanta anacgccaha egegytggag tettgtged caccaacega tgeatagete gttetttat tttgeggtt gegenaeete agaacacac y PIO Romoter tattttaca angatteaga antaegene acttacaaca agggggacta tganattatgii naraanaacgt ttetaagtet ttatgegtag tganatgttgt teeceetgat acttanatae,
121
181
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301
        taataaata gtttagtaaa oatataatta attttatgat atgacattta atgtaaaata
         ttacaatgag gatcatcaca agtttgtaca aaaaagctga acgagaaacg taaaatgata
361
         aatgttacte ctagtagtgt teaaacatgt titttegact tgetetttge attttactat,,
                                                    Int V
                                                                    attRI
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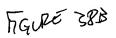


### pDEST18 6613 bp

Location (Base Nos.)

Gene Encoded

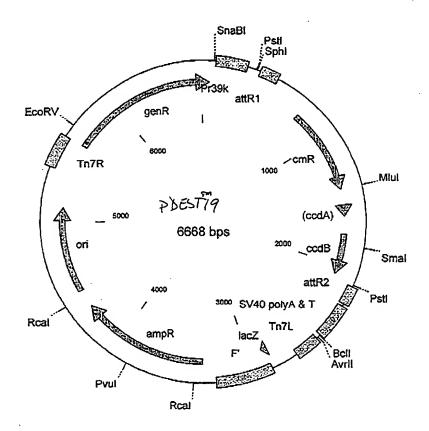
		474144	a	ampR		
		159022		ori		
		-		genR		
		273838		attR1		
		425141				
		450151		CmR	The boses	
		528053			vated ccdA	
		550258		ccdB		
		584859		attR2		
		659525	i	lacZ		
			>mm>>00000	aaaaamamaa	mccmma cccc	CACCCTCACC
1	GACGCGCCCT	GTAGCGGCGC	ATTAAGCGCG	GCGGGTGTGG	morre come	CAGCGIGACC
61	GCTACACTTG	CCAGCGCCCT	AGCGCCCGCT	CCTTTCGCTT	TCITCCCTTC	CTTTCTCGCC
121	ACGTTCGCCG	GCTTTCCCCG	TCAAGCTCTA	AATCGGGGGC	TCCCTTTAGG	DOCUMENT OF THE PARTY OF THE PA
181	AGTGCTTTAC	GGCACCTCGA	CCCCAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGGG
241	CCATCGCCCT	GATAGACGGT	TTTTCGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATAGT
301	GGACTCTTGT	TCCAAACTGG	AACAACACTC	AACCCTATCT	CGGTCTATTC	TTTTGATTTA
361	TAAGGGATTT	TGCCGATTTC	GGCCTATTGG	TTAAAAAATG	AGCTGATTTA	ACAAAAATTT
421	AACGCGAATT	TTAACAAAAT	ATTAACGTTT	ACAATTTCAG	GTGGCACTTT	TCGGGGAAAT
481	GTGCGCGGAA	CCCCTATTTG	TTTATTTTTC	TAAATACATT	CAAATATGTA	TCCGCTCATG
541	AGACAATAAC	CCTGATAAAT	GCTTCAATAA	TATTGAAAAA	GGAAGAGTAT	GAGTATTCAA
601	CATTTCCGTG	TCGCCCTTAT	TCCCTTTTTT	GCGGCATTTT	GCCTTCCTGT	TTTTGCTCAC
661	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGT	TGGGTGCACG	AGTGGGTTAC
721	ATCGAACTGG	ATCTCAACAG	CGGTAAGATC	CTTGAGAGTT	TTCGCCCCGA	AGAACGTTTT
781	CCAATGATGA	GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG	TATTATCCCG	TATTGACGCC
841	GGGCAAGAGC	AACTCGGTCG	CCGCATACAC	TATTCTCAGA	ATGACTTGGT	TGAGTACTCA
901	CCAGTCACAG	AAAAGCATCT	TACGGATGGC	ATGACAGTAA	GAGAATTATG	CAGTGCTGCC
961	ATAACCATGA	GTGATAACAC	TGCGGCCAAC	TTACTTCTGA	CAACGATCGG	AGGACCGAAG
1001	CACCTAACCG	CTOTITITIONS	CAACATGGGG	GATCATGTAA	CTCGCCTTGA	TCGTTGGGAA
1021	CCCCACCTCA	ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA	CCACGATGCC	TGTAGCAATG
1141	CCAACAACCT	TCCCCNAACT	ATTAACTCCC	GAACTACTTA	CTCTAGCTTC	CCGGCAACAA
1141	GCAACAACGI	CCATCGACGC	CCATAAACTT	GCAGGACCAC	TTCTGCGCTC	GGCCCTTCCG
1201	COMMONOR	GGAIGGAGGC	TANTOTO	GCCGGTGAGC	GTGGGTCTCG	CGGTATCATT
1261	GCTGGCTGGT	CCCCACATCC	TARRICIGGA	CGTATCGTAG	TTATCTACAC	GACGGGGAGT
1321	GCAGCACTGG	TOCATION ACC	A A BRACACACAC	ATCGCTGAGA	TACCTCCCTC	ACTGATTAAG
1381	CAGGCAACTA	TGGATGAACG	AMMIMUMUMU	TATATACTTT	ACATTCATTT	אאאסרדידראיד
1441	CATTGGTAAC	TGTCAGACCA	AGITIACICA	CTTTTTGATA	AGAIIGALII	CAAAACIICAI
1561	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG	AAAAGAICAA	ACCCCTACCA
1621	TGAGATCCTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC	ACCGCTACCA
1681	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT	TTCCGAAGGT	AACIGGCIIC
,1741	AGCAGAGCGC	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG	CCACCACTTC
						AGTGGCTGCT
1861	GCCAGTGGCG	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA	GACGATAGTT	ACCGGATAAG
1921	GCGCAGCGGT	CGGGCTGAAC	GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC
						TCCCGAAGGG
						CACGAGGGAG
						CCTCTGACTT
						CGCCAGCAAC
2221	. GCGGCCTTTT	TACGGTTCCT	GGCCTTTTGC	TGGCCTTTTG	CTCACATGTT	CTTTCCTGCG
						TACCGCTCGC
2341	CGCAGCCGAA	CGACCGAGCG	CAGCGAGTCA	GTGAGCGAGG	AAGCGGAAGA	GCGCCTGATG
2401	CGGTATTTTC	TCCTTACGCA	TCTGTGCGGT	ATTTCACACC	GCAGACCAGC	CGCGTAACCT
2461	GGCAAAATCC	GTTACGGTTG	AGTAATAAAT	GGATGCCCTG	CGTAAGCGGG	TGTGGGCGGA-



			~	CMA A A CMA CC	አር አ አጥአ አ አርፕ	בארדי א א מידיאכי
2521	CAATAAAGTC	TTAAACTGAA	CAAAATAGAT	CTAAACTATG	ACAATAAAGI	STIMMS ING
2581	ACAGAATAGT	TGTAAACTGA	AATCAGTCCA	GTTATGCTGT	ARTECOCCEC	ACIGGACIII CTATT: ACA
2641	TGTTATGGCT	AAAGCAAACT	CTTCATTTTC	TGAAGTGCAA	ATTGCCCGTC	THII I CAN C
2701	GGGGCGTGGC	CAAGGGCATG	GTAAAGACTA	TATTCGCGGC	GIIGIGACAA	COTACCEAAC
2761	AACTCCGCGG	CCGGGAAGCC	GATCTCGGCT	TGAACGAATT	GTTAGGTGGC	ACCON CECCO
2821	TCGATATCAA	AGTGCATCAC	TTCTTCCCGT	ATGCCCAACT	TIGIATAGAG	AGCCAC . GCG
2881	GGATCGTCAC	CGTAATCTGC	TTGCACGTAG	ATCACATAAG	CACCAAGCGC	GITGGCCTCA
2941	TGCTTGAGGA	GATTGATGAG	CGCGGTGGCA	ATGCCCTGCC	TCCGGTGCTC	GCCGGAGACT
3001	GCGAGATCAT	AGATATAGAT	CTCACTACGC	GGCTGCTCAA	ACCTGGGCAG	AACGTAAGCC
3061	GCGAGAGCGC	CAACAACCGC	TTCTTGGTCG	AAGGCAGCAA	GCGCGATGAA	TGTCTTACTA
3121	CGGAGCAAGT	TCCCGAGGTA	ATCGGAGTCC	GGCTGATGTT	GGGAGTAGGT	GGCTACGTCT
3181	CCGAACTCAC	GACCGAAAAG	ATCAAGAGCA	GCCCGCATGG	ATTTGACTTG	GTCAGGGCCG
3241	AGCCTACATG	TGCGAATGAT	GCCCATACTT	GAGCCACCTA	ACTTTGTTTT	AGGGCGACTG
3301	CCCTGCTGCG	TAACATCGTT	GCTGCTGCGT	AACATCGTTG	CTGCTCCATA	ACATCAAACA
3361	TCGACCCACG	GCGTAACGCG	CTTGCTGCTT	GGATGCCCGA	GGCATAGACT	GTACAAAAA
3421	ACAGTCATAA	CAAGCCATGA	AAACCGCCAC	TGCGCCGTTA	CCACCGCTGC	GTTCGGTCAA
3481	GGTTCTGGAC	CAGTTGCGTG	AGCGCATACG	CTACTTGCAT	TACAGTTTAC	GAACCGAACA
3541	GGCTTATGTC	AACTGGGTTC	GTGCCTTCAT	CCGTTTCCAC	GGTGTGCGTC	ACCCGGCAAC
3601	CTTGGGCAGC	AGCGAAGTCG	AGGCATTTCT	GTCCTGGCTG	GCGAACGAGC	GCAAGGTTTC
3661	GGTCTCCACG	CATCGTCAGG	CATTGGCGGC	CTTGCTGTTC	TTCTACGGCA	AGGTGCTGTG
3721	CACGGATCTG	CCCTGGCTTC	AGGAGATCGG	AAGACCTCGG	CCGTCGCGGC	GCTTGCCGGT
3781	GGTGCTGACC	CCGGATGAAG	TGGTTCGCAT	CCTCGGTTTT	CTGGAAGGCG	AGCATCGTTT
3841	GTTCGCCCAG	GACTCTAGCT	ATAGTTCTAG	TGGTTGGCTA	CGTATCGAGC	AAGAAAATAA
3901	AACGCCAAAC	GCGTTGGAGT	CTTGTGTGCT	ATTTTTACAA	AGATTCAGAA	ATACGCATCA
3961	CTTACAACAA	GGGGGACTAT	GAAATTATGC	ATTTTGAGGA	TGCCGGGACC	TTTAATTCAA
4021	CCCAACACAA	TATATTATAG	TTAAATAAGA	ATTATTTATC	AAATCATTTG	TATATTAATT
4021	ΤΑΤΊΔΙΙΔΙΔΟΔΑ	ACTGTAAATT	ACATTTTATT	TACAATGAGG	ATCATCACAA	GTTTGTACAA
4141	AAAAGCTGAA	CGAGAAACGT	AAAATGATAT	AAATATCAAT	ATATTAAATT	AGATTTTGCA
4201	TAAAAAAACAG	ACTACATAAT	ACTGTAAAAC	ACAACATATC	CAGTCACTAT	GGCGGCCGCT
4201	AACTTCCCAG	CATCACCCGA	CGCACTTTGC	GCCGAATAAA	TACCTGTGAC	GGAAGATCAC
4201	TTCCCAGAAT	DAATAAATCC	TGGTGTCCCT	GTTGATACCG	GGAAGCCCTG	GGCCALCTTT
4301	TCCCCAAAAT	GAGACGTTGA	TCGGCACGTA	AGAGGTTCCA	ACTITCACCA	TAATGAAATA
4301	ACATCACTAC	CCCCCCTATT		TCGAGATTTT	CAGGAGCTAA	GGAAGCTAAA
4501	AGAICACIAC	AAATCACTGG	ATATACCACC	GTTGATATAT	CCCAATGGCA	TCGTAAAGAA
4501	CAUCHGAAAA	CATTTCACTC	ACTTCCTCAD	TGTACCTATA	ACCAGACCGT	TCAGCTGGAT
4561	ATTITIONS	TTTTAAACAC	CCTAAACAAA	AATAAGCACA	AGTTTTATCC	GGCCTTTATT
4621	ATTACGGCCI	CCCCCCTGNT	COLAMONA	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT
4681	CACATICITO	TATCCCIONI	TANIOCICAL PROPERTY OF THE PRO	TGTTACACCG	TTTTCCATGA	GCAAACTGAA
4741	GAGCTGGTGA	A LAIGGGAIAG	TGIICACCCI	GACGATTTCC	GGCAGTTTCT	TATETATAT
4801	ACGITITCAL	. CGC1C1GGAG	CCCTCAAAA	CTGGCCTATT	TCCCTAAAGG	CTTTATTGAG
4861	. TCGCAAGATG	TGGCGTGTTA	COGIGAAAAC	GTGAGTTTCA	CCACTTTTCA	TTTTAAACTTC
				TTCACCATGG		
				GTTCATCATG		
5101	GTCGGCAGA	A TGCTTAATGA	ATTACAACAC	TACTGCGATG	AGTGGCAGGG	CGGGGCGTAA
5161	LACGCGTGGAT	r ccgccrtaci	. AAAAGCCAGA	TAACAGTATG	CGTATITICG	CGCTGATTTT
5221	L TGCGGTATA	A GAATATATA	TGATATGTA	r ACCCGAAGTA	TGTCAAAAAG	AGGTGTGCTA
5283	L TGAAGCAGC	3 TATTACAGTO	ACAGTTGAC	A GCGACAGCTA	TCAGTIGCTC	AAGGCATATA
534	L TGATGTCAA	r ATCTCCGGT	TGGTAAGCA	C AACCATGCAG	AATGAAGCCC	GTCGTCTGCG
540:	L TGCCGAACG	C TGGAAAGCG	AAAATCAGG	A AGGGATGGCI	GAGGTCGCCC	GGTTTATTGA
546	L AATGAACGG	C TCTTTTGCT	B ACGAGAACA	G GGACTGGTGA	AATGCAGTTT	AAGGTTTACA
552	L CCTATAAAA	G AGAGAGCCG	TATCGTCTG	r ttgtggatgi	ACAGAGTGAT	ATTATTGACA
5583	1 CGCCCGGGC	G ACGGATGGT	ATCCCCCTG	G CCAGTGCACG	TCTGCTGTCA	GATAAAGTCT
564	1 CCCGTGAAC	T TTACCCGGT	G GTGCATATC	G GGGATGAAAG	CTGGCGCATG	ATGACCACCG
570	1 ATATGGCCA	G TGTGCCGGT	C TCCGTTATC	G GGGAAGAAG1	GGCTGATCTC	AGCCACCGCG
576	1 AAAATGACA	T CAAAAACGC	C ATTAACCTG	A TGTTCTGGGG	AATATAAATO	TCAGGCTCCC
582	1 TTATACACA	G CCAGTCTGC	A GGTCGACCA	T AGTGACTGGA	A TATGTTGTGT	TTTACAGTAT
588	1 TATGTAGTC	T GTTTTTTAT	G CAAAATCTA	A TTTAATATA	TGATATTTAT	ATCATTTTAC
594	1 GTTTCTCGT	T CAGCTTTCT	T GTACAAAGT	G GTGATAGCT	r grcgagaagi	ACTAGAGGAT-

FIGURE 38C

6001	CATAATCAGC	CATACCACAT	TTGTAGAGGT	TTTACTTGCT	TTAAAAAACC	TCCCACACCT	
6061	CCCCCTGAAC	CTGAAACATA	AAATGAATGC	AATTGTTGTT	GTTAACTTGT	TTATTGCAGC	
6121	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTC	ACAAATAAAG	CATTTTTTC	
6181	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	TCTGGATCTG	
6241	ATCACTGCTT	GAGCCTAGGA	GATCCGAACC	AGATAAGTGA	AATCTAGTTC	CAAACTATTT	
6301	TGTCATTTTT	AATTTTCGTA	TTAGCTTACG	ACGCTACACC	CAGTTCCCAT	CTATTTTGTC	
6361	ACTCTTCCCT	AAATAATCCT	TAAAAACTCC	ATTTCCACCC	CTCCCAGTTC	CCAACTATTT	
6421	TGTCCGCCCA	CAGCGGGGCA	TTTTTCTTCC	TGTTATGTTT	TTAATCAAAC	ATCCTGCCAA	
6481	CTCCATGTGA	CAAACCGTCA	TCTTCGGCTA	CTTTTTCTCT	GTCACAGAAT	GAAAATTTTT	
6541	CTGTCATCTC	TTCGTTATTA	ATGTTTGTAA	TTGACTGAAT	ATCAACGCTT	ATTTGCAGCC	
6601	TGAATGGCGA	ATG					



# pDEST19 6668 bp (rotated to position 1000)

Location (Base Nos.)	Gene Encoded
515391	attR1
7651424	CmR
15441628	inactivated ccdA
17662071	ccdB
21122236	attR2
28522895	lacZ
33444319	ampR
44605114	ori
560852	genR

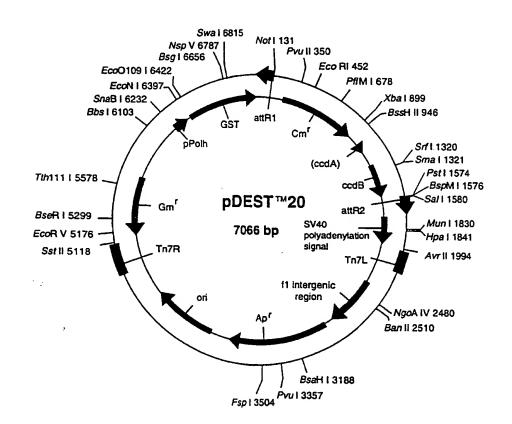
		360632		90		
1	AGTGGTTCGC	ATCCTCGGTT	TTCTGGAAGG	CGAGCATCGT	TTGTTCGCCC	AGGACTCTAG
61	CTATAGTTCT	AGTGGTTGGC	TACGTATATC	AAATACTTGT	AGGTGACGCC	GTCATCTTTC
121	CATTGTAACG	TAAATGGCAA	CTTGTAGATG	AACGCGCTGT	CAAAAAACCG	GCCAGTTTCT
181	TCCACAAACT	CGCGCACGGC	TGTCTCGTAA	ACTITITGCGT	CGCAACAATC	GCGATGACCT
241	CGTGGTATGG	AAATTTTTTC	TAAAAAAGTG	TCGTTCATGT	CGGCGGCGGG	CGCGTTCGCG
301	CTCCGGTACG	CGCGACGGGC	ACACAGCAGG	ACAGCCTTGT	CCGGCTCGAT	TATCATAAAC
361	AATCCTGCAG	GCATGCAAGC	TCGGATCATC	ACAAGTTTGT	ACAAAAAAGC	TGAACGAGAA
421	ACGTAAAATG	TATAAATAT	CAATATATTA	AATTAGATTT	TGCATAAAAA	ACAGACTACA
481	TAATACTGTA	AAACACAACA	TATCCAGTCA	CTATGGCGGC	CGCTAAGTTG	GCAGCATCAC
541	CCGACGCACT	TTGCGCCGAA	TAAATACCTG	TGACGGAAGA	TCACTTCGCA	GAATAAATAA
601	ATCCTGGTGT	CCCTGTTGAT	ACCGGGAAGC	CCTGGGCCAA	CTTTTGGCGA	AAATGAGACG
661	TTGATCGGCA	CGTAAGAGGT	TCCAACTTTC	ACCATAATGA	AATAAGATCA	CTACCGGGCG
721	TATTTTTTGA	GTTATCGAGA	TTTTCAGGAG	CTAAGGAAGC	TAAAATGGAG	AAAAAAATCA
781	CTGGATATAC	CACCGTTGAT	ATATCCCAAT	GGCATCGTAA	AGAACATTTT	GAGGCATTTC
841	AGTCAGTTGC	TCAATGTACC	TATAACCAGA	CCGTTCAGCT	GGATATTACG	GCCTTTTTAA
901	AGACCGTAAA	GAAAAATAAG	CACAAGTTTT	ATCCGGCCTT	TATTCACATT	CTTGCCCGCC
961	TGATGAATGC	TCATCCGGAA	TTCCGTATGG	CAATGAAAGA	CGGTGAGCTG	GTGATATGGG
1021	ATAGTGTTCA	CCCTTGTTAC	ACCGTTTTCC	ATGAGCAAAC	TGAAACGTTT	TCATCGCTCT
1081	GGAGTGAATA	CCACGACGAT	TTCCGGCAGT	TTCTACACAT	ATATTCGCAA	GATGTGGCGT
1141	GTTACGGTGA	AAACCTGGCC	TATTTCCCTA	AAGGGTTTAT	TGAGAATATG	TTTTTCGTCT
1201	CAGCCAATCC	CTGGGTGAGT	TTCACCAGTT	TTGATTTAAA	CGTGGCCAAT	ATGGACAACT
1261	TCTTCGCCCC	CGTTTTCACC	ATGGGCAAAT	ATTATACGCA	AGGCGACAAG	GTGCTGATGC
1321	CGCTGGCGAT	TCAGGTTCAT	CATGCCGTCT	GTGATGGCTT	CCATGTCGGC	AGAATGCTTA
1381	ATGAATTACA	ACAGTACTGC	GATGAGTGGC	AGGGCGGGC	GTAAACGCGT	GGATCCGGCT
1441	TACTAAAAGC	CAGATAACAG	TATGCGTATT	TGCGCGCTGA	TTTTTGCGGT	ATAAGAATAT
1501	ATACTGATAT	GTATACCCGA	AGTATGTCAA	AAAGAGGTGT	GCTATGAAGC	AGCGTATTAC
1561	AGTGACAGTT	GACAGCGACA	GCTATCAGTT	GCTCAAGGCA	TATATGATGT	CAATATCTCC
1621	GGTCTGGTAA	GCACAACCAT	GCAGAATGAA	GCCCGTCGTC	TGCGTGCCGA	ACGCTGGAAA
1681	GCGGAAAATC	AGGAAGGGAT	GGCTGAGGTC	GCCCGGTTTA	TTGAAATGAA	CGGCTCTTTT
1741	GCTGACGAGA	ACAGGGACTG	GTGAAATGCA	GTTTAAGGTT	TACACCTATA	AAAGAGAGAG
1801	CCGTTATCGT	CTGTTTGTGG	ATGTACAGAG	TGATATTATT	GACACGCCCG	GGCGACGGAT
,1,861	GGTGATCCCC	CTGGCCAGTG	CACGTCTGCT	GTCAGATAAA	GTCTCCCGTG	AACTTTACCC
1921	GGTGGTGCAT	ATCGGGGATG	AAAGCTGGCG	CATGATGACC	ACCGATATGG	CCAGTGTGCC
1981	GGTCTCCGTT	ATCGGGGAAG	AAGTGGCTGA	TCTCAGCCAC	CGCGAAAATG	ACATCAAAAA
2041	CGCCATTAAC	CTGATGTTCT	GGGGAATATA	AATGTCAGGC	TCCCTTATAC	ACAGCCAGTC
						GTCTGTTTTT
						CGTTCAGCTT
						ACCACATTTG
						AAACATAAAA
2341	. TGAATGCAAT	TGTTGTTGTT	' AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA
						TGTGGTTTGT
						CCTAGGAGAT
2521	CCGAACCAGA	TAAGTGAAAT	CTAGTTCCA	ACTATTTTGT	CATTTTTAAT	TTTCGTATTA
2581	L GCTTACGACG	CTACACCCAG	TTCCCATCTA	A TTTTGTCACT	CTTCCCTAAA	TAATCCTTAA-

FIGURE 39B

						~~~~
2641	AAACTCCATT	TCCACCCCTC	CCAGTTCCCA	ACTATTTTGT	CCGCCCACAG	CGGGGCATTT
2701	TTCTTCCTGT	TATGTTTTTA	ATCAAACATC	CTGCCAACTC	CATGTGACAA .	ACCGTCATCT
2761	TCGGCTACTT	TTTCTCTGTC	ACAGAATGAA	AATTTTTCTG	TCATCTCTTC	GTTATTAATG
2821	TTTGTAATTG	ACTGAATATC	AACGCTTATT	TGCAGCCTGA	ATGGCGAATG	GACGCGCCCT
2881	GTAGCGGCGC	ATTAAGCGCG	GCGGGTGTGG	TGGTTACGCG	CAGCGTGACC	GCTACACTTG
2941	CCAGCGCCCT	AGCGCCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTTCTCGCC .	ACGTTCGCCG
3001	GCTTTCCCCG	TCAAGCTCTA	AATCGGGGGC	TCCCTTTAGG	GTTCCGATTT .	AGTGCTTTAC
3061	GGCACCTCGA	CCCCAAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT
3121	GATAGACGGT	TTTTCGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATAGT	GGACTCTTGT
3181	TCCAAACTGG	AACAACACTC	AACCCTATCT	CGGTCTATTC	TTTTGATTTA	TAAGGGATTT
3241	TGCCGATTTC	GGCCTATTGG	TTAAAAAAATG	AGCTGATTTA	ACAAAAATTT	AACGCGAATT
3301	TTAACAAAAT	ATTAACGTTT	ACAATTTCAG	GTGGCACTTT	TCGGGGAAAT	GTGCGCGGAA
3361	CCCCTATTTG	TTTATTTTTC	TAAATACATT	CAAATATGTA	TCCGCTCATG	AGACAATAAC
3421	CCTGATAAAT	GCTTCAATAA	TATTGAAAAA	GGAAGAGTAT	GAGTATTCAA	CATTTCCGTG
3481	TCGCCCTTAT	TCCCTTTTTT	GCGGCATTTT	GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC
3541	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGT	TGGGTGCACG	AGTGGGTTAC	ATCGAACTGG
3601	ATCTCAACAG	CGGTAAGATC	CTTGAGAGTT	TTCGCCCCGA	AGAACGTTTT	CCAATGATGA
3661	GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG	TATTATCCCG	TATTGACGCC	GGGCAAGAGC
3721	AACTCGGTCG	CCGCATACAC	TATTCTCAGA	ATGACTTGGT	TGAGTACTCA	CCAGTCACAG
3781	AAAAGCATCT	TACGGATGGC	ATGACAGTAA	GAGAATTATG	CAGTGCTGCC	ATAACCATGA
3941	CTCATAACAC	TGCGGCCAAC	TTACTTCTGA	CAACGATCGG	AGGACCGAAG	GAGCTAACCG
3901	CTUTTUTUTUCCA	CAACATGGGG	GATCATGTAA	CTCGCCTTGA	TCGTTGGGAA	CCGGAGCTGA
3061	ATCARCCOT	ACCAAACGAC	GAGCGTGACA	CCACGATGCC	TGTAGCAATG	GCAACAACGT
3301	TCCCCAAACC	ATTAACTGGC	GAACTACTTA	CTCTAGCTTC	CCGGCAACAA	TTAATAGACT
4001	CCATCCAGCC	CCATAAACTT	GCAGGACCAC	TTCTGCGCTC	GGCCCTTCCG	GCTGGCTGGT
4001	GGMIGGMGGC	TAAATCTCCA	CCCCCTGAGC	GTGGGTCTCG	CGGTATCATT	GCAGCACTGG
4141	COCCACATOC	TANAICIGGA	CCTATCCTAC	TTATCTACAC	GACGGGGAGT	CAGGCAACTA
4201	GGCCAGAIGG	A A TO CO CO CO	ATCCCTGAGA	TAGGTGCCTC	ACTGATTAAG	CATTGGTAAC
4261	TGGATGAACG	AMAIAGACAG	TATATACTOR	AGATTGATTT	ΤΑΌΤΤΟΙΔΙΑ	TTTTAATTTA
4321	TGTCAGACCA	AGIIIACICA	THIMINCILL	ATCTCATGAC	CANANTCCCT	TAACGTGAGT
4381	AAAGGATCTA	GGTGAAGATC	CACCCCCTAC	AAAAGATCAA	ACCATCTTCT	TGAGATCCTT
4441	TTTCGTTCCA	CIGAGCGICA	GACCCCG IAG	CAAAAAAACC	ACCCCTACCA	CCCCTCCTTT
4501	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC	ACCOCIACCA	ACCACACACCCC
4561	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT	TTCCGAAGGT	CCACCACTTC	ANCANCTOTO
4621	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG	ACTCCCTCCT	CCCACTCCCC
				TCCTGTTACC		
				GACGATAGTT		
4801	CGGGCTGAAC	GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC	1 ACACCGAAC
4861	TGAGATACCT	CACAGCGTGAG	CATTGAGAAA	GCGCCACGCT	TCCCGAAGGG	AGAAAGGCGG
				CAGGAGAGCG		
				GGTTTCGCCA		
				TATGGAAAAA		
5101	TACGGTTCCT	r GGCCTTTTGC	TGGCCTTTT	CTCACATGTT	CTTTCCTGCG	TTATCCCCTG
				AGTGAGCTGA		
5221	CGACCGAGC	CAGCGAGTCA	GTGAGCGAGG	AAGCGGAAGA	GCGCCTGATG	CGGTATTTTC
,5281	L TCCTTACGC	A TCTGTGCGGI	ATTTCACAC	GCAGACCAGC	CGCGTAACCT	GGCAAAATCG
				G CGTAAGCGGG		
				ACAATAAAGT		
				r gaaaaagcat		
				A ATTGCCCGTC		
				C GTTGTGACAA		
				r GTTAGGTGGC		
				r TTGTATAGAG		
						TGCTTGAGGA
582	1 GATTGATGA	G CGCGGTGGC	A ATGCCCTGC	C TCCGGTGCTC	GCCGGAGACT	GCGAGATCAT
				A ACCTGGGCAG		
						CGGAGCAAGT
						CCGAACTCAC
						AGCCTACATG-

6121 TGCGAA	TGAT GCCCATACTT	GAGCCACCTA	ACTTTGTTTT	AGGGCGACTG	CCCTGCTGCG
6181 TAACAT	CGTT GCTGCTGCGT	AACATCGTTG	CTGCTCCATA	ACATCAAACA	TCGACCCACG
6241 GCGTAA	CGCG CTTGCTGCTT	GGATGCCCGA	GGCATAGACT	GTACAAAAAA	ACAGTCATAA
6301 CAAGCC	ATGA AAACCGCCAC	TGCGCCGTTA	CCACCGCTGC	GTTCGGTCAA	GGTTCTGGAC
6361 CAGTTG	CGTG AGCGCATACG	CTACTTGCAT	TACAGTTTAC	GAACCGAACA	GGCTTATGTC
6421 AACTGG	GTTC GTGCCTTCAT	CCGTTTCCAC	GGTGTGCGTC	ACCCGGCAAC	CTTGGGCAGC
6481 AGCGAA	GTCG AGGCATTTCT	GTCCTGGCTG	GCGAACGAGC	GCAAGGTTTC	GGTCTCCACG
6541 CATCGT	CAGG CATTGGCGGC	CTTGCTGTTC	TTCTACGGCA	AGGTGCTGTG	CACGGATCTG
6601 CCCTGG	CTTC AGGAGATCGG	AAGACCTCGG	CCGTCGCGGC	GCTTGCCGGT	GGTGCTGACC
6661 CCGGAT					

# Figure 40A: pDEST20 Glutathione-S-transferase Fusion with Polyhedron Promoter for Baculovirus Expression



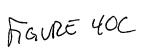
#### pDEST20 7066 bp (rotated to position 5800)

Location (Base Nos.)	Gene Encoded
5921263	GST
13971273	attR1
15062165	CmR
22852369	inactivated ccdA
25072812	ccdB
28532977	attR2
42145064	ampR
52635843	ori

1	CCACTGCGCC	GTTACCACCG	CTGCGTTCGG	TCAAGGTTCT	GGACCAGTTG	CGTGAGCGCA
61	TACGCTACTT	GCATTACAGT	TTACGAACCG	AACAGGCTTA	TGTCAACTGG	GTTCGTGCCT
121	TCATCCGTTT	CCACGGTGTG	CGTCACCCGG	CAACCTTGGG	CAGCAGCGAA	GTCGAGGCAT
181	TTCTGTCCTG	GCTGGCGAAC	GAGCGCAAGG	TTTCGGTCTC	CACGCATCGT	CAGGCATTGG
241	CGGCCTTGCT	GTTCTTCTAC	GGCAAGGTGC	TGTGCACGGA	TCTGCCCTGG	CTTCAGGAGA
301	TCGGAAGACC	TCGGCCGTCG	CGGCGCTTGC	CGGTGGTGCT	GACCCCGGAT	GAAGTGGTTC
361	GCATCCTCGG	TTTTCTGGAA	GGCGAGCATC	GTTTGTTCGC	CCAGGACTCT	AGCTATAGTT
421	CTAGTGGTTG	GCTACGTATA	CTCCGGAATA	TTAATAGATC	ATGGAGATAA	TTAAAATGAT
481	AACCATCTCG	CAAATAAATA	AGTATTTTAC	TGTTTTCGTA	ACAGTTTTGT	AATAAAAAAA
541	CCTATAAATA	TTCCGGATTA	TTCATACCGT	CCCACCATCG	GGCGCGGATC	CATGGCCCCT
601	ATACTAGGTT	ATTGGAAAAT	TAAGGGCCTT	GTGCAACCCA	CTCGACTTCT	TTTGGAATAT
661	CTTGAAGAAA	AATATGAAGA	GCATTTGTAT	GAGCGCGATG	AAGGTGATAA	ATGGCGAAAC
721	AAAAAGTTTG	AATTGGGTTT	GGAGTTTCCC	AATCTTCCTT	ATTATATTGA	TGGTGATGTT
781	AAATTAACAC	AGTCTATGGC	CATCATACGT	TATATAGCTG	ACAAGCACAA	CATGTTGGGT
841	GGTTGTCCAA	AAGAGCGTGC	AGAGATTTCA	ATGCTTGAAG	${\tt GAGCGGTTTT}$	GGATATTAGA
901		CGAGAATTGC				
	AGCAAGCTAC					
1021	AATGGTGATC	ATGTAACCCA	TCCTGACTTC	ATGTTGTATG	ACGCTCTTGA	TGTTGTTTTA
1081	TACATGGACC	CAATGTGCCT	GGATGCGTTC	CCAAAATTAG	TTTGTTTTAA	AAAACGTATT
1141	GAAGCTATCC	CACAAATTGA	TAAGTACTTG	AAATCCAGCA	AGTATATAGC	ATGGCCTTTG
1201	CAGGGCTGGC	AAGCCACGTT	TGGTGGTGGC	GACCATCCTC	CAAAATCGGA	TCTGGTTCCG
	CGTCATAATC					
1321	ATCAATATAT	TAAATTAGAT	TTTGCATAAA	AAACAGACTA	CATAATACTG	TAAAACACAA
	CATATCCAGT					
	GCTCGTATGT					
	CTAAAATGGA					
	AAGAACATTT					
	TGGATATTAC					
	TTATTCACAT					
	ACGGTGAGCT					
	CTGAAACGTT					
	TATATTCGCA					
	TTGAGAATAT					
	ACGTGGCCAA					
2041	AAGGCGACAA	GGTGCTGATG	CCGCTGGCGA	TTCAGGTTCA	TCATGCCGTC	TGTGATGGCT
2101	TCCATGTCGG	CAGAATGCTT	AATGAATTAC	AACAGTACTG	CGATGAGTGG	CAGGGCGGGG
2161	CGTAATCTAG	AGGATCCGGC	TTACTAAAAG	CCAGATAACA	GTATGCGTAT	TTGCGCGCTG
	ATTITTGCGG					
2281	TGCTATGAAG	CAGCGTATTA	CAGTGACAGT	TGACAGCGAC	AGCTATCAGT	TGCTCAAGGC
	ATATATGATG					
2401	CTGCGTGCCG	AACGCTGGAA	AGCGGAAAAT	CAGGAAGGGA	TGGCTGAGGT	CGCCCGGTTT
2461	ATTGAAATGA	ACGGCTCTTT	TGCTGACGAG	AACAGGGACT	GGTGAAATGC	AGTTTAAGGT
	TTACACCTAT					
2581	TGACACGCCC	GGGCGACGGA	TGGTGATCCC	CCTGGCCAGT	GCACGTCTGC	TGTCAGATAA
2641	AGTCTCCCGT	GAACTTTACC	CGGTGGTGCA	TATCGGGGAT	GAAAGCTGGC	GCATGATGAC-

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						, momo, aaa,
2701	CACCGATATG	GCCAGTGTGC	CGGTCTCCGT	TATCGGGGAA	GAAGTGGCTG A	ATCTCAGCCA
2761	CCGCGAAAAT	GACATCAAAA	ACGCCATTAA	CCTGATGTTC '	TGGGGAATAT	AAATGTCAGG
2821	CTCCCTTATA	CACAGCCAGT	CTGCAGGTCG	ACCATAGTGA	CTGGATATGT	TGTGTTTTAC
2881	AGTATTATGT	AGTCTGTTTT	TTATGCAAAA	TCTAATTTAA	TATATTGATA	TTTATATCAT
2941	TTTACGTTTC	TCGTTCAGCT	TTCTTGTACA	AAGTGGTTTG .	ATAGCTTGTC	GAGAAGTACT
3001	AGAGGATCAT	AATCAGCCAT	ACCACATTTG	TAGAGGTTTT	ACTTGCTTTA .	AAAAACCTCC
3061	CACACCTCCC	CCTGAACCTG	AAACATAAAA	TGAATGCAAT	TGTTGTTGTT .	AACTTGTTTA
3121	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	ATAGCATCAC	AAATTTCACA	AATAAAGCAT
3181	TTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	CAATGTATCT	TATCATGTCT
3241	GGATCTGATC	ACTGCTTGAG	CCTAGGAGAT	CCGAACCAGA	TAAGTGAAAT	CTAGTTCCAA
3301	ACTATTTCT	CATTTTTAAT	TTTCGTATTA	GCTTACGACG	CTACACCCAG	TTCCCATCTA
3361	TTTTGTCACT	CTTCCCTAAA	TAATCCTTAA	AAACTCCATT	TCCACCCCTC	CCAGTTCCCA
3421	ACTATTTTGT	CCGCCCACAG	CGGGGCATTT	TTCTTCCTGT	TATGTTTTTA	ATCAAACATC
3481	CTGCCAACTC	CATGTGACAA	ACCGTCATCT	TCGGCTACTT	TTTCTCTGTC	ACAGAATGAA
3541	AATTTTTCTG	TCATCTCTTC	<b>GTTATTAATG</b>	TTTGTAATTG	ACTGAATATC	AACGCTTATT
3601	TGCAGCCTGA	ATGGCGAATG	GACGCCCCT	GTAGCGGCGC	ATTAAGCGCG	GCGGGTGTGG
3661	TGGTTACGCG	CAGCGTGACC	GCTACACTTG	CCAGCGCCCT	AGCGCCCGCT	CCTTTCGCTT
3721	TCTTCCCTTC	CTTTCTCGCC	ACGTTCGCCG	GCTTTCCCCG	TCAAGCTCTA	AATCGGGGGC
3781	TCCCTTTAGG	GTTCCGATTT	AGTGCTTTAC	GGCACCTCGA	CCCCAAAAAA	CTTGATTAGG
3841	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT	GATAGACGGT	TTTTCGCCCT	TTGACGTTGG
3901	AGTCCACGTT	CTTTAATAGT	GGACTCTTGT	TCCAAACTGG	AACAACACTC	AACCCTATCT
3961	CGGTCTATTC	TTTTGATTTA	TAAGGGATTT	TGCCGATTTC	GGCCTATTGG	TTAAAAAATG
4021	AGCTGATTTA	ACAAAAATTT	AACGCGAATT	TTAACAAAAT	ATTAACGTTT	ACAATTTCAG
4081	GTGGCACTTT	TCGGGGAAAT	GTGCGCGGAA	CCCCTATTIG	TTTATTTTTC	TAAATACATT
4141	CAAATATGTA	TCCGCTCATG	AGACAATAAC	CCTGATAAAT	GCTTCAATAA	TATTGAAAAA
4201	GGAAGAGTAT	GAGTATTCAA	CATTTCCGTG	TCGCCCTTAT	TCCCTTTTTT	GCGGCATTTT
4261	GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGT
4201	TEGETGEACG	AGTGGGTTAC	ATCGAACTGG	ATCTCAACAG	CGGTAAGATC	CTTGAGAGTT
4321	TTCGCCCCGA	AGAACGTTTT	CCAATGATGA	GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG
4441	TATTATCCCG	TATTGACGCC	GGGCAAGAGC	AACTCGGTCG	CCGCATACAC	TATTCTCAGA
4501	ATGACTTGGT	TGAGTACTCA	CCAGTCACAG	AAAAGCATCT	TACGGATGGC	ATGACAGTAA
4501	CAGAATTATG	CAGTGCTGCC	ATAACCATGA	GTGATAACAC	TGCGGCCAAC	TTACTTCTGA
4501	CARCATCE	AGGACCGAAG	GAGCTAACCG	CTTTTTTGCA	CAACATGGGG	GATCATGTAA
4621	CTCCCCTTC	TCGTTGGGAA	CCGGAGCTGA	ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA
4741	CONCENTEC	TOTAGCAATG	GCAACAACGT	TGCGCAAACT	ATTAACTGGC	GAACTACTTA
4001	CTCTACCTTC	CCCCCAACAA	TTAATAGACT	GGATGGAGGC	GGATAAAGTT	GCAGGACCAC
4001	TTCTAGCTIC	CCCCCTTCCC	CCTCCCTGGT	TTATTGCTGA	TAAATCTGGA	GCCGGTGAGC
4001		CGCTATCATT	CCAGCACTGC	GGCCAGATGG	TAAGCCCTCC	CGTATCGTAG
4921	TOTOGGICICO	CACGGGGGAGT	CAGGCAACT	TGGATGAACG	AAATAGACAG	ATCGCTGAGA
490.	TATCIACAC	· ACTGATTAAG	CATTGGTAAC	TGTCAGACCA	AGTTTACTCA	TATATACTTT
504	L IAGGIGCCIC	י אמנוממוזאה. רא אריייריאו	ייייייייייייייייייייייייייייייייייייי	AAAGGATCTA	GGTGAAGATC	CTTTTTGATA
510	L AGAIIGAII L ATCTCATGA	י המאמשרה הי הממשמיים הממשמיי מודים מודים הממשמיים	TAACGTGAG	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG
210.	L ALCICAIGA	ACCAMPICCE	TARCOTORS	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA
522.	I AMMAGAICA	A AGGAICTIC	CCCCTCCTT	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT
520.	T CHARAGAC	r AACTGGCTTC	AGCAGAGCG	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC
7 640	COTACTTAC	CCACCACTTC	T AAGAACTCT	TAGCACCGCC	TACATACCTC	GCTCTGCTAA
540	T CGIAGIIAG	AGTGGCTGC	r GCCAGTGGC	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA
546	1 ICCIGIIAC	T ACCCCATAN	CCCABICGC	r cececteaac	GGGGGGTTCG	TGCACACAGC
227	T CONCOMING!	Y CCGPYCGY Y WCCGGYIAM	י ידארארנים. די ידאראררניאאי	TGAGATACCT	ACAGCGTGAG	CATTGAGAAA
558	· CCAGCTIGG	T TO COMMODAL(	THOMOGRAM	2 ACAGGGTATCCI	GGTAAGCGGC	AGGGTCGGAA
564	1 GUGCUAUGU	T TOCOGNAGO	TOTAL CONTRACTOR	CANACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	. СТАТСТТТАТ	AGTCCTGTCG
570	L CAGGAGAGC	B CAUGAGGGA	T CARCOTTON	P GRANCUCCIO	, סובונוונה: ברדרפדר שנפפר	GGGCGGAGCC
576	I GGTTTCGCC.	A CCCCTGACT	a coccoomm	r mycccumccu	, CICCICAGGG	TGGCCTTTTG
582	1 TATGGAAAA	A CGCCAGCAA	C GUGGUUTTT	1 AUGUIICU	, GGCCIIIIGC	ACCGCCTTTG
588	1 CTCACATGT	T CTTTCCTGC	G CCCACCCCT	ALICIGIGGE	TAMCCGIMII	CTCACCCAGG
594	1 AGTGAGCTG	A TACCGCTCG	CGCAGCCGA	A CGACCGAGCC	THUCKHUICE	GTGAGCGAGG
600	1 AAGCGGAAG	A GCGCCTGAT	G CGGTATTTT	C TCCTTACGC	, VC40101001 , VC40101001	ATTTCACACC
606	1 GCAGACCAG	C CGCGTAACC	T GGCAAAATC	G GTTACGGTTC	ACIMAIAAA)	GGATGCCCTG
612	1 CGTAAGCGG	G TGTGGGCGG	A CAATAAAGT	C TTAAACTGA	A CAAAATAGAT	CTAAACTATG



6181	ACAATAAAGT	CTTAAACTAG	ACAGAATAGT	TGTAAACTGA	AATCAGTCCA	GTTATGCTGT
6241	GAAAAAGCAT	ACTGGACTTT	TGTTATGGCT	AAAGCAAACT	CTTCATTTTC	TGAAGTGCAA
6301	ATTGCCCGTC	GTATTAAAGA	GGGGCGTGGC	CAAGGGCATG	GTAAAGACTA	TATTCGCGGC
6361	GTTGTGACAA	TTTACCGAAC	AACTCCGCGG	CCGGGAAGCC	GATCTCGGCT	TGAACGAATT
6421	GTTAGGTGGC	GGTACTTGGG	TCGATATCAA	AGTGCATCAC	TTCTTCCCGT	ATGCCCAACT
6481	TTGTATAGAG	AGCCACTGCG	GGATCGTCAC	CGTAATCTGC	TTGCACGTAG	ATCACATAAG
6541	CACCAAGCGC	GTTGGCCTCA	TGCTTGAGGA	GATTGATGAG	CGCGGTGGCA	ATGCCCTGCC
6601	TCCGGTGCTC	GCCGGAGACT	GCGAGATCAT	AGATATAGAT	CTCACTACGC	GGCTGCTCAA
6661	ACCTGGGCAG	AACGTAAGCC	GCGAGAGCGC	CAACAACCGC	TTCTTGGTCG	AAGGCAGCAA
6721	GCGCGATGAA	TGTCTTACTA	CGGAGCAAGT	TCCCGAGGTA	ATCGGAGTCC	GGCTGATGTT
6781	GGGAGTAGGT	GGCTACGTCT	CCGAACTCAC	GACCGAAAAG	ATCAAGAGCA	GCCCGCATGG
6841	ATTTGACTTG	GTCAGGGCCG	AGCCTACATG	TGCGAATGAT	GCCCATACTT	GAGCCACCTA
6901	ACTITGTTTT	AGGGCGACTG	CCCTGCTGCG	TAACATCGTT	GCTGCTGCGT	AACATCGTTG
6961	CTGCTCCATA	ACATCAAACA	TCGACCCACG	GCGTAACGCG	CTTGCTGCTT	GGATGCCCGA
7021	GGCATAGACT	GTACAAAAAA	ACAGTCATAA	CAAGCCATGA	AAACCG	

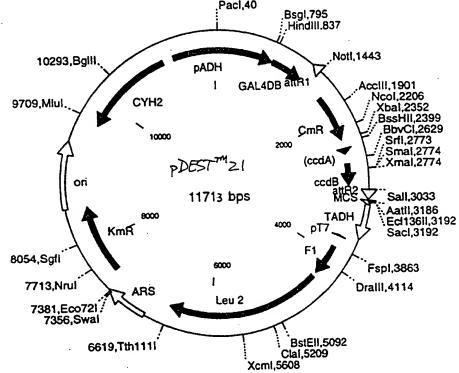
FIGURE 40)

Figure: 4 (A:

### P DEST21

## 2-Hybrid Vector with DNA-Binding Domain

The specific translation of th



### pDEST21 11713 bp (rotated to position 11000)

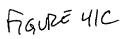
Gene Encoded

Location (Base Nos.)

	-	857132	22	GAL4D	3	
	14561332		attR1			
	17062365		CmR			
		24852	569	inactivated ccdA		
		270730		ccdB		
-		30533		attR2		
		37163	735	pT7 (1	r7 promoter:	
		389943	354	-	l intergeni:	
		44146	542	Leu2		
		75418	515	kanR		
		96681	0958	СҮН2		
		11118		HDAG	(ADH promote	er)
				•		·
1	TTTATTATGT	TACAATATGG	AAGGGAACTT	TACACTTCTC	CTATGCACAT	ATATTAATTA
61	AAGTCCAATG	CTAGTAGAGA	AGGGGGGTAA	CACCCCTCCG	CGCTCTTTTC	CGATTTTTTT
121	CTAAACCGTG	GAATATTTCG	GATATCCTTT	TGTTGTTTCC	GGGTGTACAA	TATGGACTTC
181	CTCTTTTCTG	GCAACCAAAC	CCATACATCG	GGATTCCTAT	AATACCTTCG	TTGGTCTCCC
241	TAACATGTAG	GTGGCGGAGG	GGAGATATAC	AATAGAACAG	ATACCAGACA	AGACATAATG
301	GGCTAAACAA	GACTACACCA	ATTACACTGC	CTCATTGATG	GTGGTACATA	ACGAACTAAT
361	ACTGTAGCCC	TAGACTTGAT	AGCCATCATC	ATATCGAAGT	TTCACTACCC	TTTTTCCATT
					TTCTTTTTTT	
481	TCTCCCCCGT	TGTTGTCTCA	CCATATCCGC	AATGACAAAA	AAAATGATGG	AAGACACTAA
541	AGGAAAAAAT	TAACGACAAA	GACAGCACCA	ACAGATGTCG	TTGTTCCAGA	GCTGATGAGG
601	GGTATCTTCG	AACACACGAA	ACTITITCCT	TCCTTCATTC	ACGCACACTA	CTCTCTAATG
661	AGCAACGGTA	TACGGCCTTC	CTTCCAGTTA	CTTGAATTTG	AAATAAAAA	AGTTTGCCGC
721	TTTGCTATCA	AGTATAAATA	GACCTGCAAT	TATTAATCTT	TTGTTTCCTC	GTCATTGTTC
781	TCGTTCCCTT	TCTTCCTTGT	TTCTTTTTCT	GCACAATATT	TCAAGCTATA	CCAAGCATAC
841	AATCAACTCC	AAGCTTGAAG	CAAGCCTCCT	GAAAGATGAA	GCTACTGTCT	TCTATCGAAC
901	AAGCATGCGA	TATTTGCCGA	CTTAAAAAGC	TCAAGTGCTC	CAAAGAAAAA	CCGAAGTGCG
961	CCAAGTGTCT	GAAGAACAAC	TGGGAGTGTC	GCTACTCTCC	CAAAACCAAA	AGGTCTCCGC
1021	TGACTAGGGC	ACATCTGACA	GAAGTGGAAT	CAAGGCTAGA	AAGACTGGAA	CAGCTATTTC
1081	TACTGATTTT	TCCTCGAGAA	GACCTTGACA	TGATTTTGAA	AATGGATTCT	TTACAGGATA
1141	TAAAAGCATT	GTTAACAGGA	TTATTTGTAC	AAGATAATGT	GAATAAAGAT	GCCGTCACAG
1201	ATAGATTGGC	TTCAGTGGAG	ACTGATATGC	CTCTAACATT	GAGACAGCAT	AGAATAAGTG
1261	CGACATCATC	ATCGGAAGAG	AGTAGTAACA	AAGGTCAAAG	ACAGTTGACT	GTATCGTCGA
1321	GGTCGAATCA	AACAAGTTTG	TACAAAAAAG	CTGAACGAGA	AACGTAAAAT	CATATAAATA
1381	TCAATATATT	AAATTAGATT	TTGCATAAAA	AACAGACTAC	ATAATACTGT	AAAACACAAC
1441	ATATCCAGTC	ACTATGGCGG	CCGCTAAGTT	GGCAGCATCA	CCCGACGCAC	TTTCCCCCCC
1501	ATAAATACCT	GTGACGGAAG	ATCACTTCGC	AGAATAAATA	AATCCTGGTG	TCCCTCTTCA
1561	TACCGGGAAG	CCCTGGGCCA	ACTITITGGCG	AAAATGAGAC	GTTGATCGGC	ACCTANGACC
1621	TTCCAACTTT	CACCATAATG	AAATAAGATC	ACTACCGGGC	GTATTITTG	ACCTANGAGG
1681	ATTTTCAGGA	GCTAAGGAAG	CTAAAATGGA	GAAAAAAATC	ACTGGATATA	CCACCGTTCA
1741	TATATCCCAA	TGGCATCGTA	AAGAACATTT	TGAGGCATTT	CAGTCAGTTG	CTCAATCTAC
1801	CTATAACCAG	ACCGTTCAGC	TGGATATTAC	GGCCTTTTTTA	AAGACCGTAA	ACAAAAAAAA
1861	GCACAAGTTT	TATCCGGCCT	TTATTCACAT	TCTTGCCCGC	CTGATGAATG	CTCATCCCCA
1921:	ATTCCGTATG	GCAATGAAAG	ACGGTGAGCT	GGTGATATGG	GATAGTGTTC	ACCOMPTOTES
1981	CACCGTTTTC	CATGAGCAAA	CTGAAACGTT	TTCATCCCTC	TGGAGTGAAT	ACCOLLOTIA
2041	TTTCCGGCAG	TTTCTACACA	TATATTCCCA	AGATOTOGOO	TGTTACGGTG	ALCACGACGA
2101	CTATTTCCCT	AAAGGGTTTA	TTGAGAATAT	CTATATATATA	TCAGCCAATC	CCTCCCTCAC
2161	TTTCACCACT	עעודענססטנווע	ACGTGGCCAA	TATCOACAAC	TTCTTCGCCC	CCCTTTTTTT
2221	CATGGGCAAA	TATTATACCC	ADGGCGACAA	GGTGCTCATC	CCGCTGGCGA	TTCACCOTTCAC
2281	TCATGCCGTC	TGTGATGGCT	TOCATOTOCO	CACAAMCOMM	AATGAATTAC	1 CAGGTTCA
2341	CGATGAGTGG	CAGGGCGGGC	CCTAATCTAC	ACCAMOCOCC	TTACTAAAAG	AACAGTACTG
2401	GTATGCGTAT	TTGCGCGCTG	ATTTTTCCCC	TATANCANTA	TATACTAAAAG	TOTATACCCC
~101		-10000016		IAIAAGAATA	TATACIGATA	TOTATACCCCG.

FIGURE 413

2461	AAGTATGTCA	AAAAGAGGTG	TGCTATGAAG	CAGCGTATTA	CAGTGACAGT	TGACAGCGAC
2521	AGCTATCAGT	TGCTCAAGGC	ATATATGATG	TCAATATCTC	CGGTCTGGTA	AGCACAACCA
2581	TGCAGAATGA	AGCCCGTCGT	CTGCGTGCCG	AACGCTGGAA	AGCGGAAAAT	CAGGAAGGGA
2641	TGGCTGAGGT	CGCCCGGTTT	ATTGAAATGA	ACGGCTCTTT	TGCTGACGAG	AACAGGGACT
2701	GGTGAAATGC	AGTTTAAGGT	TTACACCTAT	AAAAGAGAGA	GCCGTTATCG	TCTGTTTGTG
2761	GATGTACAGA	GTGATATTAT	TGACACGCCC	GGGCGACGGA	TGGTGATCCC	CCTGGCCAGT
2821	GCACGTCTGC	TGTCAGATAA	AGTCTCCCGT	GAACTTTACC	CGGTGGTGCA	TATCGGGGAT
2881	GAAAGCTGGC	GCATGATGAC	CACCGATATG	GCCAGTGTGC	CGGTCTCCGT	TATCGGGGAA
2941	GAAGTGGCTG	ATCTCAGCCA	CCGCGAAAAT	GACATCAAAA	ACGCCATTAA	CCTGATGTTC
3001	TGGGGAATAT	AAATGTCAGG	CTCCCTTATA	CACAGCCAGT	CTGCAGGTCG	ACCATAGTGA
3061	CTGGATATGT	TGTGTTTTAC	AGTATTATGT	AGTCTGTTTT	TTATGCAAAA	TCTAATTTAA
3121	TATATTGATA	TTTATATCAT	TTTACGTTTC	TCGTTCAGCT	TTCTTGTACA	AAGTGGTTTG
3181	ATGGCCGCTA	AGTAAGTAAG	ACGTCGAGCT	CTAAGTAAGT	AACGGCCGCC	ACCGCGGTGG
	AGCTTTGGAC					
	TACCTTGCCA					
	TGACACTTCT					
3421	ATAAAAAAA	AGTGTATACA	AATTTTAAAG	TGACTCTTAG	GTTTTAAAAC	GAAAATTCTT
	ATTCTTGAGT					
	TCTTATTGAC					
	CACCCAATTG					
	TGTCCTCAGA					
	TAGTGAGTCG					
3721	TGGCGTTACC	CAACTTAATC	GCCTTGCAGC	ACATCCCCCT	TTCGCCAGCT	GGCGTAATAG
	CGAAGAGGCC					
	GCGCCCTGTA					
	ACACTTGCCA					
	TTCGCCGGCT					
4021	GCTTTACGGC	ACCTCCACCC	CANANACTOR	CATTACCCTC	ATGGTTCACG	TAGTGGGCCA
	TCGCCCTGAT					
	CTCTTGTTCC					
4201	GGGATTTTGC	AAACIGGAAC	AALACICAAC	AAAAATCACC	TOTALICITI	אאאאאאאר
4261	GGGATTTTGC	CGATTICGGC	CIAIIGGIIA	AMAMATGAGC	CCCCTATTT	CTCCTTACCC
	GCGAATTTTA					
4381	ATCTGTGCGG	TATTTCACAC	CGCATATCGA	CCGGTCGAGG	AGAACIICIA	DARTCCACA
	ATACCTAATA					
	TCTCTTCAAA					
	TATAGGATAA					
	GGCGCCTGAT					
	AGATGCAAGA					
	CACAGGGGCG					
	AGGTCGCCTG					
	AGGCCGGAAC					
	. CAATACTTGA					
	. CAATCGTCTT					
	. TCAAGGATAT					
	GCCAGGTGAC					
5161	. TTCTGATGTT	CGTTCCAATG	TCAAGTTCGA	TTTCGAAAAT	CATTTAATTG	GTGGTGCTGC
5221	TATCGATGCT	ACAGGTGTCC	CACTTCCAGA	TGAGGCGCTG	GAAGCCTCCA	AGAAGGTTGA
5281	TGCCGTTTTG	TTAGGTGCTG	TGGGTGGTCC	TAAATGGGGT	ACCGGTAGTG	TTAGACCTGA
5341	ACAAGGTTTA	CTAAAAATCC	GTAAAGAACT	TCAATTGTAC	GCCAACTTAA	GACCATGTAA
5401	CTTTGCATCC	GACTCTCTT	TAGACTTATO	TCCAATCAAG	CCACAATTTG	CTAAAGGTAC
5461	TGACTTCGTT	GTTGTCAGAG	AATTAGTGGG	AGGTATTTAC	TTTGGTAAGA	GAAAGGAAGA
	CGATGGTGAT					
						TTTGGTCCTT
564	GGATAAAGCT	AATGTTTTG	CCTCTTCAAC	ATTATGGAGA	AAAACTGTGG	AGGAAACCAT
						CCGCCATGAT
						TGTTTGGTGA
						CATCTGCGTC
						GCCACGGTTC-



	TGCTCCAGAT					
	GATGTTGAAA					
6061	AAAGGTTTTG	GATGCAGGTA	TCAGAACTGG	TGATTTAGGT	GGTTCCAACA	GTACCACCGA
	AGTCGGTGAT					
6181	TTTATGATAT	TTGTACATAA	ACTTTATAAA	TGAAATTCAT	AATAGAAACG	ACACGAAATT
6241	ACAAAATGGA	ATATGTTCAT	AGGGTAGACG	AAACTATATA	CGCAATCTAC	ATACATTTAT
6301	CAAGAAGGAG	AAAAAGGAGG	ATAGTAAAGG	AATACAGGTA	AGCAAATTGA	TACTAATGGC
6361	TCAACGTGAT	AAGGAAAAAG	AATTGCACTT	TAACATTAAT	ATTGACAAGG	AGGAGGGCAC
6421	CACACAAAAA	GTTAGGTGTA	ACAGAAAATC	ATGAAACTAC	GATTCCTAAT	TTGATATTGG
6481	AGGATTTTCT	СТААААААА	AAAAATACAA	CAAATAAAAA	ACACTCAATG	ACCTGACCAT
6541	TTGATGGAGT	TTAAGTCAAT	ACCTTCTTGA	ACCATTTCCC	ATAATGGTGA	AAGTTCCCTC
6601	AAGAATTTTA	CTCTGTCAGA	AACGGCCTTA	CGACGTAGTC	GATATGGTGC	ACTCTCAGTA
6661	CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGCCCCGACA	CCCGCCAACA	CCCGCTGACG
6721	CGCCCTGACG	GGCTTGTCTG	CTCCCGGCAT	CCGCTTACAG	ACAAGCTGTG	ACCGTCTCCG
6781	GGAGCTGCAT	GTGTCAGAGG	TTTTCACCGT	CATCACCGAA	ACGCGCGAGA	CGAAAGGGCC
6841	TCGTGATACG	CCTATTTTTA	TAGGTTAATG	TCATGATAAT	AATGGTTTCT	TAGGACGGAT
6901	CGCTTGCCTG	TAACTTACAC	GCGCCTCGTA	TCTTTTAATG	ATGGAATAAT	TTCCCAATTT
6961	ACTCTGTGTT	TATTTATTTT	TATGTTTTGT	ATTTGGATTT	TAGAAAGTAA	ATAAAGAAGG
7021	TAGAAGAGTT	ACGGAATGAA	GAAAAAAAA	TAAACAAAGG	דעעעעעעעעעעע	TTCAACAAAA
7081	AGCGTACTTT	ACATATATAT	TTATTAGACA	AGAAAAGCAG	משמשמשמשמ	TATACATCA
7141	ATTAACGATA	AGTAAAATGT	AAAATCACAG	GATTTTCCTC	TGTGGTCTTC	TACACACACA
7201	AGATGAAACA	ATTCGGCATT	AATACCTGAG	AGCAGGAAGA	GCAAGATAAA	ACCTACTATT
7261	TGTTGGCGAT	CCCCCTAGAG	ייים בייים בייים מייים	CTTCCCAAAA	CANANACTAT	TTTTTTTTT
7321	ATTTCTTTTT	TTACTTTCTA	יוידע על העלונה. הדיני על על העלונה.	יי בייייי ביי ביי ביי ביי	ΔΤΥΛΛΑΔΙΑΙ	איירא א איירא איירא איירא א
7381	ATTATTTTTA	TAGCACGTGA	TGAAAAGGAC	CCAGGTGGCA	CTTTTTCCCCC	ANATOTOGGO
7441	GGAACCCCTA	TTTGTTTATT	TTTCTAAATA	CATTCAAATA	TGTATCCGCT	CATCACACAA
7501	TAACCCTGAT	AAATGCTTCA	ATAATCTGCA	GCTCTGGCCC	CTCTCTCAAA	ATCTCTCATC
7561	TTACATTGCA	CAAGATAAAA	ATATATCATC	ATGAACAATA	AAACTCTCTC	CTTACATAAA
	CAGTAATACA					
	ATTAAATTCC					
7741	GCAATCAGGT	GCGACAATCT	TTCCATTCTA	TECENACECE	CATCCCCCAC	ATAATGTCGG
7801	GAAACATGGC	AAAGGTAGCG	TTGCCAATGA	TGTTACAGAT	GACATGCTCA	CACTAAACTC
7861	GCTGACGGAA	TTTATGCCTC	TTCCGACCAT	CANCCAUTTE	ATCCCTACTC	CTCATCATC
7921	ATGGTTACTC	ACCACTGCGA	TCCGCGGGAA	AACAGCATTC	CACCTATTAC	AACAATATCC
7981	TGATTCAGGT	GAAAATATTG	TTGATGCGCT	GGCAGTGTTC	CAGGIATIAG	TCCATTCCAT
8041	TCCTGTTTGT	AATTGTCCTT	TTAACACCCA	TCCCCTATOT	CCTCTCCCTC	ACCCCCAADC
8101	ACGAATGAAT	AACGGTTTGG	TTGATGCGAG	TCAUTTTCATT	CACCACCCTA	AGGCGCAATC
8161	TGTTGAACAA	GTCTCCAAAC	AAATGCATAC	COTTOTOCCO	TTTCTCA CCCC	ATGGCTGGCC
8221	CACTCATGGT	GATTTCTCAC	TTCATAACCT	TATTTTTCCA	CACCCCAAAA	MARICAGICGI
8281	TATTGATGTT	GGACGAGTCG	GAATCGCAGA	CCCATACCAC	CATCTTCCCA	TAATAGGTTG
8341	CTGCCTCGGT	GAGTTTTCTC	CTTCATTACA	CANACCCCTT	GAICIIGCCA	ATTCCTATGGAA
8401	TAATCCTGAT	ATCANTANAT	TCCACTTTCA	TTTCATCCTC	CAMCACOTTO	ATGGTATTGA
8461	ATTGGTTAAT	TGGTTGTAAC	ACTCCCACAC	CATTRACCORC	CATGAGTTTT	TUTAATCAGA
8521	ACCAAAATCC	CTTAACCTCA	CTTTTTCCTTC	CATTACGCTG	ACTIGACGGG	ACGGCGCATG
8581	AAAGGATCTT	CTTCACATCC	GITITEGITE	CACTGAGCGT	CAGACCCCGT	AGAAAAGATC
8-641	CCACCGCTAC	CAGCGGTCCT	TTCTTCCC	CGCGTAATCT	GUTGUTTGCA	AACAAAAAA
8701	CTAACTCCCT	TCACCACACC	CCACATACCA	GATCAAGAGC	TACCAACTCT	TTTTCCGAAG
8761	GCCACCACT	TCAGCAGAGC	TCTACCACCC	AATACTGTCC	TTCTAGTGTA	GCCGTAGTTA
0701	GGCCACCACT	CTCCCACTCC	IGIAGCACCG	CCTACATACC	TCGCTCTGCT	AATCCTGTTA
0021	CCAGTGGCTG	ACCCCCAGIGG	CGATAAGTCG	TGTCTTACCG	GGTTGGACTC	AAGACGATAG
0001	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	CGTGCACACA	GCCCAGCTTG
0741	GAGCGAACGA	CCACAAACCGA	ACTGAGATAC	CTACAGCGTG	AGCATTGAGA	AAGCGCCACG
2001	CTTCCCGAAG	COMMISSION	GGACAGGTAT	CCGGTAAGCG	GCAGGGTCGG	AACAGGAGAG
30PT	CGCACGAGGG	AGCTTCCAGG	GGGGAACGCC	TGGTATCTTT	ATAGTCCTGT	CGGGTTTCGC
3151	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	GGGGGCCGAG	CCTATGGAAA
3181	AACGCCAGCA	ACGCGGCCTT	TITACGGTTC	CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG
9241	TTCTTTCCTG	CGTTATCCCC	TGATTCTGTG	GATAACCGTA	TTACCGCCTT	TGAGTGAGCT
9301	GATACCGCTC	GCCGCAGCCG	AACGACCGAG	CGCAGCGAGT	CAGTGAGCGA	GGAAGCGGAA
936 I	GAGUGUCCAA	TAUGUAAACC	GCCTCTCCCC	GCGCGTTGGC	CGATTCATTA	ATGCAGCTGG-
				_		

FIGURE 4LD

					NOOCH APPELA	TOTO SOME
	CACGACAGGT					
	CTCACTCATT					
	ATTGTGAGCG				ACCATGATTA	
	GGAATTAACC				TCCCGAGCTT	
	AGCCTTCGAG					
	CACGCGTCTG				AATAACGTTC	
	CATAACTATA				TGTCTAACTC	
	GGTTAGAGCG		•		GACATAACTA	
	ATCGACAAAG				TTCAAGTAGG	TAATTAAGTC
9961	GTTTCTGTCT	TTTTCCTTCT	TCAACCCACC	AAAGGCCATC	TTGGTACTTT	TTTTTTTTT
10021	TTTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TITTTTTTTT	TITTTTTTT	TTTTTTTTT
10081	TTTTTTTTTT	TTTTTTTTT	TCATAGAAAT	AATACAGAAG	TAGATGTTGA	ATTAGATTAA
10141	ACTGAAGATA	TATAATITAT	TGGAAAATAC	ATAGAGCTTT	TTGTTGATGC	GCTTAAGCGA
10201	TCAATTCAAC	AACACCACCA	GCAGCTCTGA	TTTTTTCTTC	AGCCAACTTG	GAGACGAATC
10261	TAGCTTTGAC	GATAACTGGA	ACATTTGGAA	TTCTACCCTT	ACCCAAGATC	TTACCGTAAC
10321	CGGCTGCCAA	AGTGTCAATA	ACTGGAGCAG	TTTCCTTAGA	AGCAGATTTC	AAGTATTGGT
10381	CTCTCTTGTC	TTCTGGGATC	AATGTCCACA	ATTTGTCCAA	GTTCAAGACT	GGCTTCCAGA
					ACCGAAATAA	
10501	ATTTATCCAT	GTTAATTCTG	TGGTGATGTT	GACCACCGGC	CATACCTCTA	CCACCGGGGT
10561	GCTTTCTGTG	CTTACCGATA	CGACCTTTAC	CGGCTGAGAC	GTGACCTCTG	TGCTTTCTAG
10621	TCTTAGTGAA	TCTGGAAGGC	ATTCTTGATT	AGTTGGATGA	TTGTTCTGGG	ATTTAATGCA
10681	AAAATCACTT	AAGAAGGAAA	ATCAACGGAG	AAAGCAAACG	CCATCTTAAA	TATACGGGAT
10741	ACAGATGAAA	GGGTTTGAAC	CTATCTGGAA	AATAGCATTA	AACAAGCGAA	AAACTGCGAG
10801	GAAAATTGTT	TGCGTCTCTG	CGGGCTATTC	ACGCGCCAGA	GGAAAATAGG	AAAAATAACA
10861	GGGCATTAGA	AAAATAATTT	TGATTTTGGT	AATGTGTGGG	TCCTGGTGTA	CAGATGTTAC
10921	ATTGGTTACA	GTACTCTTGT	TTTTGCTGTG	TTTTTCGATG	AATCTCCAAA	ATGGTTGTTA
10981	GCACATGGAA	GAGTCACCGA	TGCTAAGTTA	TCTCTATGTA	AGCTACGTGG	CGTGACTTTT
11041	GATGAAGCCG	CACAAGAGAT	ACAGGATTGG	CAACTGCAAA	TAGAATCTGG	GGATCCCCCC
11101	TCGAGATCCG	GGATCGAAGA	AATGATGGTA	AATGAAATAG	GAAATCAAGG	AGCATGAAGG
11161	CAAAAGACAA	ATATAAGGGT	CGAACGAAAA	ATAAAGTGAA	AAGTGTTGAT	ATGATGTATT
11221	TGGCTTTGCG	GCGCCGAAAA	AACGAGTTTA	CGCAATTGCA	CAATCATGCT	GACTCTGTGG
11281	CGGACCCGCG	CTCTTGCCGG	CCCGGCGATA	ACGCTGGGCG	TGAGGCTGTG	CCCGGCGGAG
11341	TTTTTTGCGC	CTGCATTTTC	CAAGGTTTAC	CCTGCGCTAA	GGGGCGAGAT	TGGAGAAGCA
11401	ATAAGAATGC	CGGTTGGGGT	TGCGATGATG	ACGACCACGA	CAACTGGTGT	CATTATTTAA
11461	GTTGCCGAAA	GAACCTGAGT	GCATTTGCAA	CATGAGTATA	CTAGAAGAAT	GAGCCAAGAC
11521	TTGCGAGACG	CGAGTTTGCC	GGTGGTGCGA	ACAATAGAGC	GACCATGACC	TTGAAGGTGA
11581	GACGCGCATA	ACCGCTAGAG	TACTTTGAAG	AGGAAACAGC	AATAGGGTTG	CTACCAGTAT
11641	AAATAGACAG	GTACATACAA	CACTGGAAAT	GGTTGTCTGT	TTGAGTACGC	TTTCAATTCA
11701	TTTGGGTGTG	CAC				

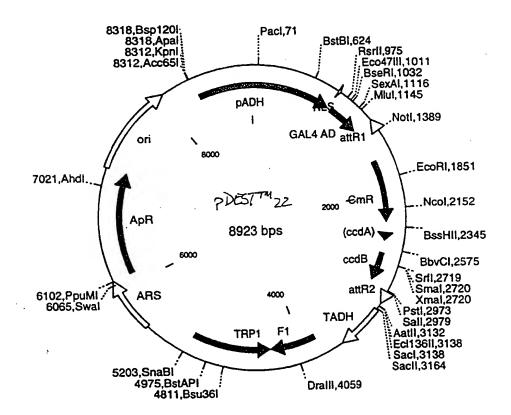
FIGURE 415

### Figure 42A:

. . . . .

PDGT22

## 2-Hybrid Vector with Activation Domain



#### pDEST22 8923 bp

	Loc	ation (Base	Nos.)	Gene I	ncoded			
		ation (Base 904124 138812	18	GAL4	AD.			
		138812	264	attR1	attR1			
		163822	297	CmR				
		241725		inact	ivated ccdA			
		263929	944	ccdB				
29853109			attR2					
		383143		f1 (f:	lintergenio	region)		
		433451	L76	TRP1				
		611071	L94	ampR				
		834486	56	PADH	(yeast ADH p	promoter)		
	TTCATTTGGG							
61	TGCACATATA	TTAATTAAAG	TCCAATGCTA	GTAGAGAAGG	GGGGTAACAC	CCCTCCGCGC		
	TCTTTTCCGA							
181	TGTACAATAT	GGACTTCCTC	TTTTCTGGCA	ACCAAACCCA	TACATCGGGA	TTCCTATAAT		
241	ACCTTCGTTG	${\tt GTCTCCCTAA}$	CATGTAGGTG	GCGGAGGGGA	GATATACAAT	AGAACAGATA		
	CCAGACAAGA							
	GTACATAACG							
	ACTACCCTTT							
	${\tt TTTTTTTTC}$							
541	ATGATGGAAG	ACACTAAAGG	AAAAAATTAA	CGACAAAGAC	AGCACCAACA	GATGTCGTTG		
601	${\tt TTCCAGAGCT}$	GATGAGGGGT	ATCTTCGAAC	ACACGAAACT	TTTTCCTTCC	TTCATTCACG		
661	CACACTACTC	TCTAATGAGC	AACGGTATAC	GGCCTTCCTT	CCAGTTACTT	GAATTTGAAA		
721	TAAAAAAAGT	TTGCCGCTTT	GCTATCAAGT	ATAAATAGAC	CTGCAATTAT	TAATCTTTTG		
781	TTTCCTCGTC	ATTGTTCTCG	TTCCCTTTCT	TCCTTGTTTC	TTTTTCTGCA	CAATATTTCA		
841	AGCTATACCA	AGCATACAAT	CAACTCCAAG	CTTATGCCCA	AGAAGAAGCG	GAAGGTCTCG		
901	AGCGGCGCCA	ATTTTAATCA	AAGTGGGAAT	ATTGCTGATA	GCTCATTGTC	CTTCACTTTC		
	ACTAACAGTA							
1021	CAACCAATTG	CCTCCTCTAA	CGTTCATGAT	AACTTCATGA	ATAATGAAAT	CACGGCTAGT		
1081	AAAATTGATG	ATGGTAATAA	TTCAAAACCA	CTGTCACCTG	GTTGGACGGA	CCAAACTGCG		
1141	TATAACGCGT	TTGGAATCAC	TACAGGGATG	TTTAATACCA	CTACAATGGA	TGATGTATAT		
1201	AACTATCTAT	TCGATGATGA	AGATACCCCA	CCAAACCCAA	AAAAAGAGGG	TGGGTCGAAT		
1261	CAAACAAGTT	TGTACAAAAA	AGCTGAACGA	GAAACGTAAA	ATGATATAAA	TATCAATATA		
1321	TTAAATTAGA	TTTTGCATAA	AAAACAGACT	ACATAATACT	GTAAAACACA	ACATATCCAG		
1381	TCACTATGGC	GGCCGCTAAG	TIGGCAGCAT	CACCCGACGC	ACTTTGCGCC	GAATAAATAC		
1441	CTGTGACGGA	AGATCACTTC	GCAGAATAAA	TAAATCCTGG	TGTCCCTGTT	GATACCGGGA		
1501	AGCCCTGGGC	CAACTTTTGG	CGAAAATGAG	ACGTTGATCG	GCACGTAAGA	GGTTCCAACT		
1201	TTCACCATAA	TGAAATAAGA	TCACTACCGG	GCGTATTTTT	TGAGTTATCG	AGATTTTCAG		
1621	GAGCTAAGGA	AGCTAAAATG	GAGAAAAAA	TCACTGGATA	TACCACCGTT	GATATATCCC		
1001	AATGGCATCG	TAAAGAACAT	TTTGAGGCAT	TTCAGTCAGT	TGCTCAATGT	ACCTATAACC		
1001	AGACCGTTCA	CTTTTATT	ACGGCCTTTT	TAAAGACCGT	AAAGAAAAAT	AAGCACAAGT		
1061	TTTATCCGGC	ACACCCTCAC	ATTCTTGCCC	GCCTGATGAA	TGCTCATCCG	GAATTCCGTA		
1001	TGGCAATGAA	ACTCARACC	CIGGIGATAT	GGGATAGTGT	TCACCCTTGT	TACACCGTTT		
1001	TCCATGAGCA	CATATATTCC	CARCATOGO	TCTGGAGTGA	ATACCACGAC	GATTTCCGGC		
1301 2041)	AGTTTCTACA	CAIAIAIICG	AMCOMMON	CGTGTTACGG	TGAAAACCTG	GCCTATTTCC		
2111	CTAAAGGGTT	AAACCTCCCC	AIGITITICG	ACTICAGCCAA	TCCCTGGGTG	AGTTTCACCA		
2161	GTTTTGATTT	CCANCOCCA C	ANCOTOOTCE	ACT TUTTUGC	CCCCGTTTTC	ACCATGGGCA		
2221	AATATTATAC TCTGTGATGG	CTTCCATCTC	CCCACAATCC	TURNATIONATION	GATTCAGGTT	CATCATGCCG		
2281	TCTGTGATGG GGCAGGGCGG	CITCCAIGIC	ACACCAMOCC	1 IAAIGAATT	ACAACAGTAC	TGCGATGAGT		
2341	ATTTGCCCCC	TCATTTTTC	CCTATAACA	GCTTACTAAA	AGCCAGATAA	CAGTATGCGT		
2401	ATTTGCGCGC CAAAAAGAGG	TGTGCTATCA	ACCACCCEA	TATATACTGA	COMPONENCE	CGAAGTATGT		
2461	GTTGCTCAAG	CCATATATCA	TCTCANTATC	TCCCCTCTCC	GTTGACAGCG	ACAGCTATCA		
2521	GAAGCCCGTC	GTCTGCGTGC	CGAACGCTCC	ANACCCCANA	ATCACCACAAC	CATGCAGAAT		
		0101000100	CONNCOC 10G	AAAGCGGAAA	MICAGGAAGG	GATGGCTGAG-		

Faure 428

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2581 GTCGCCCGGT TTATTGAAAT GAACGGCTCT TTTGCTGACG AGAACAGGGA CTGGTGAAAT
2641 GCAGTTTAAG GTTTACACCT ATAAAAGAGA GAGCCGTTAT CGTCTGTTTG TGGATGTACA
2701 GAGTGATATT ATTGACACGC CCGGGCGACG GATGGTGATC CCCCTGGCCA GTGCACGTCT
2761 GCTGTCAGAT AAAGTCTCCC GTGAACTTTA CCCGGTGGTG CATATCGGGG ATGAAAGCTG
2821 GCGCATGATG ACCACCGATA TGGCCAGTGT GCCGGTCTCC GTTATCGGGG AAGAAGTGGC
2881 TGATCTCAGC CACCGCGAAA ATGACATCAA AAACGCCATT AACCTGATGT TCTGGGGAAT
2941 ATAAATGTCA GGCTCCCTTA TACACAGCCA GTCTGCAGGT CGACCATAGT GACTGGATAT
3001 GTTGTGTTTT ACAGTATTAT GTAGTCTGTT TTTTATGCAA AATCTAATTT AATATATTGA
3061 TATTTATATC ATTTTACGTT TCTCGTTCAG CTTTCTTGTA CAAAGTGGTT TGATGGCCGC
3121 TAAGTAAGTA AGACGTCGAG CTCTAAGTAA GTAACGGCCG CCACCGCGGT GGAGCTTTGG
3181 ACTTCTTCGC CAGAGGTTTG GTCAAGTCTC CAATCAAGGT TGTCGGCTTG TCTACCTTGC
3241 CAGAAATTTA CGAAAAGATG GAAAAGGGTC AAATCGTTGG TAGATACGTT GTTGACACTT
3361 TAAGTGTATA CAAATTTTAA AGTGACTCTT AGGTTTTAAA ACGAAAATTC TTATTCTTGA
3421 GTAACTCTTT CCTGTAGGTC AGGTTGCTTT CTCAGGTATA GCATGAGGTC GCTCTTATTG
3481 ACCACACCTC TACCGGCATG CCGAGCAAAT GCCTGCAAAT CGCTCCCCAT TTCACCCAAT
3541 TGTAGATATG CTAACTCCAG CAATGAGTTG ATGAATCTCG GTGTGTATTT TATGTCCTCA
3601 GAGGACAATA CCTGTTGTAA TCGTTCTTCC ACACGGATCC CAATTCGCCC TATAGTGAGT
3661 CGTATTACAA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC CCTGGCGTTA
3721 CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG
3781 CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG ACGCGCCCTG
3841 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG CTACACTTGC
3961 CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT CCCTTTAGGG TTCCGATTTA GTGCTTTACG
4021 GCACCTCGAC CCCAAAAAAC TTGATTAGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG
4081 ATAGACGGTT TTTCGCCCTT TGACGTTGGA GTCCACGTTC TTTAATAGTG GACTCTTGTT
4141 CCAAACTGGA ACAACACTCA ACCCTATCTC GGTCTATTCT TTTGATTTAT AAGGGATTTT
4201 GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA CAAAAATTTA ACGCGAATTT
4261 TAACAAAATA TTAACGTTTA CAATTTCCTG ATGCGGTATT TTCTCCTTAC GCATCTGTGC
4321 GGTATTTCAC ACCGCAGGCA AGTGCACAAA CAATACTTAA ATAAATACTA CTCAGTAATA
4381 ACCTATTTCT TAGCATTTTT GACGAAATTT GCTATTTTGT TAGAGTCTTT TACACCATTT
4441 GTCTCCACAC CTCCGCTTAC ATCAACACCA ATAACGCCAT TTAATCTAAG CGCATCACCA
4501 ACATTTCTG GCGTCAGTCC ACCAGCTAAC ATAAAATGTA AGCTTTCGGG GCTCTCTTGC
4561 CTTCCAACCC AGTCAGAAAT CGAGTTCCAA TCCAAAAGTT CACCTGTCCC ACCTGCTTCT
4621 GAATCAAACA AGGGAATAAA CGAATGAGGT TTCTGTGAAG CTGCACTGAG TAGTATGTTG
4681 CAGTCTTTTG GAAATACGAG TCTTTTAATA ACTGGCAAAC CGAGGAACTC TTGGTATTCT
4741 TGCCACGACT CATCTCCATG CAGTTGGACG ATATCAATGC CGTAATCATT GACCAGAGCC
4801 AAAACATCCT CCTTAGGTTG ATTACGAAAC ACGCCAACCA AGTATTTCGG AGTGCCTGAA
4861 CTATTTTTAT ATGCTTTTAC AAGACTTGAA ATTTTCCTTG CAATAACCGG GTCAATTGTT
4921 CTCTTTCTAT TGGGCACACA TATAATACCC AGCAAGTCAG CATCGGAATC TAGAGCACAT
4981 TCTGCGGCCT CTGTGCTCTG CAAGCCGCAA ACTTTCACCA ATGGACCAGA ACTACCTGTG
5041 AAATTAATAA CAGACATACT CCAAGCTGCC TTTGTGTGCT TAATCACGTA TACTCACGTG
5101 CTCAATAGTC ACCAATGCCC TCCCTCTTGG CCCTCTCCTT TTCTTTTTC GACCGAATTA
5161 ATTCTTAATC GGCAAAAAAA GAAAAGCTCC GGATCAAGAT TGTACGTAAG GTGACAAGCT
5221 ATTTTTCAAT AAAGAATATC TTCCACTACT GCCATCTGGC GTCATAACTG CAAAGTACAC
5281 ATATATTACG ATGCTGTCTA TTAAATGCTT CCTATATTAT ATATATAGTA ATGTCGTTTA
5341 TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC CCGACACCCG
5401 CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA
5461 GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC
5521 GCGAGACGAA AGGGCCTCGT GATACGCCTA TTTTTATAGG TTAATGTCAT GATAATAATG
5581 GTTTCTTAGG ACGGATCGCT TGCCTGTAAC TTACACGCGC CTCGTATCTT TTAATGATGG
5641 AATAATTTGG GAATTTACTC TGTGTTTATT TATTTTTATG TTTTGTATTT GGATTTTAGA
5701 AAGTAAATAA AGAAGGTAGA AGAGTTACGG AATGAAGAAA AAAAAATAAA CAAAGGTTTA
5761 AAAAATTTCA ACAAAAAGCG TACTTTACAT ATATATTTAT TAGACAAGAA AAGCAGATTA
5821 AATAGATATA CATTCGATTA ACGATAAGTA AAATGTAAAA TCACAGGATT TTCGTGTGTG
5881 GTCTTCTACA CAGACAAGAT GAAACAATTC GGCATTAATA CCTGAGAGCA GGAAGAGCAA
5941 GATAAAAGGT AGTATTTGTT GGCGATCCCC CTAGAGTCTT TTACATCTTC GGAAAACAAA
 6001 AACTATITTT TCTTTAATTT CTTTTTTTAC TTTCTATTTT TAATTTATAT ATTTATATA-
```

FIGURE 42C

						0m0001 0mmm
6061	AAAAATTTAA	ATTATAATTA	TTTTTATAGC	ACGTGATGAA	AAGGACCCAG	GTGGCACTTT
C101	magagaa a a m	CTCCCCCCAA	CCCCTATTTG	TTTATTTTTC	TAAATACATT	CAAATATGTA
C 1 D 1	MOCCOMONTO	አርአርአልጥልልር	CCTGATAAAT	GCTTCAATAA	TATTGAAAAA	GGAAGAGTAT
C 2 4 1	CACTATTCAA	CATTTCCGTG	TCCCCCTTAT	TCCCTTTTTT	GCGGCATTT	GCCLICCIGI
C202	<b>ምምምም</b> ርርጥርእር	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGI	1 GGG 1 GCACG
6261	ACTCCCTTAC	ATCGAACTGG	ATCTCAACAG	CGGTAAGATC	CLICAGAGII	TTCGCCCCGA
6421	ACAACCTTTT	CCAATGATGA	GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG	TATTATCCCG
C401	TATTCACCCC	CCCCAAGAGC	AACTCGGTCG	CCGCATACAC	TATTCTCAGA	ATGACTTGGT
CE 41	TCACTACTCA	CCAGTCACAG	AAAAGCATCT	TACGGATGGC	ATGACAGTAA	GAGAATTATG
6601	CAGTGCTGCC	ATAACCATGA	GTGATAACAC	TGCGGCCAAC	TTACTTCTGA	CAACGATCGG
6661	ACCACCGAAG	GAGCTAACCG	CTTTTTTTCA	CAACATGGGG	GATCATGTAA	CTCGCCTTGA
6721	TOCTTOCCA	CCGGAGCTGA	ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA	CCACGATGCC
6701	TOTAGONATO	GCAACAACGT	TGCGCAAACT	ATTAACTGGC	GAACTACTTA	CTCTAGCTTC
6041	CCCCCAACAA	TTAATAGACT	GGATGGAGGC	GGATAAAGTT	GCAGGACCAC	TTCTGCGCTC
6901	CCCCCTTCCC	GCTGGCTGGT	TTATTGCTGA	TAAATCTGGA	GCCGGTGAGC	GTGGGTCTCG
6061	CCCTATCATT	GCAGCACTGG	GGCCAGATGG	TAAGCCCTCC	CGTATCGTAG	TTATCTACAC
7021	CACCCCCACT	CAGGCAACTA	TGGATGAACG	AAATAGACAG	ATCGCTGAGA	TAGGTGCCTC
7021	ACTCATTA AC	CATTGGTAAC	TGTCAGACCA	AGTTTACTCA	TATATACTTT	AGATTGATTT
7141	ACIGATIANO	TTTTAATTTA	AAAGGATCTA	GGTGAAGATC	CTTTTTGATA	ATCTCATGAC
7141	CNANATCCCT	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG	AAAAGATCAA
7201	ACCAMCTUCT	TGAGATCCTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC
7201	ACCCCTACCA	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT	TTCCGAAGGT
7321	ACCGCIACCA	AGCAGAGCGC	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG
7381	AACIGGCIIC	: AAGAACTCTG	TAGCACCGCC	TACATACCTC	GCTCTGCTAA	TCCTGTTACC
7441	. CCACCACIIC	GCCAGTGGCG	ATABGTCGTG	TCTTACCGGG	TTGGACTCAA	GACGATAGTT
7501	AGIGGCIGCI	GCGCAGCGGT	CCCCCTGAAC	GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA
7561	ACCGGATAAC	TACACCGAAC	TCACATACCT	ACAGCGTGAG	CATTGAGAAA	GCGCCACGCT
7621	. GCGAACGACC	AGAAAGGCGG	ACAGGTATCC	GGTAAGCGGC	AGGGTCGGAA	CAGGAGAGCG
7683	COCCGAAGGC	CTTCCAGGGG	CGAACGCCTG	CTATCTTAT	AGTCCTGTCG	GGTTTCGCCA
7741	CACGAGGGA	CITCCAGGGG	TOTALCOCCIO	CTCGTCAGGG	GGGCCGAGCC	TATGGAAAAA
7801	CCTCTGACT.	GCGGCCTTTT	י שאכרכישררכים	CCCCTTTTCC	TGGCCTTTTG	CTCACATGTT
786	CGCCAGCAAG	CCGGCCIII	NTTCTCTCC	TAACCGTATT	ACCGCCTTTG	AGTGAGCTGA
792:	CTTTCCTGC	TIMICCCCIO	CCACCCACCC	CACCCAGTCA	GTGAGCGAGG	AAGCGGAAGA
798:	TACCGCTCG	CGCAGCCGAF	COACCOAGCG	CAGCGAGICA	TAATTAATTA	GCAGCTGGCA
804	1 GCGCCCAAT	A CGCAAACCGC	A ACCCCCCCAC	TGAGCGCAAC	GCAATTAATO	TGAGTTACCT
810	1 CGACAGGTT	r cccgaciaga	AAGCGGGCAC	TORGCOCARC	GCTCCTATGT	TGTGTGGAAT
816	1 CACTCATTA	G GCACCCCAG	T ACACACIA	CACCTATGA	CATGATTAC	CCAAGCTCGG
822	1 TGTGAGCGG.	A TAACAAIII	, ALACAGGAA	r cagciaiga	CCCCCCCTCC	GAGATCCGGGA
828	1 AATTAACCC	T CACTAAAGG	AACAAAAGC.	A ATTENACE ACT	TATCANGGCA	AAGACAAATA
834	1 TCGAAGAAA	T GATGGTAAA	L GAAATAGGAA	TOTTO AT ATT	ATGAAGGCA ATGTATTTG	CTTTGCGGCG
840	1 TAAGGGTCG	A ACGAAAAAT	A AAGIGAAAA	J IGIIGAIAIN	TOTALIO	ACCCGCGCTC
846	1 CCGAAAAAA	C GAGTTTACG	- AAIIGCACA	A ICAIGCIGA	_	TTTGCGCCTG
852	1 TTGCCGGCC	C GGCGATAAC	1 CIGGGCGIG	a cccycynaca	Z AGAAGCAATI	A AGAATGCCGG
858	1 CATTTTCCA	A GGTTTACCC	T GCGCTAAGG	A CACCHONIEC	יייטעעה אונעריייייייייייייייייייייייייייייייייייי	r GCCGAAAGAA
864	1 TTGGGGTTG	C GATGATGAC	ACCACGACA	A CINCINICA	CONNENCTO	G CGAGACGCGA
,870	1 CCTGAGTGC	A TITIGCAACA	I GAGTATACT	A CAMCAGICA	G VYCCAGVCII	CCCCATAACC
876	1 GTTTGCCGG	T GGTGCGAAC	A ATAGAGCGA	T ACCOMPCON	A CCACTATANA:	C GCGCATAACC
882	1 GCTAGAGTA	C TTTGAAGAG	G AAACAGCAA	AGGGIIGCI.	E CYY	A TAGACAGGTA
888	1 CATACAACA	C TGGAAATGG	T TGTCTGTTT	G MGIACGCII	1 CMM	

Mare 420

### PDEST23

### His6 carboxy-fusion vector, T7 promoter,

atc ccg cga aat taa tac gac tca cta tag gga gac cac aac ggt ttc cct tag ggc gct tta att atg ctg agt gat atc cct ctg gtg ttg cca aag gga

256 cta gat cac aag ttt gta caa aaa agc tga acg aga aac gta aaa tga tat gat cta dtg ttc aaa cat gtt ttc ccd ttg cat ttt act ata gt gat cta dtg ttc aaa cat gtt ttc ccd b

1888 ttt tta tgc aaa atc taa ttt aat ata ttg ata ttt ata tca ttt tac gtt aaa aat acg ttt tag att aaa tta tat aac tat aaa tat agt aaa atg caa aag acg aga gca agt cga aag aac atg ttt cac cac taa tac agc atg atg gtg

1939 tct cgt tca gct ttc ttg tac aaa gtg gtg att atg tcg tac tac cac cac aag aga gca agt cga aag aac atg ttt cac cac taa tac agc atg atg gtg

1990 cat cac cat cac ccc gat gag caa tag cta gca tat ggg gaa ccc cgg aga

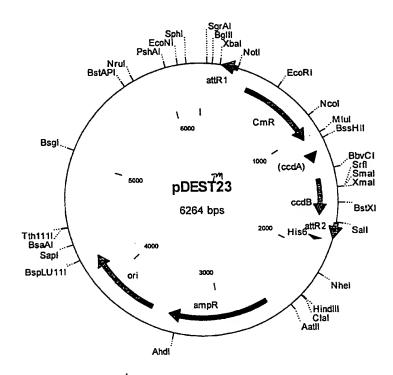


FIGURE 43A

#### pDEST23 6264 bp

Location (Base Nos.)	Gene Encoded
285161	attR1
3941053	CmR
11731257	inactivated ccdA
13951700	ccdB
17411865	attR2
18831911	his6
25743434	ampR
35834222	ori

1 TCTTCCCCAT CGGTGATGTC GGCGATATAG GCGCCAGCAA CCGCACCTGT GGCGCCGGTG 61 ATGCCGGCCA CGATGCGTCC GGCGTAGAGG ATCGAGATCT CGATCCCGCG AAATTAATAC 121 GACTCACTAT AGGGAGACCA CAACGGTTTC CCTCTAGATC ACAAGTTTGT ACAAAAAAGC 181 TGAACGAGAA ACGTAAAATG ATATAAATAT CAATATATTA AATTAGATTT TGCATAAAAA 241 ACAGACTACA TAATACTGTA AAACACAACA TATCCAGTCA CTATGGCGGC CGCATTAGGC 301 ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATAATG TGTGGATTTT GAGTTAGGAT 361 CCGGCGAGAT TTTCAGGAGC TAAGGAAGCT AAAATGGAGA AAAAAATCAC TGGATATACC 421 ACCGTTGATA TATCCCAATG GCATCGTAAA GAACATTTTG AGGCATTTCA GTCAGTTGCT 481 CAATGTACCT ATAACCAGAC CGTTCAGCTG GATATTACGG CCTTTTTAAA GACCGTAAAG 541 AAAAATAAGC ACAAGTTTTA TCCGGCCTTT ATTCACATTC TTGCCCGCCT GATGAATGCT 601 CATCCGGAAT TCCGTATGGC AATGAAAGAC GGTGAGCTGG TGATATGGGA TAGTGTTCAC 661 CCTTGTTACA CCGTTTTCCA TGAGCAAACT GAAACGTTTT CATCGCTCTG GAGTGAATAC 721 CACGACGATT TCCGGCAGTT TCTACACATA TATTCGCAAG ATGTGGCGTG TTACGGTGAA 781 AACCTGGCCT ATTTCCCTAA AGGGTTTATT GAGAATATGT TTTTCGTCTC AGCCAATCCC 841 TGGGTGAGTT TCACCAGTTT TGATTTAAAC GTGGCCAATA TGGACAACTT CTTCGCCCCC 901 GTTTTCACCA TGGGCAAATA TTATACGCAA GGCGACAAGG TGCTGATGCC GCTGGCGATT 961 CAGGTTCATC ATGCCGTCTG TGATGGCTTC CATGTCGGCA GAATGCTTAA TGAATTACAA 1021 CAGTACTGCG ATGAGTGGCA GGGCGGGGCG TAAACGCGTG GATCCGGCTT ACTAAAAGCC 1081 AGATAACAGT ATGCGTATTT GCGCGCTGAT TTTTGCGGTA TAAGAATATA TACTGATATG 1141 TATACCCGAA GTATGTCAAA AAGAGGTGTG CTATGAAGCA GCGTATTACA GTGACAGTTG 1201 ACAGCGACAG CTATCAGTTG CTCAAGGCAT ATATGATGTC AATATCTCCG GTCTGGTAAG 1261 CACAACCATG CAGAATGAAG CCCGTCGTCT GCGTGCCGAA CGCTGGAAAG CGGAAAATCA 1321 GGAAGGATG GCTGAGGTCG CCCGGTTTAT TGAAATGAAC GGCTCTTTTG CTGACGAGAA 1381 CAGGGACTGG TGAAATGCAG TTTAAGGTTT ACACCTATAA AAGAGAGAGC CGTTATCGTC 1441 TGTTTGTGGA TGTACAGAGT GATATTATTG ACACGCCCGG GCGACGGATG GTGATCCCCC 1501 TGGCCAGTGC ACGTCTGCTG TCAGATAAAG TCTCCCGTGA ACTTTACCCG GTGGTGCATA 1561 TCGGGGATGA AAGCTGGCGC ATGATGACCA CCGATATGGC CAGTGTGCCG GTCTCCGTTA 1621 TCGGGGAAGA AGTGGCTGAT CTCAGCCACC GCGAAAATGA CATCAAAAAC GCCATTAACC 1681 TGATGTTCTG GGGAATATAA ATGTCAGGCT CCCTTATACA CAGCCAGTCT GCAGGTCGAC 1741 CATAGTGACT GGATATGTTG TGTTTTACAG TATTATGTAG TCTGTTTTTT ATGCAAAATC 1801 TAATTTAATA TATTGATATT TATATCATTT TACGTTTCTC GTTCAGCTTT CTTGTACAAA 1861 GTGGTGATTA TGTCGTACTA CCATCACCAT CACCATCACC TCGATGAGCA ATAACTAGCA 1921 TAACCCCTTG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA 1981 TCCGGATATC CACAGGACGG GTGTGGTCGC CATGATCGCG TAGTCGATAG TGGCTCCAAG 2041 TAGCGAAGCG AGCAGGACTG GGCGGCGGCC AAAGCGGTCG GACAGTGCTC CGAGAACGGG 2101 TGCGCATAGA AATTGCATCA ACGCATATAG CGCTAGCAGC ACGCCATAGT GACTGGCGAT 2161 GCTGTCGGAA TGGACGATAT CCCGCAAGAG GCCCGGCAGT ACCGGCATAA CCAAGCCTAT 2221 GCCTACAGCA TCCAGGGTGA CGGTGCCGAG GATGACGATG AGCGCATTGT TAGATTTCAT 2281 ACACGGTGCC TGACTGCGTT AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTTATC 2341 GATGATAAGC TGTCAAACAT GAGAATTCTT GAAGACGAAA GGGCCTCGTG ATACGCCTAT 2401 TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC GTCAGGTGGC ACTTTTCGGG 2461 GAAATGTGCG CGGAACCCCT ATTTGTTTAT TTTTCTAAAT ACATTCAAAT ATGTATCCGC 2521 TCATGAGACA ATAACCCTGA TAAATGCTTC AATAATATTG AAAAAGGAAG AGTATGAGTA 2581 TTCAACATTT CCGTGTCGCC CTTATTCCCT TTTTTGCGGC ATTTTGCCTT CCTGTTTTTG 2641 CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT GCACGAGTGG

	GTTACATCGA					
	GTTTTCCAAT					
	ACGCCGGGCA					
	ACTCACCAGT					
2941	CTGCCATAAC	CATGAGTGAT	AACACTGCGG	CCAACTTACT	TCTGACAACG	ATCGGAGGAC
	CGAAGGAGCT					
3061	GGGAACCGGA	GCTGAATGAA	GCCATACCAA	ACGACGAGCG	TGACACCACG	ATGCCTGCAG
3121	CAATGGCAAC	AACGTTGCGC	AAACTATTAA	CTGGCGAACT	ACTTACTCTA	GCTTCCCGGC
	AACAATTAAT					
	TTCCGGCTGG					
	TCATTGCAGC					
3361	GGAGTCAGGC	AACTATGGAT	GAACGAAATA	GACAGATCGC	TGAGATAGGT	GCCTCACTGA
3421	TTAAGCATTG	GTAACTGTCA	GACCAAGTTT	ACTCATATAT	<b>ΔርጣጣጥΔር</b> Δ <b>ጥጥ</b>	GATTTAAAAC
3481	TTCATTTTTA	ATTTAAAAGG	ATCTAGGTGA	AGATCCTTTT	TCATAATCTC	ATCACCAAAA
3541	TCCCTTAACG	TGAGTTTTCG	TTCCACTGAG	CGTCAGACCC	CCTACAAAAC	ATCAACCAMMA
3601	CTTCTTGAGA	TOTTO TELESCO	CTGCGCGTAA	TCTCCTCCTT	CCARACARA	ATCAMAGGAT
3661	TACCAGCGGT	GGTTTGTTTG	CCGCATCAAG	ACCTACCAAC	TOTTTTTTTTT	AAACCACCGC
	GCTTCAGCAG					
3781	ACTTCAAGAA	CTCTCTACCA	CCCCCCTACAT	ACCITCTAGT	GTAGCCGTAG	TTAGGCCACC
3941	CTGCTGCCAG	TCCCCATAAC	TOCOCOCOCOCO	ACCICGCICI	GCTAATCCTG	TTACCAGTGG
3071	ATTARCCCCCA	CCCCTCCCCC	TCGIGICITA	CCGGGTTGGA	CTCAAGACGA	TAGTTACCGG
3061	ATAAGGCGCA	GCGGTCGGGC	TGAACGGGG	GTTCGTGCAC	ACAGCCCAGC	TTGGAGCGAA
3301	CGACCTACAC	CGAACTGAGA	TACCTACAGC	GTGAGCTATG	AGAAAGCGCC	ACGCTTCCCG
4021	AAGGGAGAAA	GGCGGACAGG	TATCCGGTAA	GCGGCAGGGT	CGGAACAGGA	GAGCGCACGA
4081	GGGAGCTTCC	AGGGGGAAAC	GCCTGGTATC	TTTATAGTCC	TGTCGGGTTT	CGCCACCTCT
4141	GACTTGAGCG	TCGATTTTTG	TGATGCTCGT	CAGGGGGGCG	GAGCCTATGG	AAAAACGCCA
4201	GCAACGCGGC	CTTTTTACGG	TTCCTGGCCT	TTTGCTGGCC	TTTTGCTCAC	ATGTTCTTTC
4261	CTGCGTTATC	CCCTGATTCT	GTGGATAACC	GTATTACCGC	CTTTGAGTGA	GCTGATACCG
4321	CTCGCCGCAG	CCGAACGACC	GAGCGCAGCG	AGTCAGTGAG	CGAGGAAGCG	GAAGAGCGCC
4381	TGATGCGGTA	TTTTCTCCTT	ACGCATCTGT	GCGGTATTTC	ACACCGCATA	TATGGTGCAC
4441	TCTCAGTACA	ATCTGCTCTG	ATGCCGCATA	GTTAAGCCAG	TATACACTCC	GCTATCGCTA
4501	CGTGACTGGG	TCATGGCTGC	GCCCCGACAC	CCGCCAACAC	CCGCTGACGC	GCCCTGACGG
4561	GCTTGTCTGC	TCCCGGCATC	CGCTTACAGA	CAAGCTGTGA	CCGTCTCCGG	GAGCTGCATG
4621	TGTCAGAGGT	TTTCACCGTC	ATCACCGAAA	CGCGCGAGGC	AGCTGCGGTA	AAGCTCATCA
4681	GCGTGGTCGT	GAAGCGATTC	ACAGATGTCT	GCCTGTTCAT	CCGCGTCCAG	CTCGTTGAGT
4741	TTCTCCAGAA	GCGTTAATGT	CTGGCTTCTG	ATAAAGCGGG	CCATGTTAAG	GGCGGTTTTT
4801	TCCTGTTTGG	TCACTGATGC	CTCCGTGTAA	GGGGGATTTC	TGTTCATGGG	GGTAATGATA
4861	CCGATGAAAC	GAGAGAGGAT	GCTCACGATA	CGGGTTACTG	ATGATGAACA	TGCCCGGTTA
4921	CTGGAACGTT	GTGAGGGTAA	ACAACTGGCG	GTATGGATGC	GGCGGGACCA	GAGAAAAATC
4981	ACTCAGGGTC	AATGCCAGCG	CTTCGTTAAT	ACAGATGTAG	GTGTTCCACA	GGGTAGCCAG
5041	CAGCATCCTG	.CGATGCAGAT	CCGGAACATA	ATGGTGCAGG	GCGCTGACTT	CCGCGTTTCC
5101	AGACTTTACG	AAACACGGAA	ACCGAAGACC	ATTCATGTTG	TTGCTCAGGT	CGCAGACGTT
5161	TTGCAGCAGC	AGTCGCTTCA	CGTTCGCTCG	CGTATCGGTG	ATTCATTCTG	СТААССАСТА
5221	AGGCAACCCC	GCCAGCCTAG	CCGGGTCCTC	AACGACAGGA	GCACGATCAT	GCGCACCCGT
5281	GGCCAGGACC	CAACGCTGCC	CGAGATGCGC	CGCGTGCGGC	TGCTGGAGAT	GGCGGACGCGI
5341	ATGGATATGT	TCTGCCAAGG	GTTGGTTTGC	GCATTCACAG	TTCTCCCCAA	CAATTCATTC
<b>'5401</b>	GCTCCAATTC	TTGGAGTGGT	GAATCCGTTA	GCGAGGTGCC	GCCGGCTTCC	ATTCACCTCC
5461	AGGTGGCCCG	GCTCCATGCA	CCGCGACGCA	ACGCGGGGAG	GCAGACAAGG	TATACCCCCC
5521	CGCCTACAAT	CCATGCCAAC	CCGTTCCATG	TGCTCGCCGA	CCCCCATA	AMCCCCCCCC
5581	CGATCAGCGG	TCCAGTGATC	GAAGTTAGGC	TGGTAAGAGG	CCCCACCCAM	AICGCCGIGA
5641	GTCCCTGATG	GTCGTCATCT	ACCTGCCTGG	ACAGCATGGG	CTCCAACCGAT	CCTTGAAGCT
5701	TGCCGCCGGA	AGCGAGAAGA	ATCATAATCC	CCAACCCCAM	CCACCAMCGCG	GUCATUCUGA
5761	CCAGCAAGAC	GTAGCCCAGC	GCGTCGCCC	CCATGCCCCC	CAMANAGE	GTCGCGAACG
5821	CGAAACGTTT	GGTGGCGGGA	CCACTCACCA	ACCOMMON CO	GATAATGGCC	TGCTTCTCGC
5881	ATACCGCAAG	CCACACGCCCC	ATCATCACCA	CCCTCCTCCTCCT	CAGGGGGTGC	AAGATTCCGA
5941	TGACCCAGAG	CONCAGGCCG	VCCATCGICG	CGACTTCCAGCG	AAAGUGGTCC	TCGCCGAAAA
6001	TGACCCAGAG	CACTACCAGC	CCCCCCCCCC	AGGGGTTGCAT	GATAAAGAAG	ACAGTCATAA
6061	GTGCGGCGAC	GATAGICAIG	ACCOMPANA	ACCGGAAGGA	GCTGACTGGG	TTGAAGGCTC
6121	TCAAGGGCAT	TCACCCCCTTT	CACCACCACCAC	TTATGCGACT	CCTGCATTAG	GAAGCAGCCC
0121	AGIAGIAGGT	TGAGGCCGTT	GAGCACCGCC	GCCGCAAGGA	ATGGTGCATG	CAAGGAGATG -

FOURE 43C

6181 GCGCCCAACA GTCCCCCGGC CACGGGGCCT GCCACCATAC CCACGCCGAA ACAAGCGCTC 6241 ATGAGCCCGA AGTGGCGAGC CCGA

FIGURE 43D

### PDEST24

### GST carboxy-fusion vector, T7 promoter

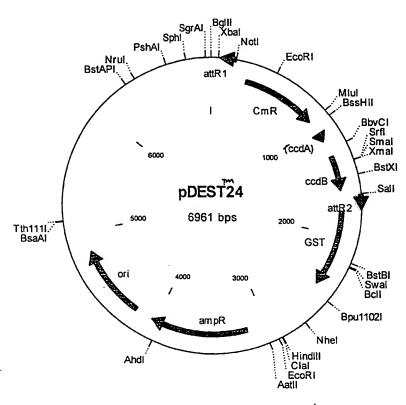


FIGURE 44A

### pDEST24 6961 bp

Location (Base Nos.)	Gene Encoded
19571	attR1
304963	CmR
10831167	inactivated ccdA
13051610	ccdB
16511775	attR2
17832451	GST
31814041	ampR
41904829	ori

1	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	GACTCACTAT	AGGGAGACCA	CAACGGTTTC
61	CCTCTAGATC	ACAAGTTTGT	ACAAAAAAGC	TGAACGAGAA	ACGTAAAATG	TATAAATATA
121	CAATATATTA	AATTAGATTT	TGCATAAAAA	ACAGACTACA	TAATACTGTA	AAACACAACA
181	TATCCAGTCA	CTATGGCGGC	CGCATTAGGC	ACCCCAGGCT	TTACACTTTA	TGCTTCCGGC
241	TCGTATAATG	TGTGGATTTT	GAGTTAGGAT	CCGGCGAGAT	TTTCAGGAGC	TAAGGAAGCT
301	AAAATGGAGA	AAAAAATCAC	TGGATATACC	ACCGTTGATA	TATCCCAATG	GCATCGTAAA
361	GAACATTTTG	AGGCATTTCA	GTCAGTTGCT	CAATGTACCT	ATAACCAGAC	CGTTCAGCTG
421	GATATTACGG	CCTTTTTAAA	GACCGTAAAG	AAAAATAAGC	ACAAGTTTTA	TCCGGCCTTT
481	ATTCACATTC	TTGCCCGCCT	GATGAATGCT	CATCCGGAAT	TCCGTATGGC	AATGAAAGAC
541	GGTGAGCTGG	TGATATGGGA	TAGTGTTCAC	CCTTGTTACA	CCGTTTTCCA	TGAGCAAACT
601	GAAACGTTTT	CATCGCTCTG	GAGTGAATAC	CACGACGATT	TCCGGCAGTT	TCTACACATA
661	TATTCGCAAG	ATGTGGCGTG	TTACGGTGAA	AACCTGGCCT	ATTTCCCTAA	AGGGTTTATT
721	GAGAATATGT	TTTTCGTCTC	AGCCAATCCC	TGGGTGAGTT	TCACCAGTTT	TGATTTAAAC
781	GTGGCCAATA	TGGACAACTT	CTTCGCCCCC	GTTTTCACCA	TGGGCAAATA	TTATACGCAA
841	GGCGACAAGG	TGCTGATGCC	GCTGGCGATT	CAGGTTCATC	ATGCCGTCTG	TGATGGCTTC
901	CATGTCGGCA	GAATGCTTAA	TGAATTACAA	CAGTACTGCG	ATGAGTGGCA	GGGCGGGGCG
961	TAAACGCGTG	GATCCGGCTT	ACTAAAAGCC	AGATAACAGT	ATGCGTATTT	GCGCGCTGAT
1021	TTTTGCGGTA	TAAGAATATA	TACTGATATG	TATACCCGAA	GTATGTCAAA	AAGAGGTGTG
1081	CTATGAAGCA	GCGTATTACA	GTGACAGTTG	ACAGCGACAG	CTATCAGTTG	CTCAAGGCAT
1141	ATATGATGTC	AATATCTCCG	GTCTGGTAAG	CACAACCATG	CAGAATGAAG	CCCGTCGTCT
1201	GCGTGCCGAA	CGCTGGAAAG	CGGAAAATCA	GGAAGGGATG	GCTGAGGTCG	CCCGGTTTAT
1261	TGAAATGAAC	GGCTCTTTTG	CTGACGAGAA	CAGGGACTGG	TGAAATGCAG	TTTAAGGTTT
				TGTTTGTGGA		
1381	ACACGCCCGG	GCGACGGATG	GTGATCCCCC	TGGCCAGTGC	ACGTCTGCTG	TCAGATAAAG
1441	TCTCCCGTGA	ACTTTACCCG	GTGGTGCATA	TCGGGGATGA	AAGCTGGCGC	ATGATGACCA
1501	CCGATATGGC	CAGTGTGCCG	GTCTCCGTTA	TCGGGGAAGA	AGTGGCTGAT	CTCAGCCACC
1561	GCGAAAATGA	CATCAAAAAC	GCCATTAACC	TGATGTTCTG	GGGAATATAA	ATGTCAGGCT
1621	CCCTTATACA	CAGCCAGTCT	GCAGGTCGAC	CATAGTGACT	GGATATGTTG	TGTTTTACAG
1681	TATTATGTAG	TCTGTTTTTT	ATGCAAAATC	TAATTTAATA	TATTGATATT	TATATCATTT
1741	TACGTTTCTC	GTTCAGCTTT	CTTGTACAAA	GTGGTGATTA	TGTCCCCTAT	ACTAGGTTAT
1801	TGGAAAATTA	AGGGCCTTGT	GCAACCCACT	CGACTTCTTT	TGGAATATCT	TGAAGAAAA
1861	TATGAAGAGC	ATTTGTATGA	GCGCGATGAA	GGTGATAAAT	GGCGAAACAA	AAAGTTTGAA
1921	TTGGGTTTGG	AGTTTCCCAA	TCTTCCTTAT	TATATTGATG	GTGATGTTAA	ATTAACACAG
1981	TCTATGGCCA	TCATACGTTA	TATAGCTGAC	AAGCACAACA	TGTTGGGTGG	TTGTCCAAAA
2041	GAGCGTGCAG	AGATTTCAAT	GCTTGAAGGA	GCGGTTTTGG	ATATTAGATA	CGGTGTTTCG
2101	AGAATTGCAT	ATAGTAAAGA	CTTTGAAACT	CTCAAAGTTG	ATTTTCTTAG	CAAGCTACCT
2161	GAAATGCTGA	AAATGTTCGA	AGATCGTTTA	TGTCATAAAA	CATATTTAAA	TGGTGATCAT
2221	GTAACCCATC	CTGACTTCAT	GTTGTATGAC	GCTCTTGATG	TTGTTTTATA	CATGGACCCA
2281	ATGTGCCTGG	ATGCGTTCCC	AAAATTAGTT	TGTTTTAAAA	AACGTATTGA	AGCTATCCCA
2341	CAAATTGATA	AGTACTTGAA	ATCCAGCAAG	TATATAGCAT	GGCCTTTGCA	GGGCTGGCAA
2401	GCCACGTTTG	GTGGTGGCGA	CCATCCTCCA	AAATCGGATC	TGGTTCCGCG	TCCATGGGGA
2461	TCCGGCTGCT	AACAAAGCCC	GAAAGGAAGC	TGAGTTGGCT	GCTGCCACCG	CTGAGCAATA
2521	ACTAGCATAA	CCCCTTGGGG	CCTCTAAACG	GGTCTTGAGG	GGTTTTTTGC	TGAAAGGAGG
2581	AACTATATCO	GGATATCCAC	AGGACGGGTG	TGGTCGCCAT	GATCGCGTAG	TCGATAGTGG
2641	CTCCAAGTAG	CGAAGCGAGC	AGGACTGGGC	GGCGGCCAAA	GCGGTCGGAC	AGTGCTCCGA-

2701	GAACGGGTGC	GCATAGAAAT	TGCATCAACG	CATATAGCGC	TAGCAGCACG	CCATAGTGAC
	TGGCGATGCT					
	AGCCTATGCC					
	ATTTCATACA					
	GCTTATCGAT					
	CGCCTATTTT					
	TTTCGGGGAA					
	TATCCGCTCA					
	ATGAGTATTC					
	GTTTTTGCTC					
	CGAGTGGGTT					
	GAAGAACGTT					
	CGTGTTGACG					
3481	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	AAGAGAATTA
3541	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	ACTTACTTCT	GACAACGATC
3601	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	CACAACATGG	GGGATCATGT	AACTCGCCTT
3661	GATCGTTGGG	AACCGGAGCT	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG
3721	CCTGCAGCAA	TGGCAACAAC	GTTGCGCAAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT
	TCCCGGCAAC					
3841	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	GAGCCGGTGA	GCGTGGGTCT
3901	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC
3961	ACGACGGGGA	GTCAGGCAAC	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC
4021	TCACTGATTA	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	CATATATACT	TTAGATTGAT
	TTAAAACTTC					
	ACCAAAATCC					
	AAAGGATCTT					
	CCACCGCTAC					
4321	GTAACTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	TTCTAGTGTA	GCCGTAGTTA
	GGCCACCACT					
4441	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG	TGTCTTACCG	GGTTGGACTC	AAGACGATAG
	TTACCGGATA					
	GAGCGAACGA					
	CTTCCCGAAG					
4681	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	ATAGTCCTGT	CGGGTTTCGC
4741	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	GGGGGCGGAG	CCTATGGAAA
4801	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC	CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG
4861	TTCTTTCCTG	CGTTATCCCC	TGATTCTGTG	GATAACCGTA	TTACCGCCTT	TGAGTGAGCT
	GATACCGCTC					
	GAGCGCCTGA					
5041	GGTGCACTCT	CAGTACAATC	TGCTCTGATG	CCGCATAGTT	AAGCCAGTAT	ACACTCCGCT
5101	ATCGCTACGT	GACTGGGTCA	TGGCTGCGCC	CCGACACCCG	CCAACACCCG	CTGACGCGCC
5161	CTGACGGGCT	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCG	TCTCCGGGAG
5221	CTGCATGTGT	CAGAGGTTTT	CACCGTCATC	ACCGANACCC	GCGAGGCAGC	TGCGGTAAAG
5281	CTCATCAGCG	TGGTCGTGAA	GCGATTCACA	GATGTCTGCC	TGTTCATCCG	CGTCCAGCTC
5341	GTTGAGTTTC	TCCAGAAGCG	TTAATGTCTG	GCTTCTGATA	AAGCGGGCCA	TGTTAAGGGC
5401	GGTTTTTTCC	TGTTTGGTCA	CTGATGCCTC	CGTGTAAGGG	CCATTTCTCT	TCATCCCCCT
5461	AATGATACCG	ATGAAACGAG	AGAGGATGCT	CACGATACGG	CTTACTCATC	ATCARGGGGG
5521	CCGGTTACTG	GAACGTTGTG	AGGGTAAACA	ACTEGEGGTA	TCCATCCCCC	CCCACCACAC
5581	AAAAATCACT	CAGGGTCAAT	GCCAGCGCTT	CGTTANTACA	CATCTACCGC	TTCCACACC
5641	TAGCCAGCAG	CATCCTGCGA	TGCAGATCCG	COLLANIACA	GTGCACGCC	CTCACAGGG
5701	CGTTTCCAGA	CTTTACGAAA	CACGGAAACC	CARCAIMAIG	CATCAGGGGG	CIGACIICCG
5761	AGACGTTTTG	CAGCAGCAGT	CCCLACCA	TCCCTCCCC	VACCCACVAN	CICAGGICGC
5821	ACCAGTAAGG	CAACCCCGCC	AGCCTAGCCC	CCTCCTCAAC	CACACCACCA	CONTONTO
5881	CACCCGTGGC	CAGGACCCAA	CCCTCCCCC	GATGCCCCAAC	GTGCCCCTCC	TOGATCATGCG
5941	GGACGCGATG	GATATGTTCT	GCCAAGGGTT	GGTTTCCCC	TTTCACACTGC	TOGAGATGGC
6001	TTGATTGGCT	CCAATTCTTC	CACTCCTCAA	TCCCTTTACCC	ACCRECAGETEC	CCCCCAAGAA
6061	CAGGTCGAGG	TGGCCCGGCT	CUSTGUEGAA	CCACCCAACC	AGGIGCCGCC	CACAACCEATT
6121	AGGGCGGCGC	CTACAATCCA	TECCANCEC	TTCCAMORCO	MOCGGGGCA	GGCATAAATC —
~-~·			- JCCAMCCCG	TICCAIGIGG	TCGCCGAGGC	GGCATAAATC—

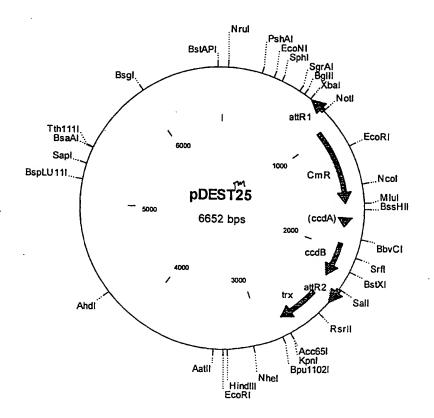
6181	CCCCTGACGA	TCAGCGGTCC	AGTGATCGAA	GTTAGGCTGG	TAAGAGCCGC	GAGCGATCCT
6161	TO A COTTON	CCTCATCGTC	GTCATCTACC	TGCCTGGACA	GCATGGCCTG	CAACGCGGGC
6241	TGAAGCIGIC	CCCCCCCAACC	CACAACAATC	ATAATGGGGA	AGGCCATCCA	GCCTCGCGTC
6301	ATCCCGATGC	CGCCGGAAGC	GAGAAGAATC	macacacaca.	TCCCCCCCAT	AATGGCCTGC
6361	GCGAACGCCA	GCAAGACGTA	GCCCAGCGCG	TCGGCCGCCA	IGCCGGCGAI	ARICOCCIOC
6421	TTCTCGCCGA	AACGTTTGGT	GGCGGGACCA	GTGACGAAGG	CTTGAGCGAG	GGCGTGCAAG
6481	ATTCCGAATA	CCGCAAGCGA	CAGGCCGATC	ATCGTCGCGC	TCCAGCGAAA	GCGGTCCTCG
6541	CCGAAAATGA	CCCAGAGCGC	TGCCGGCACC	TGTCCTACGA	GTTGCATGAT	AAAGAAGACA
6541	CEGINATION	CCCCGACGAT	AGTCATGCCC	CGCGCCCACC	GGAAGGAGCT	GACTGGGTTG
990T	GTCATAAGIG	CGGCGACGAI	MOCAMOCA CC	CTCTCCCTTA	יייברני ארייירירייף	GCATTAGGAA
6661	AAGGCTCTCA	AGGGCATCGG	TCGATCGACG	CICICCCIIA	TGCGACICCI	OMOG N MCC N N
6721	GCAGCCCAGT	AGTAGGTTGA	GGCCGTTGAG	CACCGCCGCC	GCAAGGAATG	GIGCAIGCAA
6781	GGAGATGGCG	CCCAACAGTC	CCCCGGCCAC	GGGGCCTGCC	ACCATACCCA	CGCCGAAACA
6941	ACCCCTCATG	AGCCCGAAGT	GGCGAGCCCG	ATCTTCCCCA	TCGGTGATGT	CGGCGATATA
0041	AGCGCTCHTC	ACCCCACCTC	TERCECCECT	GATGCCGGCC	ACGATGCGTC	CGGCGTAGAG
		MCCGCMCC1G	10000000			
6961	G					

FIGURE 44D

PDEST 25
Thioredoxin carboxy-fusion vector, T7 promoter

1- CmR - ccdB

1735 / Lett tac git tet egt tea get tie tig tac aaa gig gig att atg age gat aaa atg caa aga gea agt ega aag aac atg tit cae eac taa tac teg eta aaa att att cae etg act gac gac agt tit gac aeg gat gta etc aaa geg tit taa taa gig gac tig etg etg eta aaa etg tig eta eat gag tit ege



### pDEST25 6652 bp

Location (Base Nos.)	Gene Encoded
844720	attRl
9531612	CmR
17321816	inactivated ccdA
19542259	ccdB
23002424	attR2
24322794	trx

1	CCGGAAGCGA	GAAGAATCAT	AATGGGGAAG	GCCATCCAGC	CTCGCGTCGC	GAACGCCAGC
61	AAGACGTAGC	CCAGCGCGTC	GGCCGCCATG	CCGGCGATAA	TGGCCTGCTT	CTCGCCGAAA
121	CGTTTGGTGG	CGGGACCAGT	GACGAAGGCT	TGAGCGAGGG	CGTGCAAGAT	TCCGAATACC
181	GCAAGCGACA	GGCCGATCAT	CGTCGCGCTC	CAGCGAAAGC	GGTCCTCGCC	GAAAATGACC
241	CAGAGCGCTG	CCGGCACCTG	TCCTACGAGT	TGCATGATAA	AGAAGACAGT	CATAAGTGCG
301	GCGACGATAG	TCATGCCCCG	CGCCCACCGG	AAGGAGCTGA	CTGGGTTGAA	GGCTCTCAAG
361	GGCATCGGTC	GATCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAGC	AGCCCAGTAG
421	TAGGTTGAGG	CCGTTGAGCA	CCGCCGCCGC	AAGGAATGGT	GCATGCAAGG	AGATGGCGCC
481	CAACAGTCCC	CCGGCCACGG	GGCCTGCCAC	CATACCCACG	CCGAAACAAG	CGCTCATGAG
541	CCCGAAGTGG	CGAGCCCGAT	CTTCCCCATC	GGTGATGTCG	GCGATATAGG	CGCCAGCAAC
601	CGCACCTGTG	GCGCCGGTGA	TGCCGGCCAC	GATGCGTCCG	GCGTAGAGGA	TCGAGATCTC
661	GATCCCGCGA	AATTAATACG	ACTCACTATA	GGGAGACCAC	AACGGTTTCC	CTCTAGATCA
721	CAAGTTŤGTA	CAAAAAAGCT	GAACGAGAAA	CGTAAAATGA	TATAAATATC	AATATATTAA
781	ATTAGATTTT	GCATAAAAA	CAGACTACAT	AATACTGTAA	AACACAACAT	ATCCAGTCAC
841	TATGGCGGCC	GCATTAGGCA	CCCCAGGCTT	TACACTTTAT	GCTTCCGGCT	CGTATAATGT
901	GTGGATTTTG	AGTTAGGATC	CGGCGAGATT	TTCAGGAGCT	AAGGAAGCTA	AAATGGAGAA
961	AAAAATCACT	GGATATACCA	CCGTTGATAT	ATCCCAATGG	CATCGTAAAG	AACATTTTGA
1021	GGCATTTCAG	TCAGTTGCTC	AATGTACCTA	TAACCAGACC	GTTCAGCTGG	ATATTACGGC
1081	CTTTTTAAAG	ACCGTAAAGA	AAAATAAGCA	CAAGTTTTAT	CCGGCCTTTA	TTCACATTCT
1141	TGCCCGCCTG	ATGAATGCTC	ATCCGGAATT	CCGTATGGCA	ATGAAAGACG	GTGAGCTGGT
1201	GATATGGGAT	AGTGTTCACC	CTTGTTACAC	CGTTTTCCAT	GAGCAAACTG	AAACGTTTTC
1261	ATCGCTCTGG	AGTGAATACC	ACGACGATTT	CCGGCAGTTT	CTACACATAT	ATTCGCAAGA
1321	TGTGGCGTGT	TACGGTGAAA	ACCTGGCCTA	TTTCCCTAAA	GGGTTTATTG	AGAATATGTT
1381	TTTCGTCTCA	GCCAATCCCT	GGGTGAGTTT	CACCAGTTTT	GATTTAAACG	TGGCCAATAT
1441	GGACAACTTC	TTCGCCCCCG	TTTTCACCAT	GGGCAAATAT	TATACGCAAG	GCGACAAGGT
1501	GCTGATGCCG	CTGGCGATTC	AGGTTCATCA	TGCCGTCTGT	GATGGCTTCC	ATGTCGGCAG
1561	AATGCTTAAT	GAATTACAAC	AGTACTGCGA	TGAGTGGCAG	GGCGGGGCGT	AAACGCGTGG
1621	ATCCGGCTTA	CTAAAAGCCA	GATAACAGTA	TGCGTATTTG	CGCGCTGATT	TTTGCGGTAT
1681	AAGAATATAT	ACTGATATGT	ATACCCGAAG	TATGTCAAAA	. AGAGGTGTGC	TATGAAGCAG
1741	CGTATTACAG	TGACAGTTGA	CAGCGACAGC	TATCAGTTGC	TCAAGGCATA	TATGATGTCA
1801	ATATCTCCGG	TCTGGTAAGC	ACAACCATGO	: AGAATGAAGC	CCGTCGTCTG	CGTGCCGAAC
1861	GCTGGAAAGC	GGAAAATCAG	GAAGGGATGG	CTGAGGTCGC	CCGGTTTATI	GAAATGAACG
1921	GCTCTTTTGC	TGACGAGAAC	AGGGACTGGT	GAAATGCAGT	TTAAGGTTTA	CACCTATAAA
1981	. AGAGAGAGCC	GTTATCGTCT	GTTTGTGGAT	GTACAGAGTG	ATATTATTGA	CACGCCCGGG
2041	. CGACGGATGG	G TGATCCCCCT	GGCCAGTGCA	CGTCTGCTG1	CAGATAAAGT	CTCCCGTGAA
						CGATATGGCC
2161	AGTGTGCCG	TCTCCGTTAT	CGGGGAAGAA	A GTGGCTGATO	TCAGCCACC	CGAAAATGAC
2221	ATCAAAAACC	CCATTAACCT	GATGTTCTGC	GGAATATAA	A TGTCAGGCT	CCTTATACAC
2281	AGCCAGTCT	G CAGGTCGACC	ATAGTGACTO	GATATGTTGT	r GTTTTACAG1	ATTATGTAGT
						ACGTTTCTCG
						TGACTGACGA
						TCTGGGCAGA
						ACGAATATCA
						CGCCGAAATA
						CGGCAACCAA
270	1 AGTGGGTGC	A CTGTCTAAAG	GTCAGTTGA	A AGAGTTCCT	C GACGCTAAC	TGGCCGGTTC
276	1 TGGTTCTGG	T GATGACGATO	ACAAGGTAC	C CGGGGATCG	A TCCGGCTGC	r aacaaagccc -

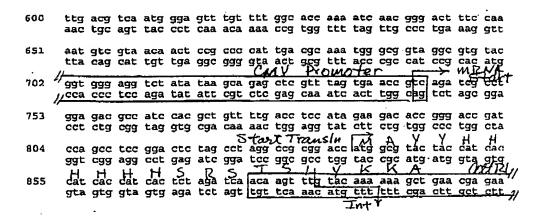
Figure 45B

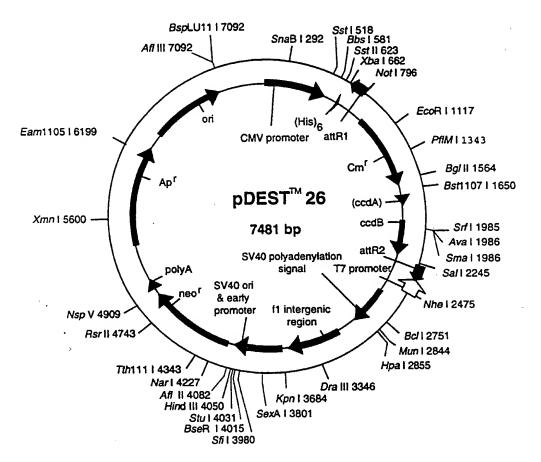
2821	GAAAGGAAGC	TGAGTTGGCT	GCTGCCACCG	CTGAGCAATA	ACTAGCATAA	CCCCTTGGGG
2881	CCTCTAAACG	GGTCTTGAGG	GGTTTTTTGC	TGAAAGGAGG	AACTATATCC	GGATATCCAC
2941	AGGACGGGTG	TGGTCGCCAT	GATCGCGTAG	TCGATAGTGG	CTCCAAGTAG	CGAAGCGAGC
		GGCGGCCAAA				
		CATATAGCGC				
		GCAAGAGGCC				
3181	AGGGTGACGG	TGCCGAGGAT	GACGATGAGC	GCATTGTTAG	ATTTCATACA	CGGTGCCTGA
		AATTTAACTG				
		AATTCTTGAA				
		ATAATGGTTT				
		TGTTTATTTT				
		ATGCTTCAAT				
		ATTCCCTTTT				
		GTAAAAGATG				
		AGCGGTAAGA				
		AAAGTTCTGC				
		CGCCGCATAC				
		CTTACGGATG				
		ACTGCGGCCA				
		CACAACATGG				
		ATACCAAACG				
		CTATTAACTG				
		GCGGATAAAG				
		GATAAATCTG				
		GGTAAGCCCT				
		CGAAATAGAC				
		CAAGTTTACT				
		TAGGTGAAGA				
		CACTGAGCGT				
		CGCGTAATCT				
		GATCAAGAGC				
		AATACTGTCC				
		CCTACATACC				
		TGTCTTACCG				
		ACGGGGGGTT				
		CTACAGCGTG				
		CCGGTAAGCG				
						TTGAGCGTCG
						ACGCGGCCTT
_		CTGGCCTTTT				
5221	TGATTCTGTG	GATAACCGTA	TTACCGCCTT	TGAGTGAGCT	GATACCGCTC	GCCGCAGCCG
						TGCGGTATTT
5341	. TCTCCTTACG	CATCTGTGCG	GTATTTCACA	CCGCATATAT	GGTGCACTCT	CAGTACAATC
						GACTGGGTCA
						TGTCTGCTCC
5521	. CGGCATCCGC	TTACAGACAA	GCTGTGACCG	TCTCCGGGAG	CTGCATGTGT	CAGAGGTTTT
						TGGTCGTGAA
						TCCAGAAGCG
						TGTTTGGTCA
5761	L CTGATGCCTC	CGTGTAAGGG	GGATTTCTGT	TCATGGGGGT	' AATGATACCO	ATGAAACGAG
5821	L AGAGGATGCT	CACGATACGG	GTTACTGATG	ATGAACATGO	CCGGTTACT	GAACGTTGTG
						CAGGGTCAAT
5943	L GCCAGCGCT1	CGTTAATACA	GATGTAGGTG	TTCCACAGGG	TAGCCAGCAG	CATCCTGCGA
600	L TGCAGATCC	GAACATAATG	GTGCAGGGCG	CTGACTTCCC	CGTTTCCAGA	CTTTACGAAA
606	L CACGGAAACO	GAAGACCATI	CATGTTGTTG	CTCAGGTCGC	AGACGTTTTC	CAGCAGCAGT
612	L CGCTTCACG	TCGCTCGCGT	ATCGGTGATI	CATTCTGCTA	ACCAGTAAGG	CAACCCCGCC
618	L AGCCTAGCC	GGTCCTCAAC	GACAGGAGCA	CGATCATGC	CACCCGTGG	CAGGACCCAA
624	L CGCTGCCCG	A GATGCGCCGC	GTGCGGCTGC	TGGAGATGG	GGACGCGAT	GATATGTTCT-

6301	CCCAAGGGTT	GGTTTGCGCA	TTCACAGTTC	TCCGCAAGAA	TTGATTGGCT	CCAATICITG
0301		macamma aca	AGGTGCCGCC	GGCTTCCATT	CAGGTCGAGG	TGGCCCGGCT
6361	GAGTGGTGAA	TCCGTTAGCG	AGGIGCCGCC		***************************************	מתא כא אתיכיכא
6421	CCATGCACCG	CGACGCAACG	CGGGGAGGCA	GACAAGGTAT	AGGGCGGCGC	CTACAATCCA
6401	madan naccc	ттеслтетее	TCGCCGAGGC	GGCATAAATC	GCCGTGACGA	TCAGCGGTCC
6481	TGCCAACCCG	TICCATGIGC	100000000	as acas maam	MON NO CONCINC	COTONTOCTO
6541	AGTGATCGAA	GTTAGGCTGG	TAAGAGCCGC	GAGCGATCCT	IGAAGCIGIC	CCTGATGGTC
	amaxmama co	TOCOTOGACA	GCATGGCCTG	CAACGCGGGC	ATCCCGATGC	CG

FIGURE 45D

### pDEST26 His6 Amino Fusion in pCMV Sport-neo Vector





#### pDEST26 7481 bp

Location (Base Nos.)	Gene Encoded
492509	his6
619519	attRl
7521411	CmR
15311615	inactivated ccdA
17532058	ccdB
20992223	attR2
24092771	SV40 polyA
29663421	fl intergenic region
34853903	SV40 promoter
39484742	neo
48064854	polyA
52656125	Apr
62746913	ori
7344385	CMV promoter

1 GTAAACTGCC CACTTGGCAG TACATCAAGT GTATCATATG CCAAGTACGC CCCCTATTGA 61 CGTCAATGAC GGTAAATGGC CCGCCTGGCA TTATGCCCAG TACATGACCT TATGGGACTT 121 TCCTACTTGG CAGTACATCT ACGTATTAGT CATCGCTATT ACCATGGTGA TGCGGTTTTG 181 GCAGTACATC AATGGGCGTG GATAGCGGTT TGACTCACGG GGATTTCCAA GTCTCCACCC 241 CATTGACGTC AATGGGAGTT TGTTTTGGCA CCAAAATCAA CGGGACTTTC CAAAATGTCG 301 TAACAACTCC GCCCCATTGA CGCAAATGGG CGGTAGGCGT GTACGGTGGG AGGTCTATAT 361 AAGCAGAGCT CGTTTAGTGA ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTTGA 421 CCTCCATAGA AGACACCGGG ACCGATCCAG CCTCCGGACT CTAGCCTAGG CCGCGGACCA 481 TGGCGTACTA CCATCACCAT CACCATCACT CTAGATCAAC AAGTTTGTAC AAAAAAGCTG 541 AACGAGAAAC GTAAAATGAT ATAAATATCA ATATATTAAA TTAGATTTTG CATAAAAAAC 601 AGACTACATA ATACTGTAAA ACACAACATA TCCAGTCACT ATGGCGGCCG CATTAGGCAC 661 CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATAATGTG TGGATTTTGA GTTAGGATCC 721 GGCGAGATTT TCAGGAGCTA AGGAAGCTAA AATGGAGAAA AAAATCACTG GATATACCAC 781 CGTTGATATA TCCCAATGGC ATCGTAAAGA ACATTTTGAG GCATTTCAGT CAGTTGCTCA 841 ATGTACCTAT AACCAGACCG TTCAGCTGGA TATTACGGCC TTTTTAAAGA CCGTAAAGAA 901 AAATAAGCAC AAGTTTTATC CGGCCTTTAT TCACATTCTT GCCCGCCTGA TGAATGCTCA 961 TCCGGAATTC CGTATGGCAA TGAAAGACGG TGAGCTGGTG ATATGGGATA GTGTTCACCC 1021 TTGTTACACC GTTTTCCATG AGCAAACTGA AACGTTTTCA TCGCTCTGGA GTGAATACCA 1081 CGACGATTTC CGGCAGTTTC TACACATATA TTCGCAAGAT GTGGCGTGTT ACGGTGAAAA 1141 CCTGGCCTAT TTCCCTAAAG GGTTTATTGA GAATATGTTT TTCGTCTCAG CCAATCCCTG 1201 GGTGAGTTTC ACCAGTTTTG ATTTAAACGT GGCCAATATG GACAACTTCT TCGCCCCCGT 1261 TTTCACCATG GGCAAATATT ATACGCAAGG CGACAAGGTG CTGATGCCGC TGGCGATTCA 1321 GGTTCATCAT GCCGTCTGTG ATGGCTTCCA TGTCGGCAGA ATGCTTAATG AATTACAACA 1381 GTACTGCGAT GAGTGGCAGG GCGGGGCGTA AAGATCTGGA TCCGGCTTAC TAAAAGCCAG 1441 ATAACAGTAT GCGTATTTGC GCGCTGATTT TTGCGGTATA AGAATATATA CTGATATGTA 1501 TACCCGAAGT ATGTCAAAAA GAGGTGTGCT ATGAAGCAGC GTATTACAGT GACAGTTGAC 1561 AGCGACAGCT ATCAGTTGCT CAAGGCATAT ATGATGTCAA TATCTCCGGT CTGGTAAGCA 1621 CAACCATGCA GAATGAAGCC CGTCGTCTGC GTGCCGAACG CTGGAAAGCG GAAAATCAGG 1681 AAGGGATGGC TGAGGTCGCC CGGTTTATTG AAATGAACGG CTCTTTTGCT GACGAGAACA 1741 GGGACTGGTG AAATGCAGTT TAAGGTTTAC ACCTATAAAA GAGAGAGCCG TTATCGTCTG 1801 TTTGTGGATG TACAGAGTGA TATTATTGAC ACGCCCGGGC GACGGATGGT GATCCCCCTG 1861 GCCAGTGCAC GTCTGCTGTC AGATAAAGTC TCCCGTGAAC TTTACCCGGT GGTGCATATC 1921 GGGGATGAAA GCTGGCGCAT GATGACCACC GATATGGCCA GTGTGCCGGT CTCCGTTATC 1981 GGGGAAGAG TGGCTGATCT CAGCCACCGC GAAAATGACA TCAAAAACGC CATTAACCTG 2041 ATGTTCTGGG GAATATAAAT GTCAGGCTCC CTTATACACA GCCAGTCTGC AGGTCGACCA 2101 TAGTGACTGG ATATGTTGTG TTTTACAGTA TTATGTAGTC TGTTTTTTAT GCAAAATCTA 2161 ATTTAATATA TTGATATTTA TATCATTTTA CGTTTCTCGT TCAGCTTTCT TGTACAAAGT 2221 GGTTGATCGC GTGCATGCGA CGTCATAGCT CTCTCCCTAT AGTGAGTCGT ATTATAAGCT 2281 AGGCACTGGC CGTCGTTTTA CAACGTCGTG ACTGGGAAAA CTGCTAGCTT GGGATCTTTG --

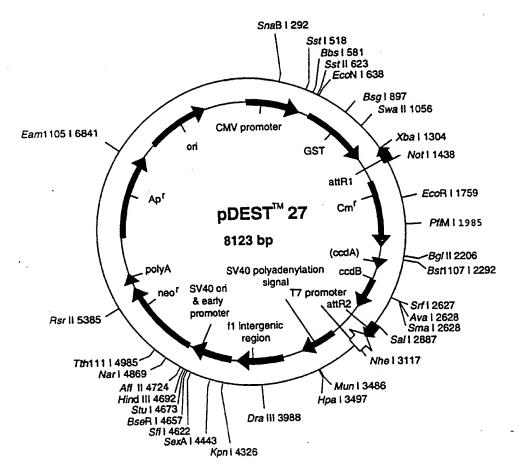
						as as moons as
2341	TGAAGGAACC	TTACTTCTGT	GGTGTGACAT	AATTGGACAA	ACTACCTACA	GAGATTTAAA
2401	GCTCTAAGGT	AAATATAAAA	TTTTTAAGTG	TATAATGTGT	TAAACTAGCT	GCATATGCTT
2461	GCTGCTTGAG	AGTTTTGCTT .	ACTGAGTATG	ATTTATGAAA	ATATTATACA	CAGGAGCTAG
2521	TGATTCTAAT	TGTTTGTGTA	TTTTAGATTC	ACAGTCCCAA	GGCTCATTTC	AGGCCCCTCA
2581	GTCCTCACAG	TCTGTTCATG	ATCATAATCA	GCCATACCAC	ATTTGTAGAG	GTTTTACTTG
2641	CTTTAAAAAA	CCTCCCACAC	CTCCCCTGA	ACCTGAAACA	TAAAATGAAT	GCAATTGTTG
2701	TTGTTAACTT	GTTTATTGCA	GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT
2761	TCACAAATAA	AGCATTTTTT	TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATG
2821	TATCTTATCA	TGTCTGGATC	GATCCTGCAT	TAATGAATCG	GCCAACGCGC	GGGGAGAGGC
2881	GGTTTGCGTA	TTGGCTGGCG	TAATAGCGAA	GAGGCCCGCA	CCGATCGCCC	TTCCCAACAG
2941	TTGCGCAGCC	TGAATGGCGA	ATGGGACGCG	CCCTGTAGCG	GCGCATTAAG	CGCGGCGGGT
3001	GTGGTGGTTA	CGCGCAGCGT	GACCGCTACA	CTTGCCAGCG	CCCTAGCGCC	CGCTCCTTTC
3061	GCTTTCTTCC	CTTCCTTTCT	CGCCACGTTC	GCCGGCTTTC	CCCGTCAAGC	TCTAAATCGG
3121	GGGCTCCCTT	TAGGGTTCCG	ATTTAGTGCT	TTACGGCACC	TCGACCCCAA	AAAACTTGAT
	TAGGGTGATG					
	TTGGAGTCCA					
	ATCTCGGTCT					
	AATGAGCTGA					
	TCGCCTGATG					
3481	ATCTGCGCAG	CACCATGGCC	TGAAATAACC	TCTGAAAGAG	GAACTTGGTT	AGGTACCTTC
3541	TGAGGCGGAA	AGAACCAGCT	GTGGAATGTG	TGTCAGTTAG	GGTGTGGAAA	GTCCCCAGGC
3601	TCCCCAGCAG	GCAGAAGTAT	GCAAAGCATG	CATCTCAATT	AGTCAGCAAC	CAGGTGTGGA
	AAGTCCCCAG					
	ACCATAGTCC					
	TCTCCGCCCC					
	TCTGAGCTAT					
	CTTGATTCTT					
	ATGGATTGCA					
4021	CACAACAGAC	AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC
4081	CGGTTCTTTT	TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG
	CGCGGCTATC					
	CTGAAGCGGG					
4261	CTCACCTTGC	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA
4321	CGCTTGATCC	GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC
4381	GTACTCGGAT	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC
	TCGCGCCAGC					
	TCGTGACCCA					
	GATTCATCGA					
	CCCGTGATAT					
	GTATCGCCGC					
4741	GAGCGGGACT	CTGGGGTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGATG
						TGTGAATCGA
						GCCGCATAGT
						TGTCTGCTCC
						CAGAGGTTTT
						TTTTTATAGG
						GGAAATGTGC
						CTCATGAGAC
						ATTCAACATT
522.	I MATAACCCI	COMMANDELL	CARIARIAL	. CAPPIPECCE	* TCCTCTTTT	GCTCACCCAG
						GGTTACATCG
						CGTTTTCCAA
						GACGCCGGGC
						TACTCACCAG
552	L AAGAGCAAC		. ATACACTATI	CICAGAATGA	Y CIIGGIIGA(	GCTGCCATAA
						CCGAAGGAGC
						TGGGAACCGG
576	1 AGCTGAATG	A AGCCATACCA	AACGACGAGC	_ GTGACACCAC	_ GMIGCCIGIT	A GCAATGGCAA -

582	21	CAACGTTGCG	CAAACTATTA	ACTGGCGAAC	TACTTACTCT	AGCTTCCCGG	CAACAATTAA
588	31	TAGACTGGAT	GGAGGCGGAT	AAAGTTGCAG	GACCACTTCT	GCGCTCGGCC	CTTCCGGCTG
594	11	GCTGGTTTAT	TGCTGATAAA	TCTGGAGCCG	GTGAGCGTGG	GTCTCGCGGT	ATCATTGCAG
600	1	CACTGGGGCC	AGATGGTAAG	CCCTCCCGTA	TCGTAGTTAT	CTACACGACG	GGGAGTCAGG
606	51	CAACTATGGA	TGAACGAAAT	AGACAGATCG	CTGAGATAGG	TGCCTCACTG	ATTAAGCATT
612	21	GGTAACTGTC	AGACCAAGTT	TACTCATATA	TACTTTAGAT	TGATTTAAAA	CTTCATTTTT
	_		GATCTAGGTG				
624	11	GTGAGTTTTC	GTTCCACTGA	GCGTCAGACC	CCGTAGAAAA	GATCAAAGGA	TCTTCTTGAG
630	01	ATCCTTTTTT	TCTGCGCGTA	ATCTGCTGCT	TGCAAACAAA	AAAACCACCG	CTACCAGCGG
636	51	TGGTTTGTTT	GCCGGATCAA	GAGCTACCAA	CTCTTTTTCC	GAAGGTAACT	GGCTTCAGCA
			ACCAAATACT				
648	31	ACTCTGTAGC	ACCGCCTACA	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG	GCTGCTGCCA
654	41	GTGGCGATAA	GTCGTGTCTT	ACCGGGTTGG	ACTCAAGACG	ATAGTTACCG	GATAAGGCGC
66	01	AGCGGTCGGG	CTGAACGGGG	GGTTCGTGCA	CACAGCCCAG	CTTGGAGCGA	ACGACCTACA
66	61	CCGAACTGAG	ATACCTACAG	CGTGAGCATT	GAGAAAGCGC	CACGCTTCCC	GAAGGGAGAA
67	21	AGGCGGACAG	GTATCCGGTA	AGCGGCAGGG	TCGGAACAGG	AGAGCGCACG	AGGGAGCTTC
67	81	CAGGGGGAAA	CGCCTGGTAT	CTTTATAGTC	CTGTCGGGTT	TCGCCACCTC	TGACTTGAGC
68	41	GTCGATTTTT	GTGATGCTCG	TCAGGGGGGC	GGAGCCTATG	GAAAAACGCC	AGCAACGCGG
69	01	CCTTTTTACG	GTTCCTGGCC	TTTTGCTGGC	CTTTTGCTCA	CATGTTCTTT	CCTGCGTTAT
			TGTGGATAAC				
		• • • • • • • • • • • • • • • • • • • •	CGAGCGCAGC				
	_		CCCCGCGCGT				
			TTGAAGCATT				
			AAATAAACAA				
			AACCATTATT				
			ATTAGATGCA				
		+	ACCCCCGCCC				AGTAACGCCA
74	41	ATAGGGACTT	TCCATTGACG	TCAATGGGTG	GAGTATTTAC	G	•

136/240 Frouter 47A

## pDEST 27 GST Amino Fusion in pCMV Sport-neo Vector

				,	4.4	., 1	· -								M	RNA	slave
	/				<u> </u>	<u>V_</u>	ىنىپ	MOT	er_	-4-			<b></b>		<del>-4-1</del>		£ 4.4-
600°	' nac	ggt	ggg	agg	tct	ata	caa	gca	gag	CEC	gut	Lag	cga	acc	900	aya.	ccg
	"ntg	cca	CGC	tee	aga	tat.	att	cgt	ctc	gag	ÇZZ	atc	acc	tgg	cag	CCC	age
1	<i></i>				~~												
651	cct	qqa	qaç	gcc	atc	cac	get	gtt	ttg	acc	tcc	ata	gaa	gac	acc	<b>9</b> 99	acc
	gga	cct	cta	cga	tag	ata	сча	caa	aac	tgg	agg	tat	ctt	ctg	tgg	CCC	tgg
	23-		5	-33		J		-		****			TAK	A .	D	I	1
702	gat	003	acc	+	~~=	010	tag	cct	agg	cca	caa	acc	ata	acc	cċt	ata	cEa
702	gat		900		990	~~~	ato	772	~33	443	-33	taa	TAC	caa	gga	tat	gat.
	cta	39 c	egg	agg	CCL	gay	aLL	440		330	300	~==	šť	w?	776	الالكه	gat GST
753	ggt	tat	tgg	aaa	att	aag	<b>ååc</b>	CCC	grg	CAA	ccc	ACL	cga			cug	gaa
	cca	ata	acc	ttt	taa	ttc	ccg	gaa	CAC	966	333	tga	gct	gaa	gaa	aaç	CLL
						-	- (	<u> </u>	Τ ΄	40	tei	n -	-				gat//
804	tat	ctt	gaa	qaa	aaa	tat	gaa	gag	cat	ttg	tat	gag	cgc	gat	gaa	ggt	gat//
	ata	даа	ctt	ctt	EEE	ata	ctt	ctc	qta	aac	ata	CLC	gcg	cta	ctt	cca	cta
		5				-		-	-						_		_
													V.	Ρ	R	5_	R
1365	<u> </u>	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt	CCC	aga
	// aaa	CCA	CCA	CCG	ctq	qta	gga	ggt	ttt	agc	cta	gac	caa	990	gca	aga	tct
	ζ,	T	S	Ľ	ΥŽ	тĸ	K	. A_					"				
1416	502	aca		ttg	rac	888	202		gaa	cga	gaa	acq	•				
~	204	it-at	-50	aac	2 = 0	FFH	ttt	CGS	CEE	act	ctt	tac					
	agu	rac	cea	aac	acy				<u> </u>		~4	101	#				
						Ţ۲	1 <del>4.</del>				at						



### pDEST27 8123 bp (rotated to position 7800)

Location (Base Nos.)	Gene Encoded
130793	GST
803927	attR1
10361695	CmR
18151899	inactivated ccdA
20372342	ccdB
23832507	attR2
26933055	SV40 polyA
32503705	fl intergenic region
37694187	SV40 promoter
42325026	neo
50905138	polyA
55496409	Apr
65587197	ori
762827	CMV promoter

						•
1	ATAAGCAGAG	CTCGTTTAGT	GAACCGTCAG	ATCGCCTGGA	GACGCCATCC	ACGCTGTTTT
61	GACCTCCATA	GAAGACACCG	GGACCGATCC	AGCCTCCGGA	CTCTAGCCTA	GGCCGCGGAC
121	CATGGCCCCT	ATACTAGGTT	ATTGGAAAAT	TAAGGGCCTT	GTGCAACCCA	CTCGACTTCT
1 0 1	тттссаатат	CTTGAAGAAA	AATATGAAGA	GCATTTGTAT	GAGCGCGATG .	AAGGTGATAA
241	ATGGCGAAAC	AAAAAGTTTG	AATTGGGTTT	GGAGTTTCCC	AATCTTCCTT	ATTATATTGA
3.01	TEGTGATGTT	AAATTAACAC	AGTCTATGGC	CATCATACGT	TATATAGCTG	ACAAGCACAA
361	CATGTTGGGT	GGTTGTCCAA	AAGAGCGTGC	AGAGATTTCA	ATGCTTGAAG	GAGCGGTTTT
421	CCATATTAGA	TACGGTGTTT	CGAGAATTGC	ATATAGTAAA	GACTTTGAAA	CTCTCAAAGT
481	TCDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AGCAAGCTAC	CTGAAATGCT	GAAAATGTTC	GAAGATCGTT	TATGTCATAA
5/1	ል TPP TP A TP A TP A T	AATGGTGATC	ATGTAACCCA	TCCTGACTTC	ATGTTGTATG	ACGCTCTTGA
601	Ադեդերեշրերեն Մահերերեն	TACATGGACC	CAATGTGCCT	GGATGCGTTC	CCAAAATTAG	TTTGTTTTAA
661	እአአአርርጥአጥጥ	GAAGCTATCC	CACAAATTGA	TAAGTACTTG	AAATCCAGCA	AGTATATAGC
721	ATGGCCTTTG	CAGGGCTGGC	AAGCCACGTT	TGGTGGTGGC	GACCATCCTC	CAAAATCGGA
781	TCTGGTTCCG	CGTTCTAGAT	CAACAAGTTT	GTACAAAAAA	GCTGAACGAG	AAACGTAAAA
0/1	тсататават	ATCAATATAT	TAAATTAGAT	TTTGCATAAA	AAACAGACTA	CATAATACIG
901	TABABCACAA	CATATCCAGT	CACTATGGCG	GCCGCATTAG	GCACCCCAGG	CTTTACACTT
961	TATGCTTCCG	GCTCGTATAA	TGTGTGGATT	TTGAGTTAGG	ATCCGGCGAG	ATTTTCAGGA
1021	GCTAAGGAAG	CTAAAATGGA	GAAAAAAATC	ACTGGATATA	CCACCGTTGA	TATATCCCAA
1081	TGGCATCGTA	AAGAACATTT	TGAGGCATTT	CAGTCAGTTG	CTCAATGTAC	CTATAACCAG
1141	ACCGTTCAGC	TGGATATTAC	GGCCTTTTTA	AAGACCGTAA	AGAAAAATAA	GCACAAGTTT
1201	TATCCGGCCT	TTATTCACAT	TCTTGCCCGC	CTGATGAATG	CTCATCCGGA	ATTCCGTATG
1261	CCAATGAAAG	ACGGTGAGCT	GGTGATATGG	GATAGTGTTC	ACCCTTGTTA	CACCGTTTTC
1321	CATGAGCAAA	CTGAAACGTT	TTCATCGCTC	TGGAGTGAAT	ACCACGACGA	TTTCCGGCAG
1381	ጥጥጥጥልሮልርል	TATATTCGCA	AGATGTGGCG	TGTTACGGTG	AAAACCTGGC	CTATTTCCCT
1 4 4 1	AAAGGGTTTA	TTGAGAATAT	GTTTTTCGTC	TCAGCCAATC	CCTGGGTGAG	TTTCACCAGT
1501	TTTC2TTT2	ACGTGGCCAA	TATGGACAAC	TTCTTCGCCC	CCGTTTTCAC	CATGGGCAAA
1561	TATTATACGO	AAGGCGACAA	GGTGCTGATG	: CCGCTGGCGA	TTCAGGTTCA	TCATGCCGTC
1621	TGTGATGGCT	TCCATGTCGG	CAGAATGCTT	: AATGAATTAC	AACAGTACTG	CGATGAGTGG
1681	CAGGGGGGG	CGTAAAGATC	TGGATCCGGC	TTACTAAAA	CCAGATAACA	GTATGCGTAT
174	TTGCGCGCTC	ATTTTTGCGG	TATAAGAATA	A TATACTGATA	A TGTATACCCG	AAGTATGTCA
180	AAAAGAGGTO	TGCTATGAAC	CAGCGTATT	A CAGTGACAGT	r TGACAGCGAC	AGCTATCAGT
186	TGCTCAAGG	ATATATGATO	TCAATATCT	C CGGTCTGGT	A AGCACAACCA	TGCAGAATGA
192	AGCCCGTCG	r CTGCGTGCCC	AACGCTGGA	A AGCGGAAAA	r caggaaggga	TGGCTGAGGT
198	1 CGCCCGGTT	r ATTGAAATGA	ACGGCTCTT	r TGCTGACGA	G AACAGGGACT	GGTGAAATGC
204	1 AGTTTTAAGG	TTACACCTAT	C AAAAGAGAGA	A GCCGTTATC	G TCTGTTTGTG	GATGTACAGA
210	1 GTGATATTA	r TGACACGCC	C GGGCGACGG	A TGGTGATCC	C CCTGGCCAGI	GCACGTCTGC
216	1 TGTCAGATA	A AGTCTCCCG	r GAACTTTAC	C CGGTGGTGC	A TATCGGGGAI	GAAAGCTGGC
222	1 CCATGATGA	C CACCGATATO	G GCCAGTGTG	C CGGTCTCCG	T TATCGGGGAA	GAAGTGGCTG
228	1 ATCTCAGCC	A CCGCGAAAA	T GACATCAAA	A ACGCCATTA	A CCTGATGTTC	TGGGGAATAT

FIGURE 47B

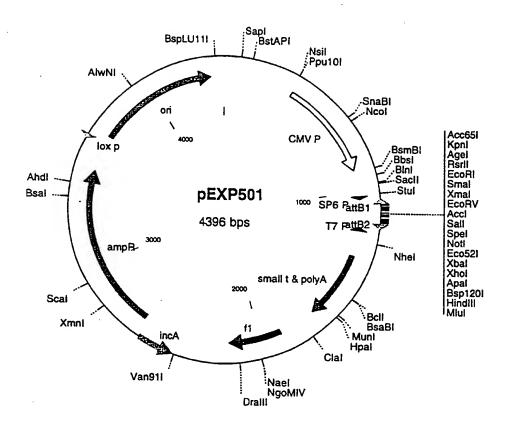
2341 AAATGTCAGG CTCCCTTATA CACAGCCAGT CTGCAGGTCG ACCATAGTGA CTGGATATGT 2401 TGTGTTTTAC AGTATTATGT AGTCTGTTTT TTATGCAAAA TCTAATTTAA TATATTGATA 2461 TTTATATCAT TTTACGTTTC TCGTTCAGCT TTCTTGTACA AAGTGGTTGA TCGCGTGCAT 2521 GCGACGTCAT AGCTCTCTCC CTATAGTGAG TCGTATTATA AGCTAGGCAC TGGCCGTCGT 2581 TTTACAACGT CGTGACTGGG AAAACTGCTA GCTTGGGATC TTTGTGAAGG AACCTTACTT 2641 CTGTGGTGTG ACATAATTGG ACAAACTACC TACAGAGATT TAAAGCTCTA AGGTAAATAT 2701 AAAATTTTTA AGTGTATAAT GTGTTAAACT AGCTGCATAT GCTTGCTGCT TGAGAGTTTT 2761 GCTTACTGAG TATGATTTAT GAAAATATTA TACACAGGAG CTAGTGATTC TAATTGTTTG 2821 TGTATTTTAG ATTCACAGTC CCAAGGCTCA TTTCAGGCCC CTCAGTCCTC ACAGTCTGTT 2881 CATGATCATA ATCAGCCATA CCACATTTGT AGAGGTTTTA CTTGCTTTAA AAAACCTCCC 2941 ACACCTCCC CTGAACCTGA AACATAAAAT GAATGCAATT GTTGTTGTTA ACTTGTTTAT 3001 TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT 3061 TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG 3121 GATCGATCCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG CGTATTGGCT 3181 GGCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGC AGCCTGAATG 3241 GCGAATGGGA CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA 3301 GCGTGACCGC TACACTTGCC AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT 3361 TTCTCGCCAC GTTCGCCGGC TTTCCCCGTC AAGCTCTAAA TCGGGGGCTC CCTTTAGGGT 3421 TCCGATTTAG TGCTTTACGG CACCTCGACC CCAAAAAACT TGATTAGGGT GATGGTTCAC 3481 GTAGTGGCC ATCGCCCTGA TAGACGGTTT TTCGCCCTTT GACGTTGGAG TCCACGTTCT 3541 TTAATAGTGG ACTCTTGTTC CAAACTGGAA CAACACTCAA CCCTATCTCG GTCTATTCTT 3601 TTGATTTATA AGGGATTTTG CCGATTTCGG CCTATTGGTT AAAAAATGAG CTGATTTAAC 3661 AAATATTTAA CGCGAATTTT AACAAAATAT TAACGTTTAC AATTTCGCCT GATGCGGTAT 3721 TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GCGGATCTGC GCAGCACCAT 3781 GGCCTGAAAT AACCTCTGAA AGAGGAACTT GGTTAGGTAC CTTCTGAGGC GGAAAGAACC 3841 AGCTGTGGAA TGTGTGTCAG TTAGGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGCAGAA 3901 GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCAGGTG TGGAAAGTCC CCAGGCTCCC 3961 CAGCAGGCAG AAGTATGCAA AGCATGCATC TCAATTAGTC AGCAACCATA GTCCCGCCCC 4021 TAACTCCGCC CATCCCGCCC CTAACTCCGC CCAGTTCCGC CCATTCTCCG CCCCATGGCT 4081 GACTAATTTT TTTTATTTAT GCAGAGGCCG AGGCCGCCTC GGCCTCTGAG CTATTCCAGA 4141 AGTAGTGAGG AGGCTTTTTT GGAGGCCTAG GCTTTTGCAA AAAGCTTGAT TCTTCTGACA 4201 CAACAGTCTC GAACTTAAGG CTAGAGCCAC CATGATTGAA CAAGATGGAT TGCACGCAGG 4261 TTCTCCGGCC GCTTGGGTGG AGAGGCTATT CGGCTATGAC TGGGCACAAC AGACAATCGG 4321 CTGCTCTGAT GCCGCCGTGT TCCGGCTGTC AGCGCAGGGG CGCCCGGTTC TTTTTGTCAA 4381 GACCGACCTG TCCGGTGCCC TGAATGAACT GCAGGACGAG GCAGCGCGGC TATCGTGGCT 4441 GGCCACGACG GGCGTTCCTT GCGCAGCTGT GCTCGACGTT GTCACTGAAG CGGGAAGGGA 4501 CTGGCTGCTA TTGGGCGAAG TGCCGGGGCA GGATCTCCTG TCATCTCACC TTGCTCCTGC 4561 CGAGAAAGTA TCCATCATGG CTGATGCAAT GCGGCGGCTG CATACGCTTG ATCCGGCTAC 4621 CTGCCCATTC GACCACCAAG CGAAACATCG CATCGAGCGA GCACGTACTC GGATGGAAGC 4681 CGGTCTTGTC GATCAGGATG ATCTGGACGA AGAGCATCAG GGGCTCGCGC CAGCCGAACT 4741 GTTCGCCAGG CTCAAGGCGC GCATGCCCGA CGGCGAGGAT CTCGTCGTGA CCCATGGCGA 4801 TGCCTGCTTG CCGAATATCA TGGTGGAAAA TGGCCGCTTT TCTGGATTCA TCGACTGTGG 4861 CCGGCTGGGT GTGGCGGACC GCTATCAGGA CATAGCGTTG GCTACCCGTG ATATTGCTGA 4921 AGAGCTTGGC GGCGAATGGG CTGACCGCTT CCTCGTGCTT TACGGTATCG CCGCTCCCGA 4981 TTCGCAGCGC ATCGCCTTCT ATCGCCTTCT TGACGAGTTC TTCTGAGCGG GACTCTGGGG 5041 TTCGAAATGA CCGACCAAGC GACGCCCAAC CTGCCATCAC GATGGCCGCA ATAAAATATC 5101 TTTATTTCA TTACATCTGT GTGTTGGTTT TTTGTGTGAA TCGATAGCGA TAAGGATCCG 5161 CGTATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA 5221. CCCGCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG 5281 ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA 5341 ACGCGCGAGA CGAAAGGGCC TCGTGATACG CCTATTTTTA TAGGTTAATG TCATGATAAT 5401 AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTTG 5461 TTTATTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT 5521 GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCGTG TCGCCCTTAT 5581 TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT 5641 AAAAGATGCT GAAGATCAGT TGGGTGCACG AGTGGGTTAC ATCGAACTGG ATCTCAACAG 5701 CGGTAAGATC CTTGAGAGTT TTCGCCCCGA AGAACGTTTT CCAATGATGA GCACTTTTAA 5761 AGTTCTGCTA TGTGGCGCGG TATTATCCCG TATTGACGCC GGGCAAGAGC AACTCGGTCG-

FIGURE 47C

5821	CCGCATACAC	TATTCTCAGA	ATGACTTGGT	TGAGTACTCA	CCAGTCACAG	AAAAGCATCT
5881	TACGGATGGC	ATGACAGTAA	GAGAATTATG	CAGTGCTGCC	ATAACCATGA	GTGATAACAC
5941	TGCGGCCAAC	TTACTTCTGA	CAACGATCGG	AGGACCGAAG	GAGCTAACCG	CTTTTTTGCA
6001	CAACATGGGG	GATCATGTAA	CTCGCCTTGA	TCGTTGGGAA	CCGGAGCTGA	ATGAAGCCAT
6061	ACCAAACGAC	GAGCGTGACA	CCACGATGCC	TGTAGCAATG	GCAACAACGT	TGCGCAAACT
6121	ATTAACTGGC	GAACTACTTA	CTCTAGCTTC	CCGGCAACAA	TTAATAGACT	GGATGGAGGC
6181	GGATAAAGTT	GCAGGACCAC	TTCTGCGCTC	GGCCCTTCCG	GCTGGCTGGT	TTATTGCTGA
6241	TAAATCTGGA	GCCGGTGAGC	GTGGGTCTCG	CGGTATCATT	GCAGCACTGG	GGCCAGATGG
6301	TAAGCCCTCC	CGTATCGTAG	TTATCTACAC	GACGGGGAGT	CAGGCAACTA	TGGATGAACG
6361	AAATAGACAG	ATCGCTGAGA	TAGGTGCCTC	ACTGATTAAG	CATTGGTAAC	TGTCAGACCA
6421	AGTTTACTCA	TATATACTTT	AGATTGATTT	AAAACTTCAT	TTTTAATTTA	AAAGGATCTA
6481	GGTGAAGATC	CTTTTTGATA	ATCTCATGAC	CAAAATCCCT	TAACGTGAGT	TTTCGTTCCA
6541	CTGAGCGTCA	GACCCCGTAG	AAAAGATCAA	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG
6601	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC	ACCGCTACCA	GCGGTGGTTT	GTTTGCCGGA
6661	TCAAGAGCTA	CCAACTCTTT	TTCCGAAGGT	AACTGGCTTC	AGCAGAGCGC	AGATACCAAA
6721	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG	CCACCACTTC	AAGAACTCTG	TAGCACCGCC
6781	TACATACCTC	GCTCTGCTAA	TCCTGTTACC	AGTGGCTGCT	GCCAGTGGCG	ATAAGTCGTG
6841	TCTTACCGGG	TTGGACTCAA	GACGATAGTT	ACCGGATAAG	GCGCAGCGGT	CGGGCTGAAC
6901	GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC	TACACCGAAC	TGAGATACCT
6961	ACAGCGTGAG	CATTGAGAAA	GCGCCACGCT	TCCCGAAGGG	AGAAAGGCGG	ACAGGTATCC
7021	GGTAAGCGGC	AGGGTCGGAA	CAGGAGAGCG	CACGAGGGAG	CTTCCAGGGG	GAAACGCCTG
7081	GTATCTTTAT	AGTCCTGTCG	GGTTTCGCCA	CCTCTGACTT	GAGCGTCGAT	TTTTGTGATG
7141	CTCGTCAGGG	GGGCGGAGCC	TATGGAAAAA	CGCCAGCAAC	GCGGCCTTTT	TACGGTTCCT
7201	GGCCTTTTGC	TGGCCTTTTG	CTCACATGTT	CTTTCCTGCG	TTATCCCCTG	ATTCTGTGGA
7261	TAACCGTATT	ACCGCCTTTG	AGTGAGCTGA	TACCGCTCGC	CGCAGCCGAA	CGACCGAGCG
7321	CAGCGAGTCA	GTGAGCGAGG	AAGCGGAAGA	GCGCCCAATA	CGCAAACCGC	CTCTCCCCGC
7381	GCGTTGGCCG	ATTCATTAAT	GCAGAGCTTG	CAATTCGCGC	GTTTTTCAAT	ATTATTGAAG
7441	CATTTATCAG	GGTTATTGTC	TCATGAGCGG	ATACATATTT	GAATGTATTT	AGAAAAATAA
7501	ACAAATAGGG	GTTCCGCGCA	CATTTCCCCG	AAAAGTGCCA	CCTGACGTCT	AAGAAACCAT
7561	TATTATCATG	ACATTAACCT	ATAAAAATAG	GCGTAGTACG	AGGCCCTTTC	ACTCATTAGA
	TGCATGTCGT					
7681	GCCCATTGAC	GTCAATAATG	ACGTATGTTC	CCATAGTAAC	GCCAATAGGG	ACTTTCCATT
	GACGTCAATG					
7801	ATATGCCAAG	TACGCCCCCT	ATTGACGTCA	ATGACGGTAA	ATGGCCCGCC	TGGCATTATG
7861	CCCAGTACAT	GACCTTATGG	GACTTTCCTA	CTTGGCAGTA	CATCTACGTA	TTAGTCATCG
	CTATTACCAT					
	CACGGGGATT					
	ATCAACGGGA			ACTCCGCCCC	ATTGACGCAA	ATGGGCGGTA
8101	GGCGTGTACG	GTGGGAGGTC	TAT			

FIGURE 47)

Figure 48 A: pEXP501: pCMV-SPORT 6 host for attB Libraries



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Figure 488: PEXP501 (contid). Features of the att B cloning vector, PEXP501. Bases within hatched area are replaced by cDNA in some LTI cDNA libraries.

+ CMV mena --- aga get egt tta gtg aac egt cag ate gee tgg aga ege cat cea --- tet ega gea aat eac ttg gea gte tag egg ace tet geg gta ggt

ege tgt ttt gae ete eat aga aga eac egg gae ega tee age ete geg aca aaa etg gag gta tet tet gtg gee etg get agg teg gag

LTI YOU PRIME SstI cgg act cta gcc tag gcc gcg gag cgg ata aca att tea cac agg gee tga gat egg ate egg ege ete gee tat tgt taa agt gtg tee

ABI rev primer Sty 586 promiter 586

aaa cag cta tga cca tta ggs cta ttt agg tga cac tat aga aca
ttt gte gat act ggt aat ccg gat aaa tcc act gtg ata tct tgt

agt tog tac aaa aaa gca ggc tog tac cog toc gga att coc ggg tca aac atg ttt ttt cgt ccg act atg gcc agg cct taa ggg ccc

ath/fieg teg/add agd tog/ova/gte gge gge ege det aga gta tee tal/age/age/tge teg agt gat day deg eeg geg aga tot cat agg Ear, I

de gag ggg coe alag ett aleg egt alee eag ett tet tet alea alag gag ede de ggg tte gal teg gda teg gte gan aga alea telt tte

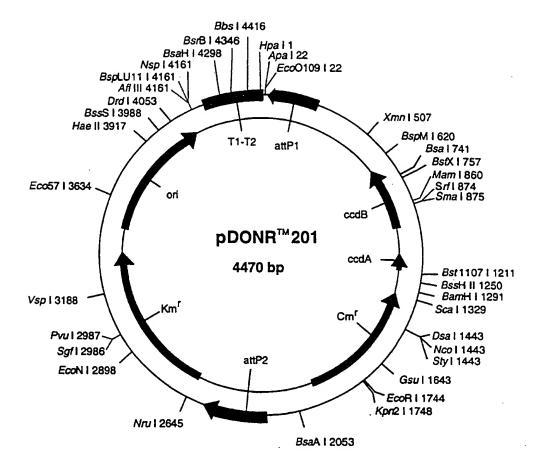
tgg tcc cta tag tga gtc gta tta taa gct agg cac tgg ccg tcg acc and gat atc act cag cat aat att cga tcc gtg acc ggc agc To promotor

nhe ttt tac aac gtc gtg act ggg aaa act gct age ttg gga tct ttg--aaa atg ttg cag cac tga ccc ttt tga cga tdg aac cct aga aac---LTI

## pEXP501 4396 bp

1	CCATTCGCCA	TTCAGGCTGC	GCAACTGTTG	GGAAGGGCGA	TCGGTGCGGG	CCTCTTCGCT
61	ATTACGCCAG	CCAATACGCA	AACCGCCTCT	CCCCGCGCGT	TGGCCGATTC	ATTAATGCAG
121	GATCGATCCA	GACATGATAA	GATACATTGA	TGAGTTTGGA	CAAACCACAA	CTAGAATGCA
181	GTGAAAAAAA	TGCTTTATTT	GTGAAATTTG	TGATGCTATT	GCTTTATTTG	TAACCATTAT
241	AAGCTGCAAT	AAACAAGTTA	ACAACAACAA	TTGCATTCAT	TTTATGTTTC	AGGTTCAGGG
301	GGAGGTGTGG	GAGGTTTTTT	AAAGCAAGTA	AAACCTCTAC	AAATGTGGTA	TGGCTGATTA
361	TGATCATGAA	CAGACTGTGA	GGACTGAGGG	GCCTGAAATG	AGCCTTGGGA	CTGTGAATCT
421	AAAATACACA	AACAATTAGA	ATCACTAGCT	CCTGTGTATA	ATATTTTCAT	AAATCATACT
481	CAGTAAGCAA	AACTCTCAAG	CAGCAAGCAT	ATGCAGCTAG	TTTAACACAT	TATACACTTA
541	AAAATTTTAT	ATTTACCTTA	GAGCTTTAAA	TCTCTGTAGG	TAGTTTGTCC	AATTATGTCA
	CACCACAGAA					
661	GTTGTAAAAC	GACGGCCAGT	GCCTAGCTTA	TAATACGACT	CACTATAGGG	ACCACTTTGT
721	ACAAGAAAGC	TGGGTACGCG	TAAGCTTGGG	CCCCTCGAGG	GATCCTCTAG	AGCGGCCGCC
781	GACTAGTGAG	CTCGTCGACG	ATATCCCGGG	AATTCCGGAC	CGGTACCAGC	CTGCTTTTTT
841	GTACAAACTT	GTTCTATAGT	GTCACCTAAA	TAGGCCTAAT	GGTCATAGCT	GTTTCCTGTG
	TGAAATTGTT					
	TCTTCTATGG					
	ACGAGCTCTG					
1021	GGCGGAGTTG	TTACGACATT	TTGGAAAGTC	CCGTTGATTT	TGGTGCCAAA	ACAAACTCCC
	ATTGACGTCA					
1201	ATTGATGTAC	TGCCAAAACC	GCATCACCAT	GGTAATAGCG	ATGACTAATA	CGTAGATGTA
1261	CTGCCAAGTA	GGAAAGTCCC	ATAAGGTCAT	GTACTGGGCA	TAATGCCAGG	CGGGCCATTT
	ACCGTCATTG					
	GTGGGCAGTT					
	TACTATGGGA					
	AGGCGGGCCA					
	TACTACGCCT					
	GCACTTTTCG					
	ATATGTATCC					
	GCGAATTGCA					
	TTGGGCGCTC					
	GAGCGGTATC					
	CAGGAAAGAA					
1921	TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO	TTTCCATACCA	CTCCCCCCC	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA
	GTCAGAGGTG					
	. CCCTCGTGCG					
						TCGGTGTAGG
						CGCTGCGCCT
						CCACTGGCAG
						GAGTTCTTGA
2341	CAGCCACTGG	TAACAGGATI	אטטאטאטטא זאראטאסאטאזייייי	CCACACTATT	TGGTATCTGC	GCTCTGCTGA
2401	AGIGGIGGCC	. TAMCIACGGC	ACACTAGAA ACACTTCCTT	CONCRUINTI	CGGCDDDCDD	ACCACCGCTG
						GGATCTCAAG
						TCACGTTAAG
						GGCATGAGAT
2641	L GGATTTTGG	CATGCCATAA	CTTCGTATAC	CATACATTAL	ACGAAGIIAI	י אאסראוטאטאו
						AAATCAATCT GAGGCACCTA
						GTGTAGATAA
2883	L CTACGATACO	GGAGGGCTTA	CCATCTGGC	CCAGTGCTGC	AATGATACCC	CGAGACCCAC
						GAGCGCAGAA
						GAAGCTAGAG
306	1 TAAGTAGTT	GCCAGTTAA1	AGTTTGCGC	A ACGTTGTTGC	CATTGCTAC	GGCATCGTGG
312	1 TGTCACGCT	C GTCGTTTGG7	ATGGCTTCA	r TCAGCTCCGC	TTCCCAACG	TCAAGGCGAG-

3181	TTACATGATC	CCCCATGTTG	TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCCT	CCGATCGTTG
3241	TCAGAAGTAA	GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC
3301	TTACTGTCAT	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT
3361	TCTGAGAATA	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA
3421	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA
3481	AACTCTCAAG	GATCTTACCG	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA
3541	ACTGATCTTC	AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC
3601	AAAATGCCGC	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC
3661	TTTTTCAATA	TTATTGAAGC	ATTTATCAGG	GTTATTGTCT	CATGCCAGGG	GTGGGCACAC
3721	ATATTTGATA	CCAGCGATCC	CTACACAGCA	CATAATTCAA	TGCGACTTCC	CTCTATCGCA
3781	CATCTTAGAC	CTTTATTCTC	CCTCCAGCAC	ACATCGAAGC	TGCCGAGCAA	GCCGTTCTCA
3841	CCAGTCCAAG	ACCTGGCATG	AGCGGATACA	TATTTGAATG	TATTTAGAAA	AATAAACAAA
3901	TAGGGGTTCC	GCGCACATTT	CCCCGAAAAG	TGCCACCTGA	AATTGTAAAC	GTTAATATTT
3961	TGTTAAAATT	CGCGTTAAAT	TTTTGTTAAA	TCAGCTCATT	TTTTAACCAA	TAGGCCGAAA
4021	TCGGCAAAAT	CCCTTATAAA	TCAAAAGAAT	AGACCGAGAT	AGGGTTGAGT	GTTGTTCCAG
4081	TTTGGAACAA	GAGTCCACTA	TTAAAGAACG	TGGACTCCAA	CGTCAAAGGG	CGAAAAACCG
4141	TCTATCAGGG	CGATGGCCCA	CTACGTGAAC	CATCACCCTA	ATCAAGTTTT	TTGGGGTCGA
4201	GGTGCCGTAA	AGCACTAAAT	CGGAACCCTA	AAGGGAGCCC	CCGATTTAGA	GCTTGACGGG
4261	GAAAGCCGGC	GAACGTGGCG	AGAAAGGAAG	GGAAGAAAGC	GAAAGGAGCG	GGCGCTAGGG
4321	CGCTGGCAAG	TGTAGCGGTC	ACGCTGCGCG	TAACCACCAC	ACCCGCCGCG	CTTAATGCGC
4381	CGCTACAGGG	CGCGTC				



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#### pDONR201 4470 bp (rotated to position 3516)

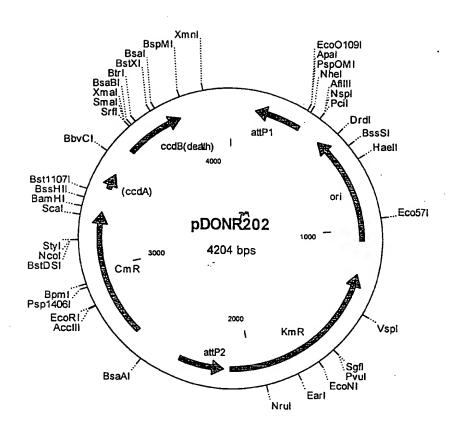
Location (Base Nos.)	Gene Encoded
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656961	ccdB
10991184	ccdA
13031962	CmR
22102442	attP2
25653374	Kmr
34954134	ori

1 GTTAACGCTA GCATGGATCT CGGGCCCCAA ATAATGATTT TATTTTGACT GATAGTGACC 61 TGTTCGTTGC AACAAATTGA TGAGCAATGC TTTTTTATAA TGCCAACTTT GTACAAAAAA 121 GCTGAACGAG AAACGTAAAA TGATATAAAT ATCAATATAT TAAATTAGAT TTTGCATAAA 181 AAACAGACTA CATAATACTG TAAAACACAA CATATCCAGT CACTATGAAT CAACTACTTA 241 GATGGTATTA GTGACCTGTA GTCGACCGAC AGCCTTCCAA ATGTTCTTCG GGTGATGCTG 301 CCAACTTAGT CGACCGACAG CCTTCCAAAT GTTCTTCTCA AACGGAATCG TCGTATCCAG 361 CCTACTCGCT ATTGTCCTCA ATGCCGTATT AAATCATAAA AAGAAATAAG AAAAAGAGGT 421 GCGAGCCTCT TTTTTGTGTG ACAAAATAAA AACATCTACC TATTCATATA CGCTAGTGTC 481 ATAGTCCTGA AAATCATCTG CATCAAGAAC AATTTCACAA CTCTTATACT TTTCTCTTAC 541 AAGTCGTTCG GCTTCATCTG GATTTTCAGC CTCTATACTT ACTAAACGTG ATAAAGTTTC 601 TGTAATTTCT ACTGTATCGA CCTGCAGACT GGCTGTGTAT AAGGGAGCCT GACATTTATA 661 TTCCCCAGAA CATCAGGTTA ATGGCGTTTT TGATGTCATT TTCGCGGTGG CTGAGATCAG 721 CCACTTCTTC CCCGATAACG GAGACCGGCA CACTGGCCAT ATCGGTGGTC ATCATGCGCC 781 AGCTTTCATC CCCGATATGC ACCACCGGGT AAAGTTCACG GGAGACTTTA TCTGACAGCA 841 GACGTGCACT GGCCAGGGG ATCACCATCC GTCGCCCGGG CGTGTCAATA ATATCACTCT 901 GTACATCCAC AAACAGACGA TAACGGCTCT CTCTTTTATA GGTGTAAACC TTAAACTGCA 961 TTTCACCAGT CCCTGTTCTC GTCAGCAAAA GAGCCGTTCA TTTCAATAAA CCGGGCGACC 1021 TCAGCCATCC CTTCCTGATT TTCCGCTTTC CAGCGTTCGG CACGCAGACG ACGGGCTTCA 1081 TTCTGCATGG TTGTGCTTAC CAGACCGGAG ATATTGACAT CATATATGCC TTGAGCAACT 1141 GATAGCTGTC GCTGTCAACT GTCACTGTAA TACGCTGCTT CATAGCACAC CTCTTTTTGA 1201 CATACTTCGG GTATACATAT CAGTATATAT TCTTATACCG CAAAAATCAG CGCGCAAATA 1261 CGCATACTGT TATCTGGCTT TTAGTAAGCC GGATCCACGC GATTACGCCC CGCCCTGCCA 1321 CTCATCGCAG TACTGTTGTA ATTCATTAAG CATTCTGCCG ACATGGAAGC CATCACAGAC 1381 GGCATGATGA ACCTGAATCG CCAGCGGCAT CAGCACCTTG TCGCCTTGCG TATAATATTT 1441 GCCCATGGTG AAAACGGGGG CGAAGAAGTT GTCCATATTG GCCACGTTTA AATCAAAACT 1501 GGTGAAACTC ACCCAGGGAT TGGCTGAGAC GAAAAACATA TTCTCAATAA ACCCTTTAGG 1561 GAAATAGGCC AGGTTTTCAC CGTAACACGC CACATCTTGC GAATATATGT GTAGAAACTG 1621 CCGGAAATCG TCGTGGTATT CACTCCAGAG CGATGAAAAC GTTTCAGTTT GCTCATGGAA 1681 AACGGTGTAA CAAGGGTGAA CACTATCCCA TATCACCAGC TCACCGTCTT TCATTGCCAT 1741 ACGGAATTCC GGATGAGCAT TCATCAGGCG GGCAAGAATG TGAATAAAGG CCGGATAAAA 1801 CTTGTGCTTA TTTTTCTTTA CGGTCTTTAA AAAGGCCGTA ATATCCAGCT GAACGGTCTG 1861 GTTATAGGTA CATTGAGCAA CTGACTGAAA TGCCTCAAAA TGTTCTTTAC GATGCCATTG 1921 GGATATATCA ACGGTGGTAT ATCCAGTGAT TTTTTTCTCC ATTTTAGCTT CCTTAGCTCC 1981 TGANAATCTC GATAACTCAA AAAATACGCC CGGTAGTGAT CTTATTTCAT TATGGTGAAA 2041 GTTGGAACCT CTTACGTGCC GATCAACGTC TCATTTTCGC CAAAAGTTGG CCCAGGGCTT 2101 CCCGGTATCA ACAGGGACAC CAGGATTTAT TTATTCTGCG AAGTGATCTT CCGTCACAGG 2161 TATTTATTCG GCGCAAAGTG CGTCGGGTGA TGCTGCCAAC TTAGTCGACT ACAGGTCACT 2221 AATACCATCT AAGTÄGTTGA TTCATAGTGA CTGGATATGT TGTGTTTTAC AGTATTATGT 2281 AGTCTGTTTT TTATGCAAAA TCTAATTTAA TATATTGATA TTTATATCAT TTTACGTTTC 2341 TCGTTCAGCT TTCTTGTACA AAGTTGGCAT TATAAGAAAG CATTGCTTAT CAATTTGTTG 2401 CAACGAACAG GTCACTATCA GTCAAAATAA AATCATTATT TGCCATCCAG CTGCAGCTCT 2461 GGCCCGTGTC TCAAAATCTC TGATGTTACA TTGCACAAGA TAAAAATATA TCATCATGAA 2521 CAATAAAACT GTCTGCTTAC ATAAACAGTA ATACAAGGGG TGTTATGAGC CATATTCAAC 2581 GGGAAACGTC GAGGCCGCGA TTAAATTCCA ACATGGATGC TGATTTATAT GGGTATAAAT 2641 GGGCTCGCGA TAATGTCGGG CAATCAGGTG CGACAATCTA TCGCTTGTAT GGGAAGCCCG 2701 ATGCGCCAGA GTTGTTTCTG AAACATGGCA AAGGTAGCGT TGCCAATGAT GTTACAGATG~

2761	AGATGGTCAG	ACTAAACTGG	CTGACGGAAT	TTATGCCTCT	TCCGACCATC	AAGCATTTTA
2821	TCCGTACTCC	TGATGATGCA	TGGTTACTCA	CCACTGCGAT	CCCCGGAAAA	ACAGCATTCC
2881	AGGTATTAGA	AGAATATCCT	GATTCAGGTG	AAAATATTGT	TGATGCGCTG	GCAGTGTTCC
2941	TGCGCCGGTT	GCATTCGATT	CCTGTTTGTA	ATTGTCCTTT	TAACAGCGAT	CGCGTATTTC
3001	GTCTCGCTCA	GGCGCAATCA	CGAATGAATA	ACGGTTTGGT	TGATGCGAGT	GATTTTGATG
3061	ACGAGCGTAA	TGGCTGGCCT	GTTGAACAAG	TCTGGAAAGA	AATGCATAAA	CTTTTGCCAT
3121	TCTCACCGGA	TTCAGTCGTC	ACTCATGGTG	ATTTCTCACT	TGATAACCTT	ATTTTTGACG
3181	AGGGGAAATT	AATAGGTTGT	ATTGATGTTG	GACGAGTCGG	AATCGCAGAC	CGATACCAGG
3241	ATCTTGCCAT	CCTATGGAAC	TGCCTCGGTG	AGTTTTCTCC	TTCATTACAG	AAACGGCTTT
3301	TTCAAAAATA	TGGTATTGAT	AATCCTGATA	TGAATAAATT	GCAGTTTCAT	TTGATGCTCG
3361	ATGAGTTTTT	CTAATCAGAA	TTGGTTAATT	GGTTGTAACA	CTGGCAGAGC	ATTACGCTGA
3421	CTTGACGGGA	CGGCGCAAGC	TCATGACCAA	AATCCCTTAA	CGTGAGTTTT	CGTTCCACTG
3481	AGCGTCAGAC	CCCGTAGAAA	AGATCAAAGG	ATCTTCTTGA	GATCCTTTTT	TTCTGCGCGT
3541	AATCTGCTGC	TTGCAAACAA	AAAAACCACC	GCTACCAGCG	GTGGTTTGTT	TGCCGGATCA
3601	AGAGCTACCA	ACTCTTTTTC	CGAAGGTAAC	TGGCTTCAGC	AGAGCGCAGA	TACCAAATAC
3661	TGTCCTTCTA	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	CACCGCCTAC
3721	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT
3781	TACCGGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	CAGCGGTCGG	GCTGAACGGG
3841	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG	AACGACCTAC	ACCGAACTGA	GATACCTACA
3901	GCGTGAGCTA	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGCGGACA	GGTATCCGGT
3961	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA
4021	TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	TGTGATGCTC
4081	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	CAGCAACGCG	GCCTTTTTAC	GGTTCCTGGC
4141	CTTTTGCTGG	CCTTTTGCTC	ACATGTTCTT	TCCTGCGTTA	TCCCCTGATT	CTGTGGATAA
4201	CCGTATTACC	GCTAGCCAGG	AAGAGTTTGT	AGAAACGCAA	AAAGGCCATC	CGTCAGGATG
4261	GCCTTCTGCT	TAGTTTGATG	CCTGGCAGTT	TATGGCGGGC	GTCCTGCCCG	CCACCCTCCG
4321	GGCCGTTGCT	TCACAACGTT	CAAATCCGCT	CCCGGCGGAT	TTGTCCTACT	CAGGAGAGCG
4381	TTCACCGACA	AACAACAGAT	AAAACGAAAG	GCCCAGTCTT	CCGACTGAGC	CTTTCGTTTT
4441	ATTTGATGCC	TGGCAGTTCC	CTACTCTCGC			

FIGURE 49C

0/52027 147/240 FIGURE 50A: PDONRZOZ (KanĒ)



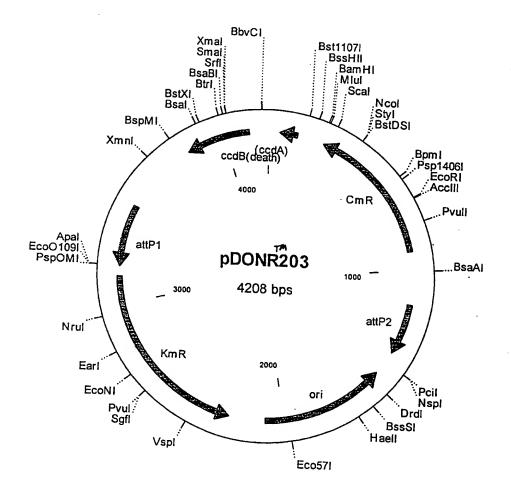
Gene Encoded

### pDONR202 4204 bp

Location (Base Nos.)

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		122821	.07	KmR		
		238121		attP2		
		262932		CmR		
		340834			vated ccdA	
		363039		ccdB	.vacca ccan	
				0000		
1	CGGCATTGAG	GACAATAGCG	AGTAGGCTGG	ATACGACGAT	TCCGTTTGAG	AAGAACATTT
				ATCACCCGAA		
121	GTCGACTACA	GGTCACTAAT	ACCATCTAAG	TAGTTGATTC	ATAGTGACTG	GATATGTTGT
181	GTTTTACAGT	ATTATGTAGT	CTGTTTTTTA	TGCAAAATCT	AATTTAATAT	ATTGATATTT
241	ATATCATTTT	ACGTTTCTCG	TTCAGCTTTT	TTGTACAAAG	TTGGCATTAT	AAAAAAGCAT
				ACTATCAGTC		
				TTATCCACAG		
				GCCAGGAACC		
				GAGCATCACA		
541	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	TTCCCCCTGG	AAGCTCCCTC
601	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	TGTCCGCCTT	TCTCCCTTCC
661	GGAAGCGTGG	CGCTTTCTCA	TAGCTCACGC	TGTAGGTATC	TCAGTTCGGT	CTACCTCCTT
				CCCGTTCAGC		
				AGACACGACT		
				GTAGGCGGTG		
				GTATTTGGTA		
961	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA	AACAAACCAC	CCCTCCTACC
1021	GGTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	ACGCGCAGAA	AAAAAGGATC	TCAAGAAGAT
1081	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAACG	AAAACTCACG	TTAACCCATT
1141	TTGGTCATGA	GCTTGCGCCG	TCCCGTCAAG	TCAGCGTAAT	CCTCTCCCAC	TCTTACAGCATI
1201	AATTAACCAA	TTCTGATTAG	AAAAACTCAT	CGAGCATCAA	ATGAAACTGC	A A TOTAL A TOTAL A
1261	TATCAGGATT	ATCAATACCA	ממטיידידידים	AAAGCCGTTT	CTCTANTCAN	CCACAAAACT
				CCTGGTATCG		
1381	CAACATCAAT	ACAACCTATT	AATTTCCCCT	CGTCAAAAAT	ANGGTTATCA	ACTCACACAC
1441	CACCATGAGT	GACGACTGAA	TCCGGTGAGA	ATGGCAAAAG	TOTALCA	TOTTTCCACA
1501	CTTGTTCAAC	AGGCCAGCCA	TTACGCTCGT	CATCAAAATC	TITALGCALL	ACCANACCOM
1561	TATTCATTCG	TGATTGCGCC	TGAGCGAGAC	GAAATACGCG	ACTOGCATCA	ACCAAACCGI
1621	TACAAACAGG	AATCGAATGC	AACCGCCGCA	GGAACACTGC	CACCCCATCA	AAAGGACAA1
1681	CACCTGAATC	AGGATATTCT	TOTALTACOT	GGAATGCTGT	TTTTTCCCCCC	ACAATATTT
1741	TGAGTAACCA	TGCATCATCA	GCAGTACCCA	TAAAATGCTT	CATCCTCCCA	ACCCCAGTGG
1801	ATTCCGTCAG	CCAGTTTAGT	CTGACCATCT	CATCTGTAAC	AMCAMMCCCA	AGAGGCATAA
1861	TGCCATGTTT	CAGAAACAAC	TOTOGCOCAT	CGGGCTTCCC	ATCATIGGCA	ACGCTACCTT
1921	CACCTGATTG	CCCGACATTA	TCGCGAGCCC	ATTTATACCC	ATACAAGCGA	CCAMGGAMGM
1981	TGGAATTTAA	TCGCGGCCTC	GACGTTTCCC	GTTGAATATG	CCTCATAACA	COCOMMONA
2041	ТАСТСТТТАТ	GTAAGCAGAC	ACTTTTTATTC	TTCATGATGA	TATA TOTAL	CCCCTTGTAT
2101	ТСТААСАТСА	GAGATTTTCA	GACACGGGGG	AGAGCTGCAG	CECCAECCA	1CTTGTGCAA
2161	TTATTTTCAC	TCATACTCAC	CTCTTCCTTC	CAACAAATTG	ATTACCATO	AATAATGATT
2221	ATGCCAACTT	TOTACAACAA	ACCTCAACCA	GAAACGTAAA	ATAAGCAATG	CTTTCTTATA
2281	TTAAATTAGA	TTTTCCARGAA	ANDROGACOM	ACATAATACT	ATGATATAAA	TATCAATATA
2341	TCACTATGAA	TCDDCTAC	ACATCOTATE	ACATAATACT	JAAAACACA	ACATATCCAG
2401	TCACCCCACC	CPCLACIACII	CCANTANANT	CCTGTGACGG	AGTCGACTAA	GTTGGCAGCA
2461	ATANATOOTO	GTGTCCCTCT	TCAMIMAMIA	AAGCCCTGGG	AAGATCACTT	CGCAGAATAA
2521	CDCCTTCTC	GCCACCTGI	ACCUMPOUS SO	MAGCCCTGGG	CCAACTTTTG	GCGAAAATGA
2521	CCCCTATORIC	THE PERSONAL	CACATTOCAAC	TTTCACCATA	ATGAAATAAG	ATCACTACCG
2641	ATCACTCCAT	ATACCACCOM	TCATATATATCA	GGAGCTAAGG CAATGGCATC	AAGCTAAAAT	GGAGAAAAA
2701	TOTAL TOTAL	TTCCTCAAAC	TOMINIALCC	CAATGGCATC	GTAAAGAACA	TTTTGAGGCA
2 / U I	TITCAGICAG	LIGCICAATG	TACCTATAAC	CAGACCGTTC	AGCTGGATAT	TACGGCCTTT ~

2761	TTAAAGACCG	TAAAGAAAAA	TAAGCACAAG	TTTTATCCGG	${\tt CCTTTATTCA}$	CATTCTTGCC
2821	CGCCTGATGA	ATGCTCATCC	GGAATTCCGT	ATGGCAATGA	AAGACGGTGA	GCTGGTGATA
2881	TGGGATAGTG	TTCACCCTTG	TTACACCGTT	TTCCATGAGC	AAACTGAAAC	GTTTTCATCG
2941	CTCTGGAGTG	AATACCACGA	CGATTTCCGG	CAGTTTCTAC	ACATATATTC	GCAAGATGTG
3001	GCGTGTTACG	GTGAAAACCT	GGCCTATTTC	CCTAAAGGGT	TTATTGAGAA	TATGTTTTTC
3061	GTCTCAGCCA	ATCCCTGGGT	GAGTTTCACC	AGTTTTGATT	TAAACGTGGC	CAATATGGAC
3121	AACTTCTTCG	CCCCCGTTTT	CACCATGGGC	AAATATTATA	CGCAAGGCGA	CAAGGTGCTG
3181	ATGCCGCTGG	CGATTCAGGT	TCATCATGCC	GTCTGTGATG	GCTTCCATGT	CGGCAGAATG
3241	CTTAATGAAT	TACAACAGTA	CTGCGATGAG	TGGCAGGGCG	GGGCGTAATC	GCGTGGATCC
3301	GGCTTACTAA	AAGCCAGATA	ACAGTATGCG	TATTTGCGCG	CTGATTTTTG	CGGTATAAGA
3361	ATATATACTG	ATATGTATAC	CCGAAGTATG	TCAAAAAGAG	GTGTGCTATG	AAGCAGCGTA
3421	TTACAGTGAC	AGTTGACAGC	GACAGCTATC	AGTTGCTCAA	GGCATATATG	ATGTCAATAT
3481	CTCCGGTCTG	GTAAGCACAA	CCATGCAGAA	TGAAGCCCGT	CGTCTGCGTG	CCGAACGCTG
3541	GAAAGCGGAA	AATCAGGAAG	GGATGGCTGA	GGTCGCCCGG	TTTATTGAAA	TGAACGGCTC
3601	TTTTGCTGAC	GAGAACAGGG	ACTGGTGAAA	TGCAGTTTAA	GGTTTACACC	TATAAAAGAG
3661	AGAGCCGTTA	TCGTCTGTTT	GTGGATGTAC	AGAGTGATAT	TATTGACACG	CCCGGGCGAC
3721	GGATGGTGAT	CCCCCTGGCC	AGTGCACGTC	TGCTGTCAGA	TAXAGTCTCC	CGTGAACTTT
3781	ACCCGGTGGT	GCATATCGGG	GATGAAAGCT	GGCGCATGAT	GACCACCGAT	ATGGCCAGTG
3841	TGCCGGTCTC	CGTTATCGGG	GAAGAAGTGG	CTGATCTCAG	CCACCGCGAA	AATGACATCA
3901	AAAACGCCAT	TAACCTGATG	TTCTGGGGAA	TATAAATGTC	AGGCTCCCTT	ATACACAGCC
3961	AGTCTGCAGG	TCGATACAGT	AGAAATTACA	GAAACTTTAT	CACGTTTAGT	AAGTATAGAG
4021	GCTGAAAATC	CAGATGAAGC	CGAACGACTT	GTAAGAGAAA	AGTATAAGAG	TTGTGAAATT
4081	GTTCTTGATG	CAGATGATTT	TCAGGACTAT	GACACTAGCG	TATATGAATA	GGTAGATGTT
4141	TTTATTTTGT	CACACAAAAA	AGAGGCTCGC	ACCTCTTTTT	CTTATTTCTT	TTTATGATTT
4201	AATA					



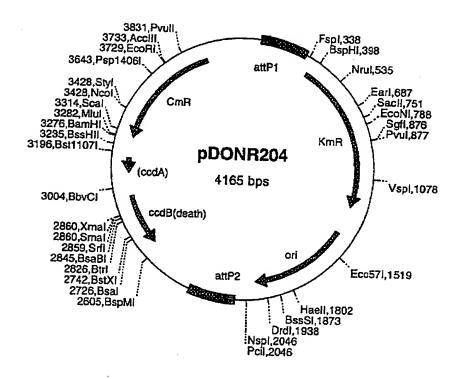
### pDONR203 4208 bp

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15092082	ori
22513130	KmR
34643174	attP1
38124117	ccdB

		381241	17	ccdB		
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		TATATGCCTT				
		TAGCACACCT				
		AAAATCAGCG				
		TTACGCCCCG				
		ATGGAAGCCA				
		GCCTTGCGTA				
		CACGTTTAAA				
		CTCAATAAAC				
		ATATATGTGT				
		TTCAGTTTGC				
		ACCGTCTTTC				
		AATAAAGGCC				
		ATCCAGCTGA				
		TTCTTTACGA				
		TTTAGCTTCC				
		TATTTCATTA				
		AAAGTTGGCC				
		GTGATCTTCC				
		AGTCGACTAC				
		TGTTTTACAG				
		TATATCATTT				
		TTGCTTATCA				
		CCATCCAGCT				
		TGTGAGCAAA				
		TCCATAGGCT				
		GAAACCCGAC				
		CTCCTGTTCC				
		TGGCGCTTTC				
		AGCTGGGCTG				
		ATCGTCTTGA				
		ACAGGATTAG				
		ACTACGGCTA				
		TCGGAAAAAG				
		TTTTTGTTTG				
		TCTTTTCTAC				
		TGAGCTTGCG				
		CAATTCTGAT				
		ATTATCAATA				
		GCAGTTCCAT				
		AATACAACCT				
		AGTGACGACT				
		AACAGGCCAG				
		TCGTGATTGC				
		AGGAATCGAA				
2701	L TTTCACCTGA	A ATCAGGATAT	TCTTCTAATA	A CCTGGAATGO	TGTTTTTCCG	GGGATCGCAG-

2761	TGGTGAGTAA	CCATGCATCA	TCAGGAGTAC	GGATAAAATG	CTTGATGGTC	GGAAGAGGCA
2821	TAAATTCCGT	CAGCCAGTTT	AGTCTGACCA	TCTCATCTGT	AACATCATTG	GCAACGCTAC
2881	CTTTGCCATG	TTTCAGAAAC	AACTCTGGCG	CATCGGGCTT	CCCATACAAG	CGATAGATTG
2941	TCGCACCTGA	TTGCCCGACA	TTATCGCGAG	CCCATTTATA	CCCATATAAA	TCAGCATCCA
3001	TGTTGGAATT	TAATCGCGGC	CTCGACGTTT	CCCGTTGAAT	ATGGCTCATA	ACACCCCTTG
3061	TATTACTGTT	TATGTAAGCA	GACAGTTTTA	TTGTTCATGA	TGATATATTT	TTATCTTGTG
3121	CAATGTAACA	TCAGAGATTT	TGAGACACGG	GCCAGAGCTG	CAGCTAGCAT	GGATCTCGGG
3181	CCCCAAATAA	TGATTTTATT	TTGACTGATA	GTGACCTGTT	CGTTGCAACA	AATTGATGAG
3241	CAATGCTTTT	TTATAATGCC	AACTTTGTAC	AAAAAAGCTG	AACGAGAAAC	GTAAAATGAT
3301	ATAAATATCA	ATATATTAAA	TTAGATTTTG	CATAAAAAAC	AGACTACATA	ATACTGTAAA
3361	ACACAACATA	TCCAGTCACT	ATGAATCAAC	TACTTAGATG	GTATTAGTGA	CCTGTAGTCG
3421	ACCGACAGCC	TTCCAAATGT	TCTTCGGGTG	ATGCTGCCAA	CTTAGTCGAC	CGACAGCCTT
3481	CCAAATGTTC	TTCTCAAACG	GAATCGTCGT	ATCCAGCCTA	CTCGCTATTG	TCCTCAATGC
3541	CGTATTAAAT	CATAAAAAGA	AATAAGAAAA	AGAGGTGCGA	GCCTCTTTTT	TGTGTGACAA
3601	AATAAAAACA	TCTACCTATT	CATATACGCT	AGTGTCATAG	TCCTGAAAAT	CATCTGCATC
3661	AAGAACAATT	TCACAACTCT	TATACTTTTC	TCTTACAAGT	CGTTCGGCTT	CATCTGGATT
3721	TTCAGCCTCT	ATACTTACTA	AACGTGATAA	AGTTTCTGTA	ATTTCTACTG	TATCGACCTG
3781	CAGACTGGCT	GTGTATAAGG	GAGCCTGACA	TTTATATTCC	CCAGAACATC	AGGTTAATGG
3841	CGTTTTTGAT	GTCATTTTCG	CGGTGGCTGA	GATCAGCCAC	TTCTTCCCCG	ATAACGGAGA
3901	CCGGCACACT	GGCCATATCG	GTGGTCATCA	TGCGCCAGCT	TTCATCCCCG	ATATGCACCA
3961	CCGGGTAAAG	TTCACGGGAG	ACTTTATCTG	ACAGCAGACG	TGCACTGGCC	AGGGGGATCA
4021	CCATCCGTCG	CCCGGGCGTG	TCAATAATAT	CACTCTGTAC	ATCCACAAAC	AGACGATAAC
4081	GGCTCTCTCT	TTTATAGGTG	TAAACCTTAA	ACTGCATTTC	ACCAGTCCCT	GTTCTCGTCA
4141	GCAAAAGAGC	CGTTCATTTC	AATAAACCGG	GCGACCTCAG	CCATCCCTTC	CTGATTTTCC
4201	GCTTTCCA					

NO 00/52027 153/240 FIGURE 52A PDOURZOY (KANR)



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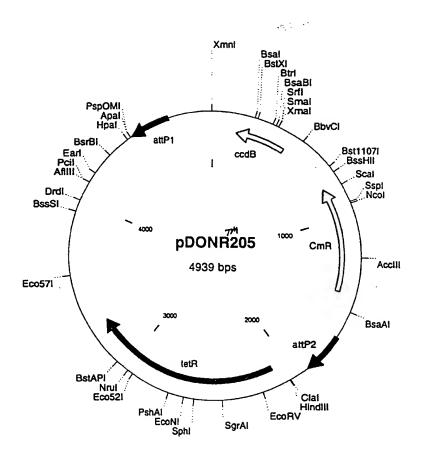
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121	TGGATATGTT	GTGTTTTACA	GTATTATGTA	GTCTGTTTTT	TATGCAAAAT	CTAATTTAAT
181	ATATTGATAT	TTATATCATT	TTACGTTTCT	CGTTCAGCTT	TTTTGTACAA	AGTTGGCATT
241	ATAAAAAAGC	ATTGCTTATC	AATTTGTTGC	AACGAACAGG	TCACTATCAG	TCAAAATAAA
301	ATCATTATTT	GGGGCCCGAG	ATCCATGCTA	GCTGCAGTGC	GCAGGGCCCG	TGTCTCAAAA
361	TCTCTGATGT	TACATTGCAC	AAGATAAAAA	TATATCATCA	TGAACAATAA	AACTGTCTGC
421	TTACATAAAC	AGTAATACAA	GGGGTGTTAT	GAGCCATATT	CAACGGGAAA	CGTCTTGCTG
481	GAGGCCGCGA	TTAAATTCCA	ACATGGATGC	TGATTTATAT	GGGTATAAAT	GGGCTCGCGA
541	TAATGTCGGG	CAATCAGGTG	CGACAATCTT	TCGATTGTAT	GGGAAGCCCG	ATGCGCCAGA
601	GTTGTTTCTG	AAACATGGCA	AAGGTAGCGT	TGCCAATGAT	GTTACAGATG	AGATGGTCAG
661	ACTAAACTGG	CTGACGGAAT	TTATGCCTCT	TCCGACCATC	AAGCATTTTA	TCCGTACTCC
721	TGATGATGCA	TGGTTACTCA	CCACTGCGAT	CCGCGGGAAA	ACAGCATTCC	AGGTATTAGA
781	AGAATATCCT	GATTCAGGTG	AAAATATTGT	TGATGCGCTG	GCAGTGTTCC	TGCGCCGGTT
841	GCATTCGATT	CCTGTTTGTA	ATTGTCCTTT	TAACAGCGAT	CGCGTATTTC	GTCTCGCTCA
901	GGCGCAATCA	CGAATGAATA	ACGGTTTGGT	TGATGCGAGT	GATTTTGATG	ACGAGCGTAA
961	TGGCTGGCCT	GTTGAACAAG	TCTGGAAAGA	AATGCATACG	CTTTTGCCAT	TCTCACCGGA
1021	TTCAGTCGTC	ACTCATGGTG	ATTTCTCACT	TGATAACCTT	ATTTTTGACG	AGGGGAAATT
1081	AATAGGTTGT	ATTGATGTTG	GACGAGTCGG	AATCGCAGAC	CGATACCAGG	ATCTTGCCAT
1141	CCTATGGAAC	TGCCTCGGTG	AGTTTTCTCC	TTCATTACAG	AAACGGCTTT	TTCAAAAATA
1201	TGGTATTGAT	AATCCTGATA	TGAATAAATT	GCAGTTTCAT	TTGATGCTCG	ATGAGTTTTT
1261	CTAATCAGAA	TTGGTTAATT	GGTTGTAACA	CTGGCAGAGC	ATTACGCTGA	CTTGACGGGA
1321	CGGCGNCATG	ACCAAAATCC	CTTAACGTGA	GTTTTCGTTC	CACTGAGCGT	CAGACCCCGT
1381	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTCTG	CGCGTAATCT	GCTGCTTGCA
1441	AACAAAAAA	CCACCGCTAC	CAGCGGTGGT	TTGTTTGCCG	GATCAAGAGC	TACCAACTCT
1501	TTTTCCGAAG	GTAACTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	TTCTAGTGTA
1561	GCCGTAGTTA	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC	TCGCTCTGCT
1621	AATCCTGTTA	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG	TGTCTTACCG	GGTTGGACTC
1681	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	CGTGCACACA
1741	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC	CTACAGCGTG	AGCTATGAGA
1801	AAGCGCCACG	CTTCCCGAAG	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	GCAGGGTCGG
1861	AACAGGAGAG	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	ATAGTCCTGT
1921	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	GGGGGCGGAG
1981	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC	CTGGCCTTTT	GCTGGCCTTT
2041	TGCTCACATG	TTCTTTCCTG	CGTTATCCCC	TGATTCTGTG	GATAACCGTA	TTACCGCTAG
2101	CTGGATCGGC	AAATAATGAT	TTTATTTTGA	CTGATAGTGA	CCTGTTCGTT	GCAACAAATT
2161	GATAAGCAAT	GCTTTTTTAT	AATGCCAACT	TTGTACAAGA	AAGCTGAACG	AGAAACGTAA
2221	AATGATATAA	ATATCAATAT	ATTAAATTAG	ATTTTGCATA	AAAAACAGAC	TACATAATAC
2281	TGTAAAACAC	AACATATCCA	GTCACTATGA	TTCAACTACT	TAGATGGTAT	TAGTGACCTG
2341	TAGTCGACTA	AGTTGGCAGC	ATCACCCGAC	GCACTTTGCG	CCGAATAAAT	ACCTGTGACG
2401	GAAGATCACT	TCGCAGAATA	AATAAATCCT	GGTGTCCCTG	TTGATACCGG	GAAGCCCTGG
2461	GCCAACTTTT	GGCGAAAATG	AGACGTTGAT	CGGCACATTT	CACAACTCTT	ATACTTTTCT
2521	CTTACAAGTC	GTTCGGCTTC	ATCTGGATTT	TCAGCCTCTA	TACTTACTAA	ACGTGATAAA
2581	GTTTCTGTAA	TTTCTACTGT	ATCGACCTGC	AGACTGGCTG	TGTATAACGG	AGCCTGACAT
2641	TTATATTCCC	CAGAACATCA	GGTTAATGGC	GTTTTTGATG	TCATTTTCGC	GGTGGCTGAG
2701	ATCAGCCACT	TCTTCCCCGA	TAACGGAGAC	CGGCACACTG	GCCATATCGG	TGGTCATCAT
2761	GCGCCAGCTT	TCATCCCCGA	TATGCACCAC	CGGGTAAAGT	TCACGGGAGA	CTTTATCTGA
2821	CAGCAGACGT	GCACTGGCCA	GGGGGATCAC	CATCCGTCGC	CCGGGCGTGT	CAATAATATC
2881	ACTCTGTACA	TCCACAAACA	GACGATAACG	GCTCTCTCTT	TTATAGGTGT	AAACCTTAAA
2941	CTGCATTTCA	CCAGTCCCTG	TTCTCGTCAG	CAAAAGAGCC	GTTCATTTCA	ATAAACCGGG
3001	CGACCTCAGC	CATCCCTTCC	TGATTTTCCG	CTTTCCAGCG	TTCGGCACGC	AGACGACGGG
						ATGCCTTGAG
3121	CAACTGATAG	CTGTCGCTGT	CAACTGTCAC	TGTAATACGC	TGCTTCATAG	CACACCTCTT-

FIGURE 52B

3181	TTTGACATAC	TTCGGGTATA	CATATCAGTA	TATATTCTTA	TACCGCAAAA	ATCAGCGCGC
3241	AAATACGCAT	ACTGTTATCT	GGCTTTTAGT	AAGCCGGATC	CACGCGTTTA	CGCCCCGCCC
3301	TGCCACTCAT	CGCAGTACTG	TTGTAATTCA	TTAAGCATTC	TGCCGACATG	GAAGCCATCA
3361	CAGACGGCAT	GATGAACCTG	AATCGCCAGC	GGCATCAGCA	CCTTGTCGCC	TTGCGTATAA
3421	TATTTGCCCA	TGGTGAAAAC	GGGGGCGAAG	AAGTTGTCCA	TATTGGCCAC	GTTTAAATCA
3481	AAACTGGTGA	AACTCACCCA	GGGATTGGCT	GAGACGAAAA	ACATATTCTC	AATAAACCCT
3541	TTAGGGAAAT	AGGCCAGGTT	TTCACCGTAA	CACGCCACAT	CTTGCGAATA	TATGTGTAGA
3601	AACTGCCGGA	AATCGTCGTG	GTATTCACTC	CAGAGCGATG	AAAACGTTTC	AGTTTGCTCA
3661	TGGAAAACGG	TGTAACAAGG	GTGAACACTA	TCCCATATCA	CCAGCTCACC	GTCTTTCATT
3721	GCCATACGGA	ATTCCGGATG	AGCATTCATC	AGGCGGGCAA	GAATGTGAAT	AAAGGCCGGA
3781	TAAAACTTGT	GCTTATTTTT	CTTTACGGTC	TTTAAAAAGG	CCGTAATATC	CAGCTGAACG
3841	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	TGAAATGCCT	CAAAATGTTC	TTTACGATGC
3901	CATTGGGATA	TATCAACGGT	GGTATATCCA	GTGATTTTTT	TCTCCATTTT	AGCTTCCTTA
3961	GCTCCTGAAA	ATCTCGATAA	CTCAAAAAAT	ACGCCCGGTA	GTGATCTTAT	TTCATTATGG
4021	TGAAAGTTGG	AACCTCTTAC	TGTTCTTGAT	GCAGATGATT	TTCAGGACTA	TGACACTAGC
4081	ATATATGAAT	AGGTAGATGT	TTTTATTTTG	TCACACAAAA	AAGAGGCTCG	CACCTCTTTT
4141	TCTTATTTCT	TTTTATGATT	TAATA			

FIGURE 52C

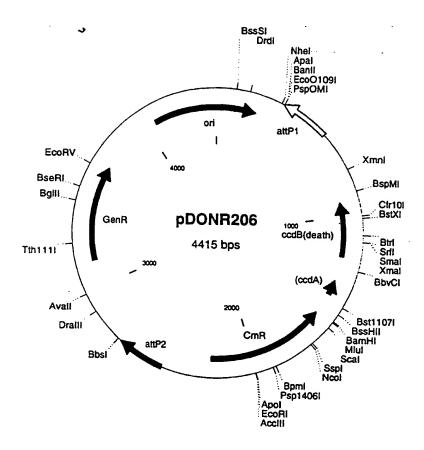
Figure 53A; pDONR205 (tetR)



#### pDONR205 4939 bp

GGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGGGCGAAG AAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACCCAGGGATTGGCT GAGACGAAAAACATATTCTCAATAAACCCTTTAGGGAAATAGGCCAGGTTTTCACCGTAA CACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATCGTCGTGGTATTCACTC  ${\tt CAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAAGGGTGAACACTA}$ TCCCATATCACCAGCTCACCGTCTTTCATTGCCATACGGAATTCCGGATGAGCATTCATC AGGCGGGCAAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTTTTCTTTACGGTC TTTAAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACATTGAGCAACTGAC TGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCA GTGATTTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGATAACTCAAAAAAT  ${\tt ACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTTACGTGCCGATCA}$ ACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAGGA GGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCAT AGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAA TTTAATATATGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTT GGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAA AATAAAATCATTATTTGCCATCCAGCTGCAGCTCTGGCCCGTGTCTCAAAATCTCTGATG TTACATTGCACAAGATAAAAATATATCATCATGAATTCTCATGTTTGACAGCTTATCATC GATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGCACCGTGT ATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGCTGTAGGC ATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTCCGACAGC ATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGCGCA CCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCCCAGTCCTGCTTCGCTA CTTGGAGCCACTATCGACTACGCGATCATGGCGACCACCCCGTCCTGTGGATCCTCTAC GCCGGACGCATCGTGGCCGCCATCACCGGCGCCCACAGGTGCGGTTGCTGGCGCCTATATC GCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGCTTGTTTC GGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGGACTGTTGGGCGCCATCTCCTTGCAT GCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACCTACTACTGGGCTGCTTCCTA ATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTC AGCTCCTTCCGGTGGGCGCGGGCATGACTATCGTCGCCGCACTTATGACTGTCTTCTTT ATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGC TTTCGCTGGAGCGCGATGATCGGCCTGTCGCTTGCGGTATTCGGAATCTTGCACGCC CTCGCTCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCGAGAAGCAGGCCATT ATCGCCGGCATGGCGGCCGACGCGTGGGCTACGTCTTGCTGGCGTTCGCGACGCGAGGC TGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCATCGGGATGCCCGCGTTG CAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGACAGCTTCAAGGATCGCTC GCGGCTCTTACCAGCCTAACTTCGATCATTGGACCGCTGATCGTCACGGCGATTTATGCC GCCTCGGCGAGCACATGGAACGGGTTGGCATGGATTGTAGGCGCCGCCCTATACCTTGTC TGCCTCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAATGGAAGCC GAACTGTGAATGCGCAAACCAACCCTTGGCAGAACATATCCATCGCATGACCAAAATCCC TTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTC AGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTT CAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTT CAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGC TGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA GGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACCCCAGCTTGGAGCGAACGAC CTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGG GAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGA GCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACT  CGCGGCCTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGC GTTATCCCCTGATTCTGTGGATAACCGTATTACCGCTAGCCAGGAAGAGTTTGTAGAAAC GCAAAAAGGCCATCCGTCAGGATGGCCTTCTGCTTAGTTTGATGCCTGGCAGTTTATGGC GGGCGTCCTGCCCGCCACCCTCCGGGCCGTTGCTTCACAACGTTCAAATCCGCTCCCGGC GGATTTGTCCTACTCAGGAGAGCGTTCACCGACAAACAACAGATAAAACGAAAGGCCCAG TCTTCCGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTCTCGCGTTAAC GCTAGCATGGATCTCGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCG TTGCAACAAATTGATGAGCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAAGCTGAA CGAGAAACGTAAAATGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAACAG ACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGT ATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACT TAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACT CTCTTTTTTGTGTGACAAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTC CTGAAAATCATCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCG TTCGGCTTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAAT  ${\tt TTCTACTGTATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCC}$ AGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTT CTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTT CATCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTG CACTGGCCAGGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACAT CCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCAC CAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCC ATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGGGCTTCATTCTGC ATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGC TGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTTGACATACT TCGGGTATACATATCAGTATATATTCTTATACCGCAAAAATCAGCGCGCAAATACGCATA CTGTTATCTGGCTTTTAGTAAGCCGGATCCACGCGATTACGCCCCGCCCTGCCACTCATC GCAGTACTGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAGACGGCATG ATGAACCTGAATCGCCAGC

FIGURE 53C



#### pDONR206 4415 bp

CGGCATTGAGGACAATAGCGAGTAGGCTGGATACGACGATTCCGTTTGAGAAGAACATTT GGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGAATCATAGTGAC TGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAAT ATATTGATATTTATCATTTTACGTTTCTCGTTCAGCTTTTTTGTACAAAGTTGGCATT ATAAAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAA ATCATTATTTGGGGCCCGAGATCCATGCTAGCGGTAATACGGTTATCCACAGAATCAGGG GATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAG GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC TTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCG GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCT ACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA TCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA CGTTAAGGGATTTTGGTCATGNCGCCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGT TACAACCAATTAACCAATTCTGATTAGAAAAACTCATCGAGCATCAAATGAAACTGCAAT TTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGA GAAAACTCACCGAGGCAGTTCCATAGGATGCCAAGATCCTGGTATCGGTCTGCGATTCCG ACTCGTCCAACATCAATACAACCTATTAGCCGAGGTCTTCCGATCTCCTGAAGCCAGGGC AGATCCGTGCACAGCACCTTGCCGTAGAAGAACAGCAAGGCCGCCAATGCCTGACGATGC GTGGAGACCGAAACCTTGCGCTCGTTCGCCAGCCAGGACAGAAATGCCTCGACTTCGCTG CTGCCCAAGGTTGCCGGGTGACGCACACCGTGGAAACGGATGAAGGCACGAACCCAGTTG ACATAAGCCTGTTCGGTTCGTAAACTGTAATGCAAGTAGCGTATGCGCTCACGCAACTGG TCCAGAACCTTGACCGAACGCAGCGGTGGTAACGCCGCAGTGGCGGTTTTCATGGCTTGT TATGACTGTTTTTTTGTACAGTCTATGCCTCGGGCATCCAAGCAGCAGCGCGTTACGCC GTGGGTCGATGTTTGATGTTATGGAGCAGCAACGATGTTACGCAGCAGCAACGATGTTAC GCAGCAGGCCAGTCGCCCTAAAACAAAGTTAGGTGGCTCAAGTATGGGCATCATTCGCAC ATGTAGGCTCGGCCCTGACCAAGTCAAATCCATGCGGGCTGCTCTTGATCTTTTCGGTCG TGAGTTCGGAGACGTAGCCACCTACTCCCAACATCAGCCGGACTCCGATTACCTCGGGAA CTTGCTCCGTAGTAAGACATTCATCGCGCTTGCTGCCTTCGACCAAGAAGCGGTTGTTGG CGCTCTCGCGGCTTACGTTCTGCCCAGGTTTGAGCAGCCGCGTAGTGAGATCTATATCTA TGATCTCGCAGTCTCCGGCGAGCACCGGAGGCAGGCATTGCCACCGCGCTCATCAATCT  $\verb|CCTCAAGCATGAGGCCAACGCGCTTGGTGCTTATGTGATCTACGTGCAAGCAGATTACGG|\\$ TGACGATCCCGCAGTGGCTCTCTATACAAAGTTGGGCATACGGGAAGAAGTGATGCACTT TGATATCGACCCAAGTACCGCCACCTAACAATTCGTTCAAGCCGAGATCGGCTTCCCGGC CTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTG AATCCGGTGAGAATGGCAAAAGCGTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGC CCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAAT GCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATT CTTCTAATACCTGGAATGCTGTTTTCCCGCGGATCGCAGTGGTGAGTAACCATGCATCAT CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACA  ${\tt ACTCTGGCGCATCGGGCTTCCCATACAATCGAAAGATTGTCGCACCTGATTGCCCGACAT}$ TATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCC TCCAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGT AAGCAGACAGTTTTATTGTTCATGATGATATTTTTTATCTTGTGCAATGTAACATCAGA ACTGATAGTGACCTGTTCGTTGCAACAAATTGATAAGCAATGCTTTTTTATAATGCCAAC -

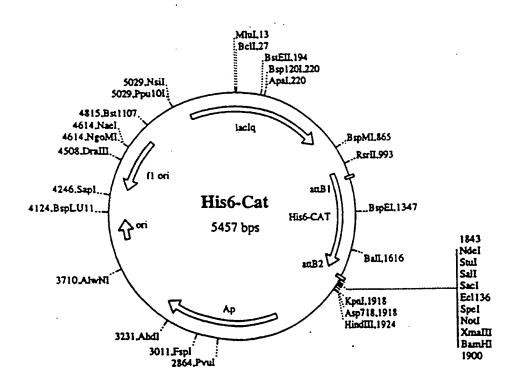
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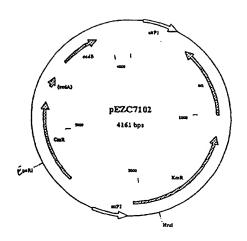
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TEV potesse Tyr Phe Gin Gy The Met Gy Lys Lys The The Gy Tyr The The Vol According that tet can gga acc atg gag and and atc act gga tat acc acc get gat ata and get cet tgg tac etc tet tet tag tga cet ata tgg tgg can eta





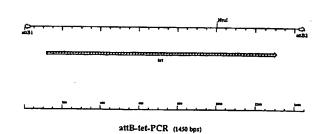
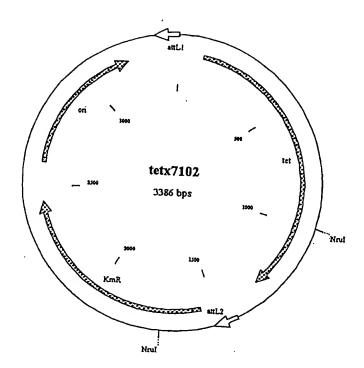


FIGURE 5%



MGURE 57

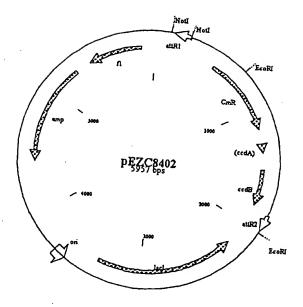
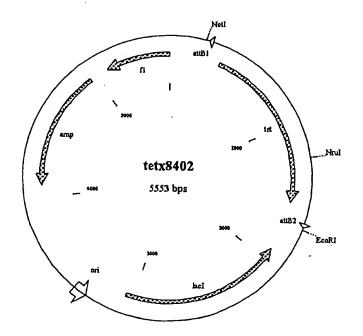
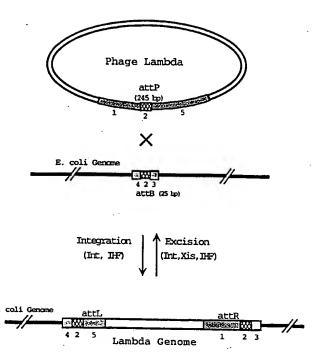


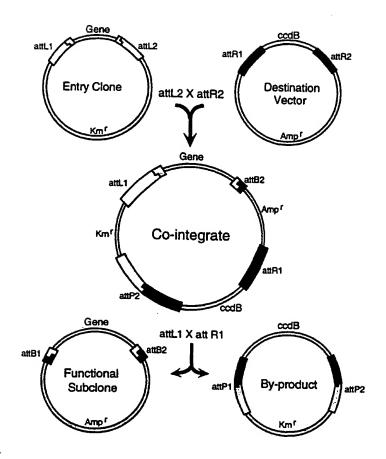
FIGURE 58



FGURE 59



Fauzt 60



Maure 61

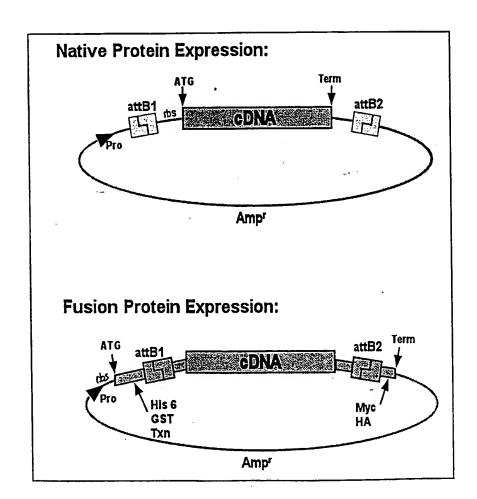
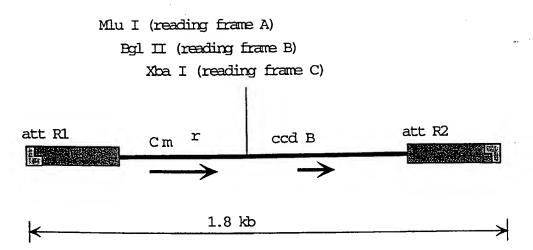
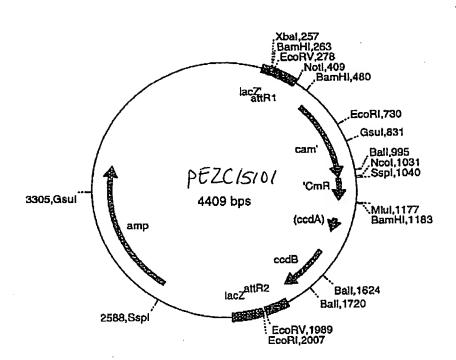


FIGURE 62

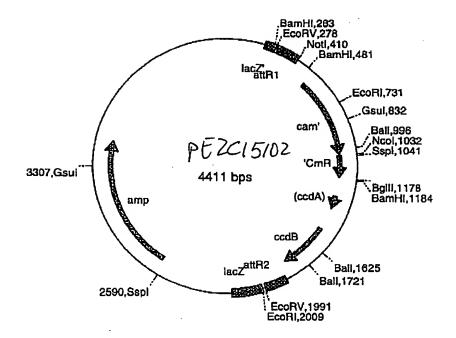


FOURE 63

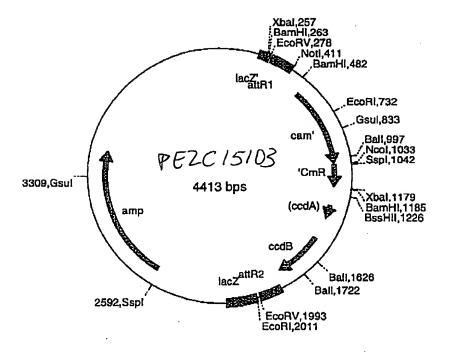
FIGURE 64A



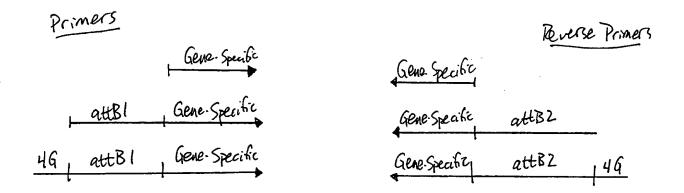
172/240 FIGURE CUB



5



Primers for Amplifying tet R and ample for Cloning by Recombination



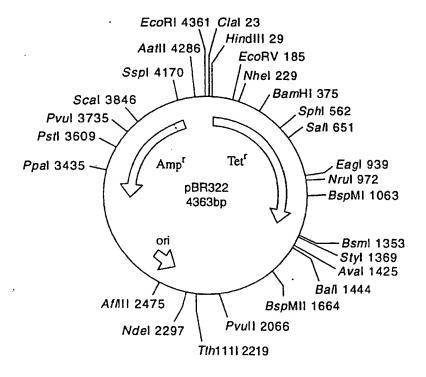
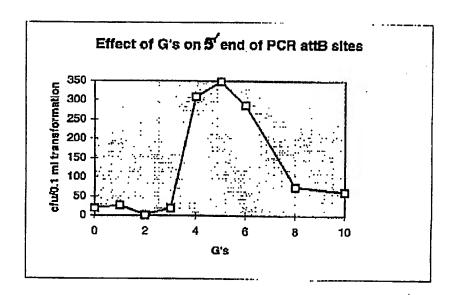


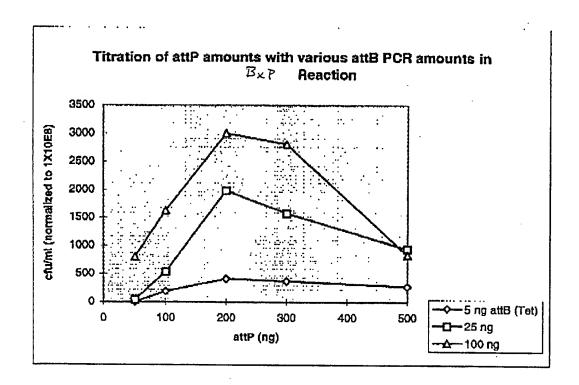
FIGURE 65

## Results of Cloning tet and amp PCR Products by Recombination

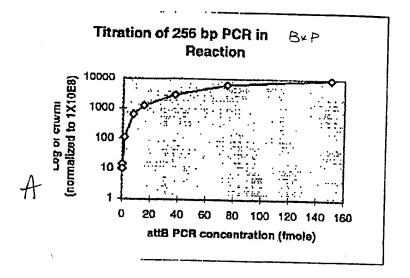
PCR Product Used in GCS Reactions	No. Colonies Obtained (100 ul plated)	Form of DNA Analyzed	Colonies Obtained of Predicted Size
tet	6, 10	SC	0 of 8
attB-tet	9, 6	SC	1 of 8
attB+4G-tet	824, 1064	SC	7 of 7
	ŕ	AvaI+Bam	7 of 7
amp	7, 13	SC	0 of 8
attB-amp	18, 22	SC	3 of 8
attB+4G-amp	3020, 3540	SC	8 of 8
	, , , , , ,	PstI	8 of 8
attB Plasmid (Pos. Control)	320, 394		

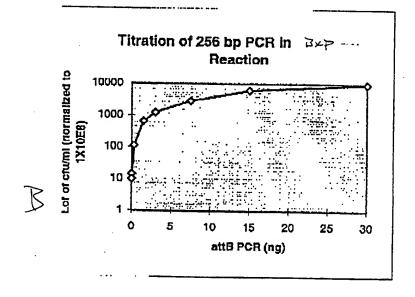


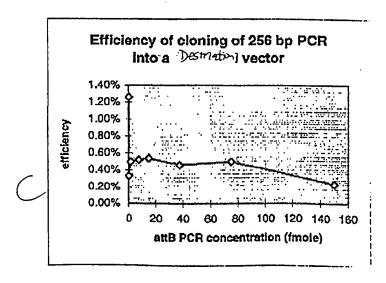
DOURE 67

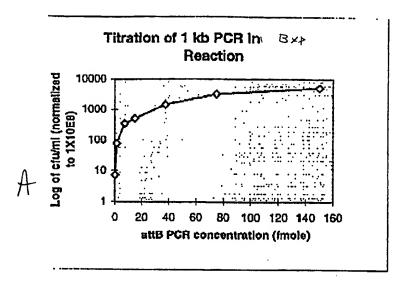


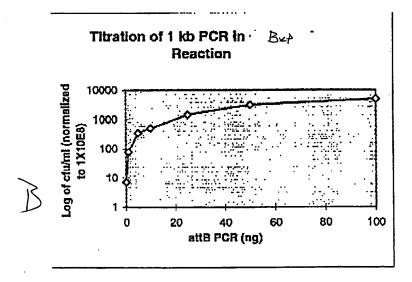
TIGUTÉ 69

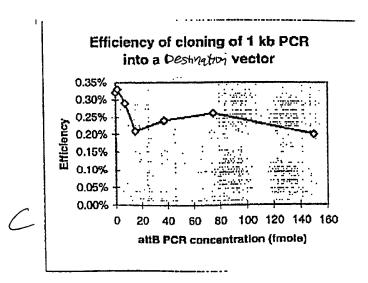




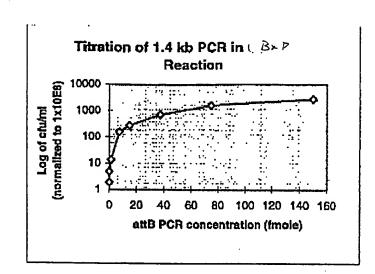




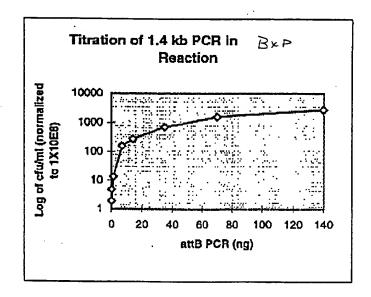




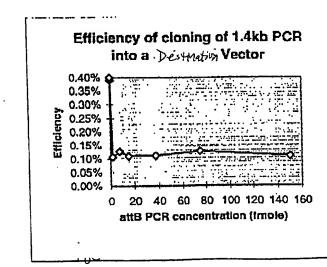
FOURE 71

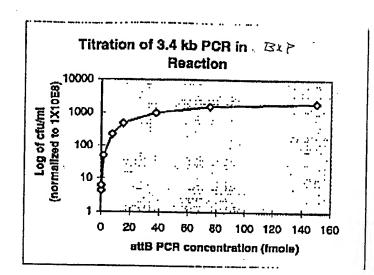


A

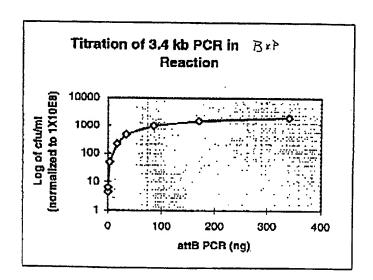


B

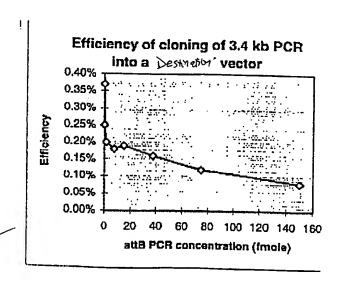


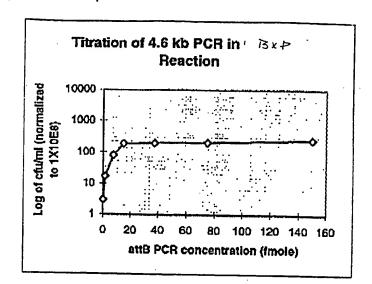


Ĥ

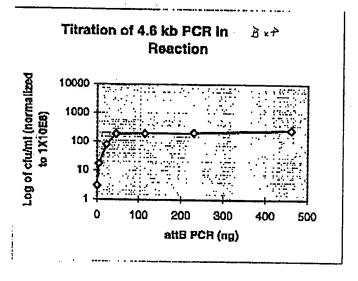


B

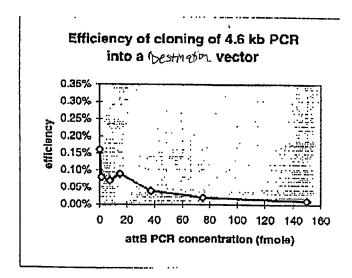




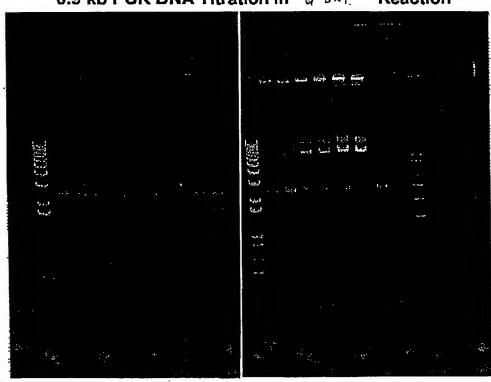
A



B



6.9 kb PCR DNA Titration in [a Bx P Reaction



FOURE 74

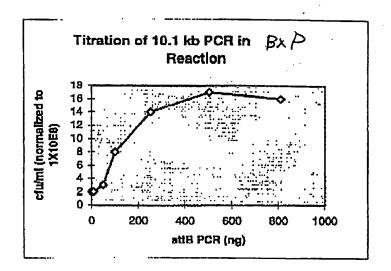
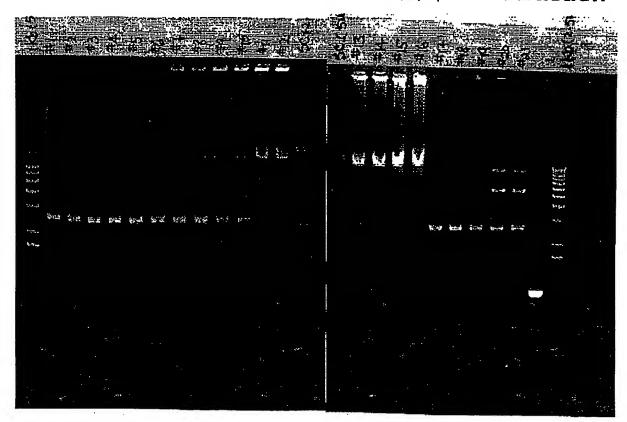


Figure 75-

#### 10.1 kb PCR DNA Titration in $\exists x \vdash$ Reaction



## Cloning of PCR Products of Different Sizes with the GATEWAY™ PCR Cloning System

Size	fmols PCR DNA	ng PCR DNA	Cols/ml Transformation (pUC=108CFU/ml)	Correct Clones/Total Examined**
0.26 kb*	15 37.5	3 7.5	1223 2815	10/10 (a)
1.0 kb	15 37.5	10 25	507 1447	49/50 (b)
1.4 <b>k</b> b	15 37.5	14 35	271 683	48/50 (c)
3.4 kb	15 37.5	34 85	478 976	9/10 (a)
4.6 kb	15 37.5	46 115	190 195	10/10 (a)
6.9 kb	15 37.5	69 173	30 (235)** 54 (463)**	47/50 (b)

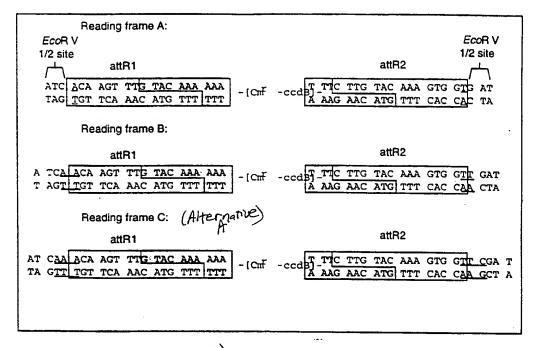
<sup>\*</sup>The 0.26 kb PCR product was used unpurified; all the others were purified by precipitation with PEG/MgCl<sub>2</sub> as described in the text of Example 9, to remove primer dimers potentially present. Standard incubations were for 60 min.

- (a) DNA minipreps
- (b) ampR/kanR
- (c) tetR/kanR

Figure 77

<sup>\*\*</sup>overnight incubation

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Reading frame C: (Alternative)

att R1

AT CAA ACA AGT TTE/TAX ABA/AAX

TA GTT TGT TCA AAC ATG TTT ATT

CMR-ccdB)—

AAC/ AAC/ AAC/ ATC/ TTT CAC CAA ACT A

Fusion protein codon Reading frame A cassette

--- nnn nnn atc aca agt ttg tac aaa aaa gct --- nnn nnn tag tgt tca aac atg ttt ttt cga --- attr 1

Reading frame B cassette

--- nnn nnn nna tca aca agt ttg tac aaa aaa gct ----- nnn nnn nnt agt tgt tca aac atg ttt ttt cga ---

\* cannot be TG or TA

#### Reading frame C cassette

--- nnn nnn nat c<u>aa a</u>ca agt ttg tac aaa aaa gct ----- nnn nnn nta gtt tgt tca aac atg ttt ttt cga ---

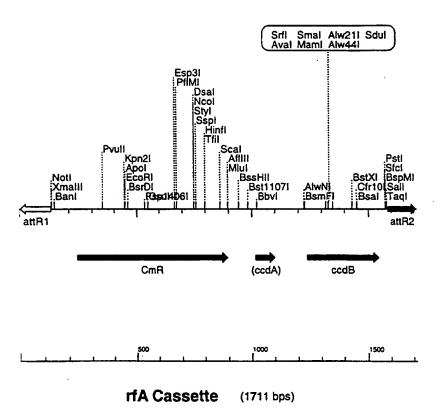
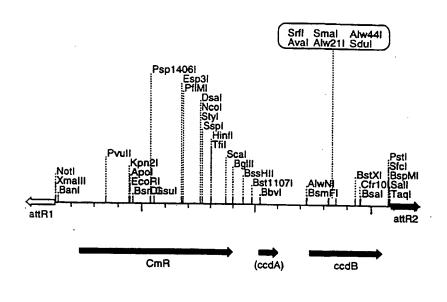
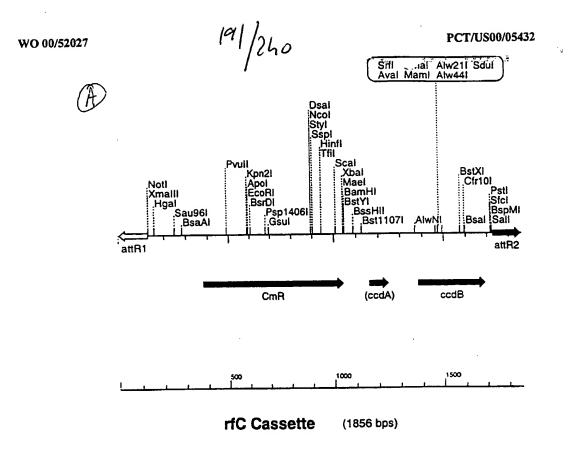
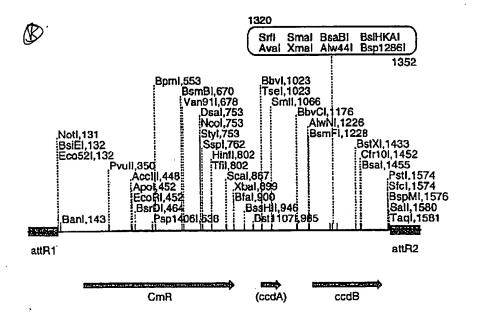


FIGURE 80









rfC cassette (1715 bps)

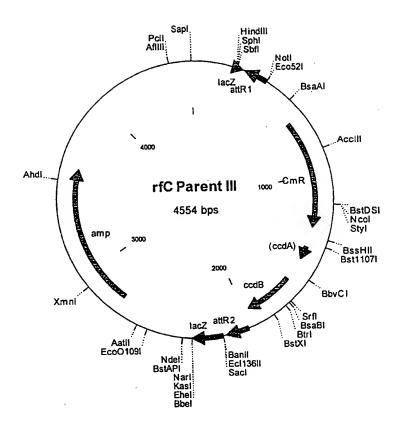


FIGURE 83 A

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#### prfC Parent III 4554 bp

Location (Base Nos.)	Gene Encoded
410286	attR1
6601319	CmR
14391523	inactivated ccdA
16611966	ccdB
20072131	attR2
27533613	amp

1	GCGCCCAATA	CGCAAACCGC	CTCTCCCCGC	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA
61	CGACAGGTTT	CCCGACTGGA	AAGCGGGCAG	TGAGCGCAAC	GCAATTAATG	TGAGTTAGCT
121	CACTCATTAG	GCACCCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	TGTGTGGAAT
181	TGTGAGCGGA	TAACAATTTC	ACACAGGAAA	CAGCTATGAC	CATGATTACG	CCAAGCTTGC
241	ATGCCTGCAG	GTCGACTCTA	GAGGATCCCC	GGGTACCGAT	ATCAAACAAG	TTTGTACAAA
301	AAAGCTGAAC	GAGAAACGTA	AAATGATATA	AATATCAATA	TATTAAATTA	GATTTTGCAT
361	AAAAAACAGA	CTACATAATA	CTGTAAAACA	CAACATATCC	AGTCACTATG	GCGGCCGCTA
421	AGTTGGCAGC	ATCACCCGAC	GCACTTTGCG	CCGAATAAAT	ACCTGTGACG	GAAGATCACT
481	TCGCAGAATA	AATAAATCCT	GGTGTCCCTG	TTGATACCGG	GAAGCCCTGG	GCCAACTTTT
	GGCGAAAATG					
601	GATCACTACC	GGGCGTATTT	TTTGAGTTAT	CGAGATTTTC	AGGAGCTAAG	GAAGCTAAAA
	TGGAGAAAA					
721	ATTTTGAGGC	ATTTCAGTCA	GTTGCTCAAT	GTACCTATAA	CCAGACCGTT	CAGCTGGATA
781	TTACGGCCTT	TTTAAAGACC	GTAAAGAAAA	ATAAGCACAA	GTTTTATCCG	GCCTTTATTC
841	ACATTCTTGC	CCGCCTGATG	AATGCTCATC	CGGAATTCCG	TATGGCAATG	AAAGACGGTG
	AGCTGGTGAT					
961	CGTTTTCATC	GCTCTGGAGT	GAATACCACG	ACGATTTCCG	GCAGTTTCTA	CACATATATT
1021	CGCAAGATGT	GGCGTGTTAC	GGTGAAAACC	TGGCCTATTT	CCCTAAAGGG	TTTATTGAGA
1081	ATATGTTTTT	CGTCTCAGCC	AATCCCTGGG	TGAGTTTCAC	CAGTTTTGAT	TTAAACGTGG
1141	CCAATATGGA	CAACTTCTTC	GCCCCCGTTT	TCACCATGGG	CAAATATTAT	ACGCAAGGCG
1201	ACAAGGTGCT	GATGCCGCTG	GCGATTCAGG	TTCATCATGC	CGTCTGTGAT	GGCTTCCATG
1261	TCGGCAGAAT	GCTTAATGAA	TTACAACAGT	ACTGCGATGA	GTGGCAGGGC	GGGGCGTAAT
1321	CTAGAGGATC	CGGCTTACTA	AAAGCCAGAT	AACAGTATGC	GTATTTGCGC	GCTGATTTTT
1381	GCGGTATAAG	AATATATACT	GATATGTATA	CCCGAAGTAT	GTCAAAAAGA	GGTGTGCTAT
1441	GAAGCAGCGT	ATTACAGTGA	CAGTTGACAG	CGACAGCTAT	CAGTTGCTCA	AGGCATATAT
	GATGTCAATA					
1561	GCCGAACGCT	GGAAAGCGGA	AAATCAGGAA	GGGATGGCTG	AGGTCGCCCG	GTTTATTGAA
1621	ATGAACGGCT	CTTTTGCTGA	CGAGAACAGG	GACTGGTGAA	ATGCAGTTTA	AGGTTTACAC
	CTATAAAAGA					
1741	GCCCGGGCGA	CGGATGGTGA	TCCCCCTGGC	CAGTGCACGT	CTGCTGTCAG	ATAAAGTCTC
1801	CCGTGAACTT	TACCCGGTGG	TGCATATCGG	GGATGAAAGC	TGGCGCATGA	TGACCACCGA
1861	TATGGCCAGT	GTGCCGGTCT	CCGTTATCGG	GGAAGAAGTG	GCTGATCTCA	GCCACCGCGA
	AAATGACATC					
1981	TATACACAGC	CAGTCTGCAG	GTCGACCATA	GTGACTGGAT	ATGTTGTGTT	TTACAGTATT
	ATGTAGTCTG					
	TTTCTCGTTC					
	L GGCCGTCGTT					
	L TGCAGCACAT					
	L TTCCCAACAG					
	GCATCTGTGC					
	1 CGCATAGTTA					
	1 TCTGCTCCCG					
	1 GAGGTTTTCA					
	1 TTTATAGGTI					
	1 AAATGTGCGC					
270	1 CATGAGACA	TAACCCTGAT	AAATGCTTC	A ATAATATTG	A AAAAGGAAGA	GTATGAGTAT
276	1 TCAACATTTO	CGTGTCGCCC	TTATTCCCT	r TTTTGCGGC	A TTTTGCCTTC	CTGTTTTTGC-

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2	821	TCACCCAGAA	ACGCTGGTGA	AAGTAAAAGA	TGCTGAAGAT	CAGTTGGGTG	CACGAGTGGG
2	881	TTACATCGAA	CTGGATCTCA	ACAGCGGTAA	GATCCTTGAG	AGTTTTCGCC	CCGAAGAACG
2	941	TTTTCCAATG	ATGAGCACTT	TTAAAGTTCT	GCTATGTGGC	GCGGTATTAT	CCCGTATTGA
3	001	CGCCGGGCAA	GAGCAACTCG	GTCGCCGCAT	ACACTATTCT	CAGAATGACT	TGGTTGAGTA
3	061	CTCACCAGTC	ACAGAAAAGC	ATCTTACGGA	TGGCATGACA	GTAAGAGAAT	TATGCAGTGC
3	121	TGCCATAACC	ATGAGTGATA	ACACTGCGGC	CAACTTACTT	CTGACAACGA	TCGGAGGACC
3	181	GAAGGAGCTA	ACCGCTTTTT	TGCACAACAT	GGGGGATCAT	GTAACTCGCC	TTGATCGTTG
3	241	GGAACCGGAG	CTGAATGAAG	CCATACCAAA	CGACGAGCGT	GACACCACGA	TGCCTGTAGC
3	301	AATGGCAACA	ACGTTGCGCA	AACTATTAAC	TGGCGAACTA	CTTACTCTAG	CTTCCCGGCA
3	361	ACAATTAATA	GACTGGATGG	AGGCGGATAA	AGTTGCAGGA	CCACTTCTGC	GCTCGGCCCT
3	421	TCCGGCTGGC	TGGTTTATTG	CTGATAAATC	TGGAGCCGGT	GAGCGTGGGT	CTCGCGGTAT
3	481	CATTGCAGCA	CTGGGGCCAG	ATGGTAAGCC	CTCCCGTATC	GTAGTTATCT	ACACGACGGG
3	541	GAGTCAGGCA	ACTATGGATG	AACGAAATAG	ACAGATCGCT	GAGATAGGTG	CCTCACTGAT
3	601	TAAGCATTGG	TAACTGTCAG	ACCAAGTTTA	CTCATATATA	CTTTAGATTG	ATTTAAAACT
3	661	TCATTTTTAA	TTTAAAAGGA	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT
3	721	CCCTTAACGT	GAGTTTTCGT	TCCACTGAGC	GTCAGACCCC	GTAGAAAAGA	TCAAAGGATC
3	781	TTCTTGAGAT	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT
3	841	ACCAGCGGTG	GTTTGTTTGC	CGGATCAAGA	GCTACCAACT	CTTTTTCCGA	AGGTAACTGG
3	901	CTTCAGCAGA	GCGCAGATAC	CAAATACTGT	CCTTCTAGTG	TAGCCGTAGT	TAGGCCACCA
3	961	CTTCAAGAAC	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC
4	021	TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA
4	081	TAAGGCGCAG	CGGTCGGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC
4	141	GACCTACACC	GAACTGAGAT	ACCTACAGCG	TGAGCTATGA	GAAAGCGCCA	CGCTTCCCGA
4	201	AGGGAGAAAG	GCGGACAGGT	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG
4	261	GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG
4	321	ACTTGAGCGT	CGATTTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG
_			TTTTTACGGT				
			CCTGATTCTG				
4	1501	TCGCCGCAGC	CGAACGACCG	AGCGCAGCGA	GTCAGTGAGC	GAGGAAGCGG	AAGA

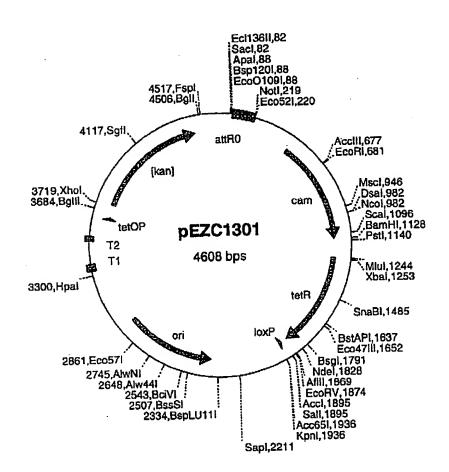
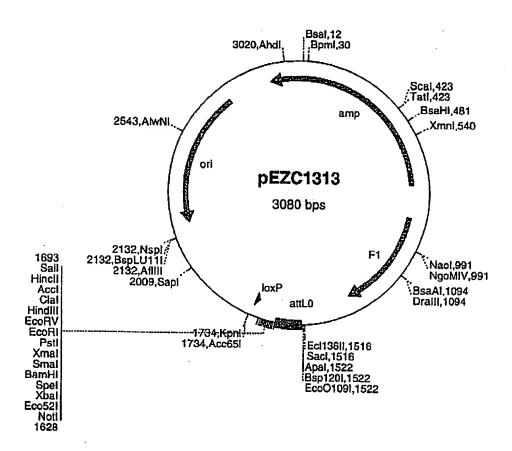
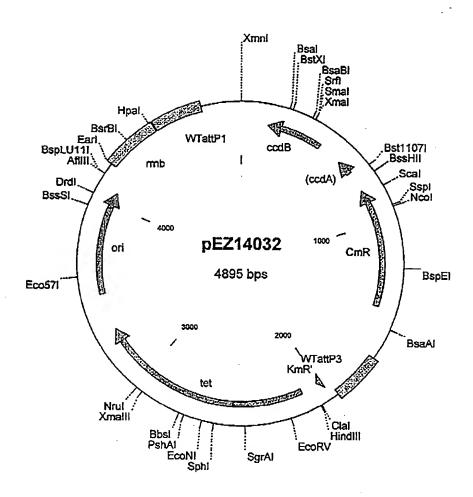
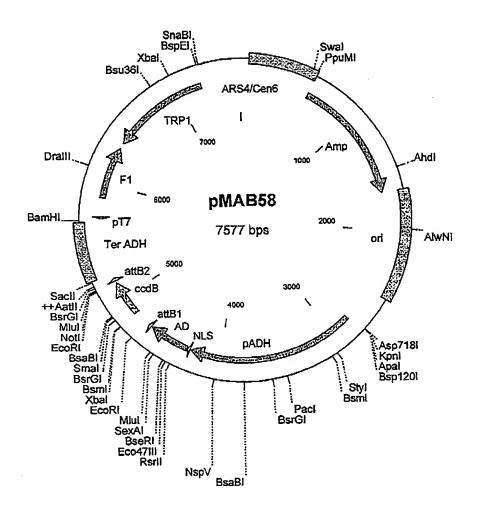


FIGURE 84

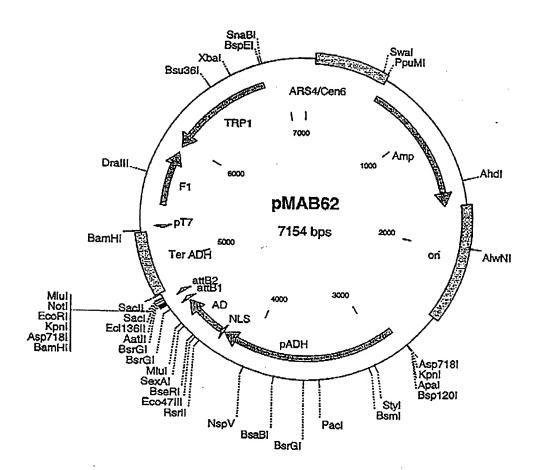




198/240 FIGURE 87



# 199/240 FIGURE 88



DNA to be emplified (5' -> 3'): attBI primer! 9999 ABCD stable primer: Denature, anneal hybrid primers, textend with polymerase Hybrid primers (port atto, part gene specific): CD W. ed x' 1 amplification aycles Denoture, anneal attB primers, extend with polymersse CDW xd'c' ..... dc ba 1939 9339. ... c'D'w' x'dc 1 amplification cycles

Figure 89

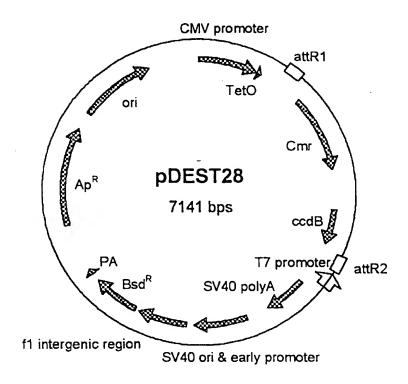


FIGURE 90A

pDEST28 7141 bp

ATGCATGTCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCC CGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTAT GCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC GCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAC AATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGT AGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCCCTATCAGTGATAGAGATCTC CCTATCAGTGATAGAGATCGTCGACGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGACT CTAGAGGATCCCTACCGGTGATATCCTCGAGCCCATCAACAAGTTTGTACAAAAAAGCTG AACGAGAAACGTAAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAAC AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGGCGGCCGCATTAGGCAC CCCAGGCTTTACACTTTATGCTTCCGGCTCGTATAATGTGTGGATTTTGAGTTAGGATCC GGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCAC ATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAA AAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCA TCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCC TTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCA CGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAA CCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTG GGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGT TTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCA GGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACA ATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTA TACCCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGAC AGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCA CAACCATGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGG AAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACA TTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTG GCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATC GGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATC GGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTG ATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACCA TAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTA ATTTAATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGT GGTTGATGGGCGGCCGCTCTAGAGGGCCCAAGCTTACGCGTGCATGCGACGTCATAGCTC TCTCCCTATAGTGAGTCGTATTATAAGCTAGGCACTGGCCGTCGTTTTACAACGTCGTGA CTGGGAAAACTGCTAGCTTGGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATA ATTGGACAAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATATAAAATTTTTAAGTGT ATAATGTGTTAAACTAGCTGCATATGCTTGCTGCTTGAGAGTTTTTGCTTACTGAGTATGA CAGTCCCAAGGCTCATTTCAGGCCCCTCAGTCCTCACAGTCTGTTCATGATCATAATCAG CCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAA CCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGG TTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTC AGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGC CCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACAC TTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTTCTCTCGCCACGTTCG  ${\tt CCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTT-}$  TACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGC CCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCT TGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGA TTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAATATTTAACGCGA ATTTTAACAAATTTTAACGTTTACAATTTCGCCTGATGCGGTATTTTCTCCTTACGCAT CTGTGCGGTATTTCACACCGCATACGCGGATCTGCGCAGCACCATGGCCTGAAATAACCT CTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATGTGT TGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCC TTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCT TTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTTGATTCTTCTGACACAACAGTCTCGAACT TAAGACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGC CGACGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGA ACTCGTGGTGCTGGGCACTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGC GATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCT CGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGT TGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTCGTGGCCG AGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGATGGCCGCAATAAAATA TCTTTATTTTCATTACATCTGTGTGTTTGTTTTTTTGTGTGAATCGATAGCGATAAGGATC CACCCGCCAACACCCGCTGACGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTAC AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCG AAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATA ATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATT TGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAA ATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTT ATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAA GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAAC AGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTT AAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGT CGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCAT CTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAC ACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTG ATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAA GATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGAT GGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAA CGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGAC CAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAAGGATC TAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTC CACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTG GATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCA AATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCG CCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCG TGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGA ACGGGGGGTTCGTGCACACACCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATAC CTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTAT TGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGA TGCTCGTCAGGGGGGGGGGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTC CTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTG GATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAG-

FIGURE 90C

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CGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCC GCGCGTTGGCCGATTCATTAATGCAGAGCTTGCAATTCGCGCGTTTTTCAATATTATTGA AGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAT AAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACC ATATTATCATGACATTAACCTATAAAAATAGGCGTAGTACGAGGCCCTTTCACTCATTA

FIGURE 90D

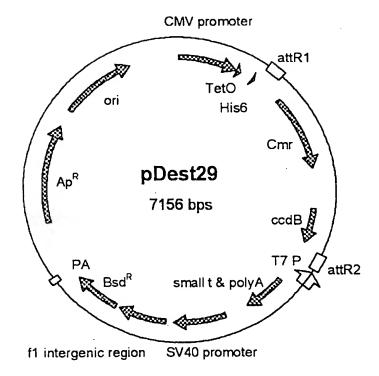


FIGURE 91 A

pDEST29 7156 bp

ATGCATGTCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCC CGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTAT GCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC GCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAC AATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGT AGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCCCTATCAGTGATAGAGATCTC CCTATCAGTGATAGAGATCGTCGACGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGACC ATGGCGTACTACCATCACCATCACCACCACCGGTGATATCCTCGAGCCCATCACAAGT TTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATATTAAATTAG ATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGG CGGCCGCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATAATGTGTGGA TTTTGAGTTAGGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAA TCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAT TTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTT TAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCC GCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATAT GGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGC TCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGG CGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCG TCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACA ACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGA TGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGC TTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGGGTAAACGCGTGGATCCG GCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAA TATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTAT TACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATC TCCGGTCTGGTAAGCACAACCATGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGG AAAGCGGAAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCT TTTGCTGACGAGAACAGGGACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGA GAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACG GATGGTGATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTA CCCGGTGGTGCATATCGGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGT GCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAA AAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCTCCGTTATACACAGCCA GTCTGCAGGTCGACCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTT TTTTATGCAAAATCTAATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAG CTTTCTTGTACAAAGTGGTGATGGGCGGCCGCTCTAGAGGGCCCAAGCTTACGCGTGCAT GCGACGTCATAGCTCTCTCCCTATAGTGAGTCGTATTATAAGCTAGGCACTGGCCGTCGT TTTACAACGTCGTGACTGGGAAAACTGCTAGCTTGGGATCTTTGTGAAGGAACCTTACTT CTGTGGTGTGACATAATTGGACAAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATAT GCTTACTGAGTATGATTTATGAAAATATTATACACAGGAGCTAGTGATTCTAATTGTTTG TGTÄTTTTAGATTCACAGTCCCAAGGCTCATTTCAGGCCCCTCAGTCCTCACAGTCTGTT CATGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCC ACACCTCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTAT TGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATT TTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTG GATCGATCCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGCT GGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG GCGAATGGGACGCCCTGTAGCGGCGCATTAAGCGCGGGGGGTGTGGTGGTTACGCGCA GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT- TCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCAC GTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCT TTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTT TTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAAC AAATATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTTCGCCTGATGCGGTAT TTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATACGCGGATCTGCGCAGCACCAT GGCCTGAAATAACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACC GTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCC CAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCC TAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCCATTCTCCGCCCCATGGCT GACTAATTTTTTTTTTTTTTTTTCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGA AGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTTGATTCTTCTGACA CAACAGTCTCGAACTTAAGACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCAT TGAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG CGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACTGG GGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCTGCGGCAGCTGGCAACCT GACTTGTATCGTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTG CCGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGG ACAGCCGACGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA AGCACTTCGTGGCCGAGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAT GGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCG ATAGCGATAAGGATCCGCGTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAG TTAAGCCAGCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTC CCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTT TCACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAG GTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTG CGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGA CAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACAT TTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCA GAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATC GAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCA ATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGG CAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCA GTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATA ACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAG CTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCG GAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCA ACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTA ATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCT GGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCA GCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAG GCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCAT TAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAA CGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGA GTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGC AGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAG AACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCCC AGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG CAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTAC ACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGA AAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTT CCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAG CGTCGATTTTTGTGATGCTCGTCAGGGGGGGGGGGCCTATGGAAAAACGCCAGCAACGCG GCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTA 

11:

AGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGC AAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGAGCTTGCAATTCGCGCGTT TTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAA TGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT GACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTAGTACGAGG CCCTTTCACTCATTAG

FIGURE 91D

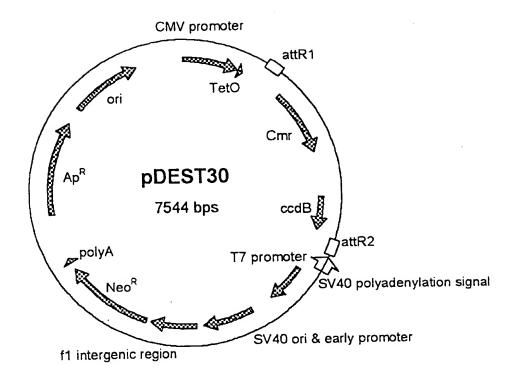


FIGURE 92A

PDEST30

7544 bp

ATGCATGTCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCC CGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT CATATGCCAAGTACGCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTAT GCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC GCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAC AATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGT AGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCCCTATCAGTGATAGAGATCTC CCTATCAGTGATAGAGATCGTCGACGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGACT CTAGAGGATCCCTACCGGTGATATCCTCGAGCCCATCAACAAGTTTGTACAAAAAAGCTG AACGAGAAACGTAAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAAC AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGGCGGCCGCATTAGGCAC CCCAGGCTTTACACTTTATGCTTCCGGCTCGTATAATGTGTGGATTTTGAGTTAGGATCC GGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCAC ATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAA AAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCA TCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCC TTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCA CGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAA CCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTG GGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGT TTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCA GGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACA GTACTGCGATGAGTGGCAGGGCGGGGCGTAAAGATCTGGATCCGGCTTACTAAAAGCCAG ATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTA TACCCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGAC AGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCA CAACCATGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGG AAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACA TTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTG GCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATC GGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATC GGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTG ATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACCA TAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTA ATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGT GGTTGATGGGCGGCCGCTCTAGAGGGCCCAAGCTTACGCGTGCATGCGACGTCATAGCTC TCTCCCTATAGTGAGTCGTATTATAAGCTAGGCACTGGCCGTCGTTTTACAACGTCGTGA  $\tt CTGGGAAAACTGCTAGCTTGGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATA$ ATTGGACAAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATATAAAATTTTTAAGTGT ATAATGTGTTAAACTAGCTGCATATGCTTGCTGCTTGAGAGTTTTGCTTACTGAGTATGA CAGTCCCAAGGCTCATTTCAGGCCCCTCAGTCCTCACAGTCTGTTCATGATCATAATCAG CCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCTGAA CCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGG TTACAAATAAAGCAATAGCATCACAAATTCACAAATAAAGCATTTTTTTCACTGCATTC AGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGC CCTGTAGCGGCGCATTAAGCGCGGGGGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACAC CCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTT- TACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGC CCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCT TGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGA TTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAATATTTAACGCGA ATTTTAACAAAATATTAACGTTTACAATTTCGCCTGATGCGGTATTTTCTCCTTACGCAT CTGTGCGGTATTTCACACCGCATACGCGGATCTGCGCAGCACCATGGCCTGAAATAACCT CTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATGTGT TGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCC TTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCT TTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTTGATTCTTCTGACACAACAGTCTCGAACT TAAGGCTAGAGCCACCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTG GGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGC TCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGG CGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCAT CATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCA CCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCA GGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAA GGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAA TATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGC GGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGA ATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGC CTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGAC CAAGCGACGCCCAACCTGCCATCACGATGGCCGCAATAAAATATCTTTATTTTCATTACA TCTGTGTGTTGTTTTTTGTGTGAATCGATAGCGATAAGGATCCGCGTATGGTGCACTCT CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCCGCCAACACCCCGC TGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGT CTCCGGGAGCTGCATGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGACGAAA GGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGAC GTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAAT ACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTG AAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGC ATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGA TCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGA GAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGG CGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTC TCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGAC AGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACT TCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCA TGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACT ACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGG TGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT CGTAGTTATCTACACGACGGGGGGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC TGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATAT ACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTT TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC CGTAGAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTT GCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAAC TCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGT GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCT GCTAATCCTGTTACCAGTGGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGA CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCAC-

FIGURE 92C

12.

ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTG
AGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGT
CGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCC
TGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCAGGGGGGCG
GAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCC
TTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGC
CTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAG
CGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCA
TTAATGCAGAGCTTGCAATTCGCGCGTTTTTCAATATTATTGAAGCATTTATCAGGGTTC
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCC
GCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATT
AACCTATAAAAATAGGCGTAGTACGAGGCCCTTTCACTCATTAG

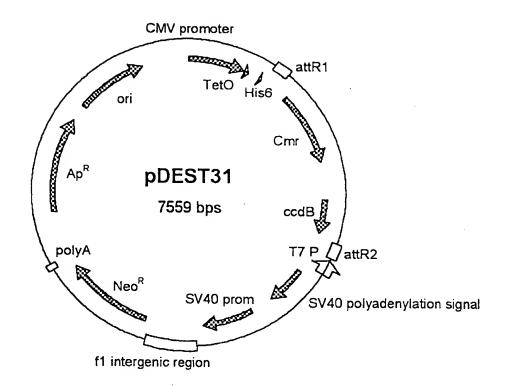


FIGURE 93A

214/240

pDEST31

7559 bp

ATGCATGTCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCC CGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT CATATGCCAAGTACGCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTAT GCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC GCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAC AATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGT AGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCCCTATCAGTGATAGAGATCTC CCTATCAGTGATAGAGATCGTCGACGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGACC ATGGCGTACTACCATCACCATCACCATCACCAGGTGATATCCTCGAGCCCATCACAAGT TTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATAAATTAG ATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGG CGGCCGCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATAATGTGTGGA TTTTGAGTTAGGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAA TCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAT TTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTT TAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCC GCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATAT GGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGC TCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGG CGTGTTACGGTGAAAACCTGGCCTATTCCCTAAAGGGTTTATTGAGAATATGTTTTTCG TCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACA ACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGA TGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGC TTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGGCGTAAACGCGTGGATCCG GCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAA TATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTAT TACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATC TCCGGTCTGGTAAGCACAACCATGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGG AAAGCGGAAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCT TTTGCTGACGAGAACAGGGACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGA GAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACG GATGGTGATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTA CCCGGTGGTGCATATCGGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGT GCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAA AAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCTCCGTTATACACAGCCA GTCTGCAGGTCGACCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTT TTTTATGCAAAATCTAATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAG CTTTCTTGTACAAAGTGGTGATGGGCGGCCGCTCTAGAGGGCCCAAGCTTACGCGTGCAT GCGACGTCATAGCTCTCTCCCTATAGTGAGTCGTATTATAAGCTAGGCACTGGCCGTCGT TTTACAACGTCGTGACTGGGAAAACTGCTAGCTTGGGATCTTTGTGAAGGAACCTTACTT CTGTGGTGTGACATAATTGGACAAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATAT GCTTACTGAGTATGATTATGAAAATATTATACACAGGAGCTAGTGATTCTAATTGTTTG TGTATTTTAGATTCACAGTCCCAAGGCTCATTTCAGGCCCCTCAGTCCTCACAGTCTGTT CATGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCC ACACCTCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTAT TGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATT TTTTTCACTGCATTCTAGTTGTGGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTG GATCGATCCTGCATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGCT GGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG GCGAATGGGACGCCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGGTGGTTACGCGCA GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT- TCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCAC GTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCT TTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTT TTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAAC AAATATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTTCGCCTGATGCGGTAT TTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATACGCGGATCTGCGCAGCACCAT GGCCTGAAATAACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACC GTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCC CAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCC TAACTCCGCCCATCCCGCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCT GACTAATTTTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGA AGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTTGATTCTTCTGACA CAACAGTCTCGAACTTAAGGCTAGAGCCACCATGATTGAACAAGATGGATTGCACGCAGG TTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGG CTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAA GACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCT GGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGA CTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGC CGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC CGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACT GTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGA TGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGG CCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGA TTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGG TTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGATGGCCGCAATAAAATATC TTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGATAGCGATAAGGATCCG CCCGCCAACACCCGCTGACGCGCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAG ACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAA ACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAAT AATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTG TTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAAT GCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTAT TCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGT AAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAG CGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAA AGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCG CCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCT TACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACAC TGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCA ACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACT TAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGG TAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACG AAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCA AGTTTACŢCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTA GGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCA CTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCG TCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAA TACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCC TCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAAC-

FIGURE 93C

FIGURE 93D

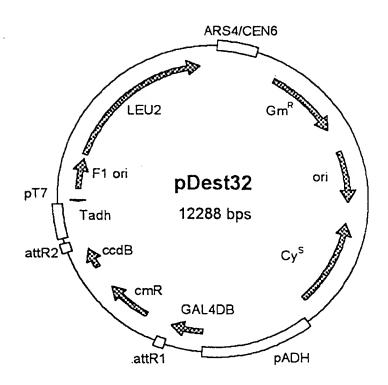


FIGURE 94A

pDEST32

12288 bp

GACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTT CTTAGGACGGATCGCTTGCCTGTAACTTACACGCGCCTCGTATCTTTTAATGATGGAATA ATTTGGGAATTTACTCTGTGTTTATTTATTTTTATGTTTTGTATTTGGATTTTAGAAAGT ATTTCAACAAAAAGCGTACTTTACATATATATTTATTAGACAAGAAAAGCAGATTAAATA TCTACACAGACAAGATGAAACAATTCGGCATTAATACCTGAGAGCAGGAAGAGCAAGATA AAAGGTAGTATTTGTTGGCGATCCCCCTAGAGTCTTTTACATCTTCGGAAAACAAAACT ATTTAAATTATATTTTTTATAGCACGTGATGAAAAGGACCCAGGTGGCACTTTTCGG GGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCG CTCATGAGACAATAACCCTGATAAATGCTTCAATAATCTGCAGTGCGCAGGGCCCGTGTC TCAAAATCTCTGATGTTACATTGCACAAGATAAAAATATATCATCATGAACAATAAAACT GTCTGCTTACATAAACAGTAATACAAGGGGTGTTATGAGCCATATTCAACGGGAAACGTC TTGCTGGAGGCCGCGATTAAATTCCAACATGGATGCTGATTTATATGGGTATAAATGGGC TCGGTAGCCAACCACTAGAACTATAGCTAGAGTCCTGGGCGAACAAACGATGCTCGCCTT CCAGAAAACCGAGGATGCGAACCACTTCATCCGGGGTCAGCACCACCGGCAAGCGCCGCG ACGGCCGAGGTCTTCCGATCTCCTGAAGCCAGGGCAGATCCGTGCACAGCACCTTGCCGT AGAAGAACAGCAAGGCCGCCAATGCCTGACGATGCGTGGAGACCGAAACCTTGCGCTCGT TCGCCAGCCAGGACAGAAATGCCTCGACTTCGCTGCTGCCCAAGGTTGCCGGGTGACGCA CACCGTGGAAACGGATGAAGGCACGAACCCAGTTGACATAAGCCTGTTCGGTTCGTAAAC TGTAATGCAAGTAGCGTATGCGCTCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCG TGCCTCGGGCATCCAAGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGA GCAGCAACGATGTTACGCAGCAGCAGCAGCAGCAGCAGGGCAGTCGCCCTAAAACA AAGTTAGGTGGCTCAAGTATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCAAGTC AAATCCATGCGGGCTGCTCTTGATCTTTTCGGTCGTGAGTTCGGAGACGTAGCCACCTAC TCCCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGCTCCGTAGTAAGACATTCATC GCGCTTGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTCGCGGGCTTACGTTCTGCCC AGGTTTGAGCAGCCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGCGAGCAC CGGAGGCAGGCATTGCCACCGCGCTCATCAATCTCCTCAAGCATGAGGCCAACGCGCTT GGTGCTTATGTGATCTACGTGCAAGCAGATTACGGTGACGATCCCGCAGTGGCTCTCTAT ACAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATCGACCCAAGTACCGCCACC TAACAATTCGTTCAAGCCGAGATCGGCTTCCCGGCCTAATAGGTTGTATTGATGTTGGAC GAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGCCTCGGTGAGT TTTCTCCTTCATTACAGAAACGGCTTTTTCAAAAATATGGTATTGATAATCCTGATATGA ATAAATTGCAGTTTCATTTGATGCTCGATGAGTTTTTCTAATCAGAATTGGTTAATTGGT TGTAACACTGGCAGAGCATTACGCTGACTTGACGGGACGGCGNCATGACCAAAATCCCTT AACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTT  ${\tt CGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCA}$ GCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCA AGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTG CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT ACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGA GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC TTCCAGGGGGGAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCCGAGCCTATGGAAAAACGCCAGCAACG CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT GCAGCCGAACGACCGAGCGCGAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATAC GCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTC CACCCCAGGCTTTACACTTTATGCTTCCGGCTCCTATGTTGTGTGGAATTGTGAGCGGAT AACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCGGAATTAACCCTC- ACTAAAGGGAACAAAAGCTGGTACCGATCCCGAGCTTTGCAAATTAAAGCCTTCGAGCGT CCCAAAACCTTCTCAAGCAAGGTTTTCAGTATAATGTTACATGCGTACACGCGTCTGTAC AGAAAAAAAAGAAAATTTGAAATATAAATAACGTTCTTAATACTAACATAACTATAAAA GTGGGGGGGGGGGGGTGAATGTAAGCGTGACATAACTAATTACATGATATCGACAAAGGAA AAGGGGCCTGTTTACTCACAGGCTTTTTTCAAGTAGGTAATTAAGTCGTTTCTGTCTTTT TTTTTTTTCATAGAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATAT AATTTATTGGAAAATACATAGAGCTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAAC ACCACCAGCAGCTCTGATTTTTTCTTCAGCCAACTTGGAGACGAATCTAGCTTTGACGAT AACTGGAACATTTGGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGT GTCAATAACTGGAGCAGTTTCCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTC TGGGATCAATGTCCACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTTG CTTGTGGAAGTATCTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTT AATTCTGTGGTGATGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTT ACCGATACGACCTTTACCGGCTGAGACGTGACCTCTGTGCTTTCTAGTCTTAGTGAATCT GGAAGGCATTCTTGATTAGTTGGATGATTGTTCTGGGATTTAATGCAAAAATCACTTAAG AAGGAAAATCAACGGAGAAAGCAAACGCCATCTTAAATATACGGGATACAGATGAAAGGG TTTGAACCTATCTGGAAAATAGCATTAAACAAGCGAAAAACTGCGAGGAAAATTGTTTGC GTCTCTGCGGGCTATTCACGCGCCAGAGGAAAATAGGAAAAATAACAGGGCATTAGAAAA ATAATTTTGATTTTGGTAATGTGTGGGTCCTGGTGTACAGATGTTACATTGGTTACAGTA CTCTTGTTTTTGCTGTGTTTTTCGATGAATCTCCAAAATGGTTGTTAGCACATGGAAGAG TCACCGATGCTAAGTTATCTCTATGTAAGCTACGTGGCGTGACTTTTGATGAAGCCGCAC TCGAAGAAATGATGGTAAATGAAATAGGAAATCAAGGAGCATGAAGGCAAAAGACAAATA TAAGGGTCGAACGAAAAATAAAGTGAAAAGTGTTGATATGATGTATTTGGCTTTGCGGCG CCGAAAAAACGAGTTTACGCAATTGCACAATCATGCTGACTCTGTGGCGGACCCGCGCTC TTGCCGGCCCGGCGATAACGCTGGGCGTGAGGCTGTGCCCGGCGGAGTTTTTTGCGCCTG CATTTTCCAAGGTTTACCCTGCGCTAAGGGGCGAGATTGGAGAAGCAATAAGAATGCCGG TTGGGGTTGCGATGATGACGACCACGACAACTGGTGTCATTATTTAAGTTGCCGAAAGAA CCTGAGTGCATTTGCAACATGAGTATACTAGAAGAATGAGCCAAGACTTGCGAGACGCGA GTTTGCCGGTGGTGCGAACAATAGAGCGACCATGACCTTGAAGGTGAGACGCGCATAACC GCTAGAGTACTTTGAAGAGGAAACAGCAATAGGGTTGCTACCAGTATAAATAGACAGGTA CATACAACACTGGAAATGGTTGTCTGTTTGAGTACGCTTTCAATTCATTTGGGTGTGCAC AAGTCCAATGCTAGTAGAGAAGGGGGGTAACACCCCTCCGCGCTCTTTTCCGATTTTTTT CTAAACCGTGGAATATTTCGGATATCCTTTTGTTGTTTCCGGGTGTACAATATGGACTTC CTCTTTTCTGGCAACCAAACCCATACATCGGGATTCCTATAATACCTTCGTTGGTCTCCC TAACATGTAGGTGGCGGAGGGGAGATATACAATAGAACAGATACCAGACAAGACATAATG GGCTAAACAAGACTACACCAATTACACTGCCTCATTGATGGTGGTACATAACGAACTAAT ACTGTAGCCCTAGACTTGATAGCCATCATCATATCGAAGTTTCACTACCCTTTTTCCATT AGGAAAAATTAACGACAAAGACAGCACCAACAGATGTCGTTGTTCCAGAGCTGATGAGG GGTATCTTCGAACACGAAACTTTTTCCTTCCTTCATTCACGCACACTACTCTCTAATG AGCAACGGTATACGGCCTTCCTTCCAGTTACTTGAATTTGAAATAAAAAAAGTTTGCCGC TTTGCTATCAAGTATAAATAGACCTGCAATTATTAATCTTTTGTTTCCTCGTCATTGTTC TCGTTCCCTTTCTTCTTTTTTTTCTGCACAATATTTCAAGCTATACCAAGCATAC AATCAACTCCAAGCTTGAAGCAAGCCTCCTGAAAGATGAAGCTACTGTCTTCTATCGAAC AAGCATGCGATATTTGCCGACTTAAAAAGCTCAAGTGCTCCAAAGAAAAACCGAAGTGCG CCAAGTGTCTGAAGAACAACTGGGAGTGTCGCTACTCTCCCAAAACCAAAAGGTCTCCGC TGACTAGGGCACATCTGACAGAAGTGGAATCAAGGCTAGAAAGACTGGAACAGCTATTTC TACTGATTTTTCCTCGAGAAGACCTTGACATGATTTTGAAAATGGATTCTTTACAGGATA TAAAAGCATTGTTAACAGGATTATTTGTACAAGATAATGTGAATAAAGATGCCGTCACAG ATAGATTGGCTTCAGTGGAGACTGATATGCCTCTAACATTGAGACAGCATAGAATAAGTG CGACATCATCATCGGAAGAGAGTAGTAACAAAGGTCAAAGACAGTTGACTGTATCGTCGA GGTCGAATCAAACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATA-

FIGURE 94C

TCAATATTTAAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAAC ATATCCAGTCACTATGGCGGCCGCTAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGA TACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGG TTCCAACTTTCACCATAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTATCGAG ATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATACCACCGTTGA CTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAA GCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGA ATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTA CACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGA TTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGC CTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAG TTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCAC CATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCA TCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTG CGATGAGTGGCAGGGCGGGCGTAATCTAGAGGATCCGGCTTACTAAAAGCCAGATAACA GTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTATACCCG AAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGAC AGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCA TGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGA TGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGGACT GATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGT GCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATCGGGGAT GAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAA GAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTC TGGGGAATATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACCATAGTGA CTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAA TATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTGGTTTG AGCTTTGGACTTCTTCGCCAGAGGTTTGGTCAAGTCTCCAATCAAGGTTGTCGGCTTGTC TACCTTGCCAGAAATTTACGAAAAGATGGAAAAGGGTCAAATCGTTGGTAGATACGTTGT TGACACTTCTAAATAAGCGAATTTCTTATGATTTATGATTTTTATTAAATAAGTTAT AAAAAAATAAGTGTATACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCTT GTTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTCTCAGGTATAGCATGAGGTCGC TCTTATTGACCACACCTCTACCGGCATGCCGAGCAAATGCCTGCAAATCGCTCCCCATTT CACCCAATTGTAGATATGCTAACTCCAGCAATGAGTTGATGAATCTCGGTGTGTATTTTA TGTCCTCAGAGGACAATACCTGTTGTAATCGTTCTTCCACACGGATCCCAATTCGCCCTA TAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCC TGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAG CGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAC GCGCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGGTGGTTACGCGCAGCGTGACCGCT ACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTTCTCGCCACG TTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGT GCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCA TCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGA CTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAA GGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAAC GCGAATTTTAACAAAATATTAACGTTTACAATTTCCTGATGCGGTATTTTCTCCTTACGC ATCTGTGCGGTATTTCACACCGCATATCGACCGGTCGAGGAGAACTTCTAGTATATCCAC ATACCTAATATTATTGCCTTATTAAAAATGGAATCGGAACAATTACATCAAAATCCACAT TCTCTTCAAAATCAATTGTCCTGTACTTCCTTGTTCATGTGTGTTCAAAAACGTTATATT TATAGGATAATTATACTCTATTTCTCAACAAGTAATTGGTTGTTTGGCCGAGCGGTCTAA GGCGCCTGATTCAAGAAATATCTTGACCGCAGTTAACTGTGGGAATACTCAGGTATCGTA AGATGCAAGAGTTCGAATCTCTTAGCAACCATTATTTTTTTCCTCAACATAACGAGAACA CACAGGGGCGCTATCGCACAGAATCAAATTCGATGACTGGAAATTTTTTTGTTAATTTCAG AGGTCGCCTGACGCATATACCTTTTTCAACTGAAAAATTGGGAGAAAAAGGAAAGGTGAG-

FIGURE 94D

AGGCCGGAACCGGCTTTTCATATAGAATAGAGAAGCGTTCATGACTAAATGCTTGCATCA CAATACTTGAAGTTGACAATATTATTTAAGGACCTATTGTTTTTTCCAATAGGTGGTTAG TCAAGGATATACCATTCTAATGTCTGCCCCTATGTCTGCCCCTAAGAAGATCGTCGTTTT GCCAGGTGACCACGTTGGTCAAGAAATCACAGCCGAAGCCATTAAGGTTCTTAAAGCTAT TTCTGATGTTCGTTCCAATGTCAAGTTCGATTTCGAAAATCATTTAATTGGTGGTGCTGC TATCGATGCTACAGGTGTCCCACTTCCAGATGAGGCGCTGGAAGCCTCCAAGAAGGTTGA TGCCGTTTTGTTAGGTGCTGTGGGTGGTCCTAAATGGGGTACCGGTAGTGTTAGACCTGA ACAAGGTTTACTAAAAATCCGTAAAGAACTTCAATTGTACGCCAACTTAAGACCATGTAA CTTTGCATCCGACTCTCTTTTAGACTTATCTCCAATCAAGCCACAATTTGCTAAAGGTAC TGACTTCGTTGTTGTCAGAGAATTAGTGGGAGGTATTTACTTTGGTAAGAGAAAGGAAGA CGATGGTGATGGTGTCGCTTGGGATAGTGAACAATACACCGTTCCAGAAGTGCAAAGAAT CACAAGAATGGCCGCTTTCATGGCCCTACAACATGAGCCACCATTGCCTATTTGGTCCTT GGATAAAGCTAATGTTTTGGCCTCTTCAAGATTATGGAGAAAAACTGTGGAGGAAAACCAT CCTAGTTAAGAACCCAACCCACCTAAATGGTATTATAATCACCAGCAACATGTTTGGTGA TATCATCTCCGATGAAGCCTCCGTTATCCCAGGTTCCTTGGGTTTGTTGCCATCTGCGTC CTTGGCCTCTTTGCCAGACAAGAACACCGCATTTGGTTTGTACGAACCATGCCACGGTTC TGCTCCAGATTTGCCAAAGAATAAGGTTGACCCTATCGCCACTATCTTGTCTGCTGCAAT GATGTTGAAATTGTCATTGAACTTGCCTGAAGAAGGTAAGGCCATTGAAGATGCAGTTAA AAAGGTTTTGGATGCAGGTATCAGAACTGGTGATTTAGGTGGTTCCAACAGTACCACCGA AGTCGGTGATGCTGTCGCCGAAGAAGTTAAGAAAATCCTTGCTTAAAAAAGATTCTCTTTT TTTATGATATTTGTACATAAACTTTATAAATGAAATTCATAATAGAAACGACACGAAATT CAAGAAGGAGAAAAAGGAGATAGTAAAGGAATACAGGTAAGCAAATTGATACTAATGGC TCAACGTGATAAGGAAAAGAATTGCACTTTAACATTAATATTGACAAGGAGGAGGCAC CACACAAAAAGTTAGGTGTAACAGAAAATCATGAAACTACGATTCCTAATTTGATATTGG TTGATGGAGTTTAAGTCAATACCTTCTTGAACCATTTCCCCATAATGGTGAAAGTTCCCTC AAGAATTTTACTCTGTCAGAAACGGCCTTACGACGTAGTCGATATGGTGCACTCTCAGTA CAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCCGCCAACACCCCGCTGACG CGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCG GGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGA

FIGURE 94E

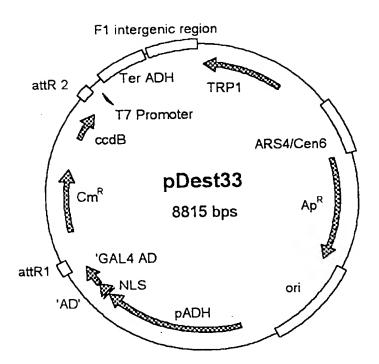


FIGURE 95A

pDEST33

8815 bp

AATACTACTCAGTAATAACCTATTTCTTAGCATTTTTTGACGAAATTTGCTATTTTGTTAG AGTCTTTTACACCATTTGTCTCCACACCTCCGCTTACATCAACACCAATAACGCCATTTA ATCTAAGCGCATCACCAACATTTTCTGGCGTCAGTCCACCAGCTAACATAAAATGTAAGC TTTCGGGGCTCTCTTGCCTTCCAACCCAGTCAGAAATCGAGTTCCAATCCAAAAGTTCAC CTGTCCCACCTGCTTCTGAATCAAACAAGGGAATAAACGAATGAGGTTTCTGTGAAGCTG CACTGAGTAGTATGTTGCAGTCTTTTGGAAATACGAGTCTTTTAATAACTGGCAAACCGA GGAACTCTTGGTATTCTTGCCACGACTCATCTCCATGCAGTTGGACGATATCAATGCCGT ATTTCGGAGTGCCTGAACTATTTTTATATGCTTTTACAAGACTTGAAATTTTCCTTGCAA TAACCGGGTCAATTGTTCTCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCAT CGGAATCTAGAGCACATTCTGCGGCCTCTGTGCTCTGCAAGCCGCAAACTTTCACCAATG GACCAGAACTACCTGTGAAATTAATAACAGACATACTCCAAGCTGCCTTTGTGTGCTTAA TTTTTTCGACCGAATTAATTCTTAATCGGCAAAAAAAGAAAAGCTCCGGATCAAGATTGT ACGTAAGGTGACAAGCTATTTTTCAATAAAGAATATCTTCCACTACTGCCATCTGGCGTC TATAGTAATGTCGTTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAA GCCAGCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGG CATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCAC CGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTA ATGTCATGATAATAATGGTTTCTTAGGACGGATCGCTTGCCTGTAACTTACACGCGCCTC ACAAGAAAAGCAGATTAAATAGATATACATTCGATTAACGATAAGTAAAATGTAAAATCA  ${\tt CAGGATTTTCGTGTGTGTCTTCTACACAGACAAGATGAAACAATTCGGCATTAATACCT}$ GAGAGCAGGAAGACAAGATAAAAGGTAGTATTTGTTGGCGATCCCCCTAGAGTCTTTTA GACCCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAA ATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT TGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCG GCATTTTGCCTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAA GATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTT GAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGT GGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCCAACTCGGTCGCCGCATACACTAT TCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATG ACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTA CTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTTCACAACATGGGGGAT CGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAA GGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCC GGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGT ATCGTAGTTATCTACACGACGGCCAGTCAGGCAACTATGGATGAACGAAATAGACAGATC GCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATAT ATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTT TTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGAC CCCGTAGÂAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGC ACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTA GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT CTGCTAATCCTGTTACCAGTGGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT- TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG GTCGGAACAGGAGGCGCACGAGGGAGCTTCCAGGGGGGAACGCCTGGTATCTTTATAGT CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG CCGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGG CCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACC GCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTG AGCGAGGAAGCGCGCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATT CATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCA ATTAATGTGAGTTACCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCT CCTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCAT GATTACGCCAAGCTCGGAATTAACCCTCACTAAAGGGAACAAAAGCTGGGTACCGGGCCC CCCCTCGAGATCCGGGATCGAAGAAATGATGATGAAATGAAATAGGAAATCAAGGAGCATG AAGGCAAAAGACAAATATAAGGGTCGAACGAAAAATAAAGTGAAAAGTGTTGATATGATG TATTTGGCTTTGCGGCGCCGAAAAAACGAGTTTACGCAATTGCACAATCATGCTGACTCT GTGGCGGACCCGCGCTCTTGCCGGCCCGGCGATAACGCTGGGCGTGAGGCTGTGCCCGGC GGAGTTTTTTGCGCCTGCATTTTCCAAGGTTTACCCTGCGCTAAGGGGCGAGATTGGAGA AGCAATAAGAATGCCGGTTGGGGTTGCGATGATGACGACCACGACAACTGGTGTCATTAT TTAAGTTGCCGAAAGAACCTGAGTGCATTTGCAACATGAGTATACTAGAAGAATGAGCCA AGACTTGCGAGACGCGAGTTTGCCGGTGGTGCGAACAATAGAGCGACCATGACCTTGAAG GTGAGACGCGCATAACCGCTAGAGTACTTTGAAGAGGAAACAGCAATAGGGTTGCTACCA GTATAAATAGACAGGTACATACAACACTGGAAATGGTTGTCTGTTTGAGTACGCTTTCAA TTCATTTGGGTGTGCACTTTATTATGTTACAATATGGAAGGGAACTTTACACTTCTCCTA TGCACATATATTAATTAAAGTCCAATGCTAGTAGAGAAGGGGGGTAACACCCCTCCGCGC TCTTTTCCGATTTTTTCTAAACCGTGGAATATTTCGGATATCCTTTTGTTGTTTCCGGG TGTACAATATGGACTTCCTCTTTTCTGGCAACCAAACCCATACATCGGGATTCCTATAAT ACCTTCGTTGGTCTCCCTAACATGTAGGTGGCGGAGGGGAGATATACAATAGAACAGATA CCAGACAAGACATAATGGGCTAAACAAGACTACACCAATTACACTGCCTCATTGATGGTG GTACATAACGAACTAATACTGTAGCCCTAGACTTGATAGCCATCATCATATCGAAGTTTC ACTACCCTTTTTCCATTTGCCATCTATTGAAGTAATAATAGGCGCATGCAACTTCTTTTC TTTTTTTTTTTTCTCTCTCCCCCGTTGTTGTCTCACCATATCCGCAATGACAAAAAA ATGATGGAAGACACTAAAGGAAAAATTAACGACAAAGACAGCACCAACAGATGTCGTTG TAAAAAAAGTTTGCCGCTTTGCTATCAAGTATAAATAGACCTGCAATTATTAATCTTTTG AGCTATACCAAGCATACAATCAACTCCAAGCTTATGCCCAAGAAGAAGCGGAAGGTCTCG AGCGGCGCCAATTTTAATCAAAGTGGGAATATTGCTGATAGCTCATTGTCCTTCACTTTC CAACCAATTGCCTCCTCTAACGTTCATGATAACTTCATGAATAATGAAATCACGGCTAGT TATAACGCGTTTGGAATCACTACAGGGATGTTTAATACCACTACAATGGATGATGTATAT CAAACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATA TTAAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAACATATCCAG CTGTGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGA AGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACT TTCACCATAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTATCGAGATTTTCAG GAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCC TTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTA TGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTT TCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGC AGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCC CTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCA GTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCA AATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCG-

FRUE 95C

TCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGT GGCAGGGCGGGCGTAATCTAGAGGATCCGGCTTACTAAAAGCCAGATAACAGTATGCGT ATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTATACCCGAAGTATGT CAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACAGCTATCA GTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCATGCAGAAT GAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAG GTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGGACTGGTGAAAT GCAGTTTAAGGTTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTACA GAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGCACGTCT GCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATCGGGGATGAAAGCTG GCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAAGTGGC TGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCTGGGGAAT ATAAATGTCAGGCTCCGTTATACACAGCCAGTCTGCAGGTCGACCATAGTGACTGGATAT GTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGA TATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTGGTTTGATGGCCGC TAAGTAAGTAAGACGTCGAGCTCCCTATAGTGAGTCGTATTACACTGGCCGTCGTTTTAC GAGCTTTGGACTTCTTCGCCAGAGGTTTGGTCAAGTCTCCAATCAAGGTTGTCGGCTTGT CTACCTTGCCAGAAATTTACGAAAAGATGGAAAAGGGTCAAATCGTTGGTAGATACGTTG TAAAAAAAATAAGTGTATACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCT TGTTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTCTCAGGTATAGCATGAGGTCG CTCTTATTGACCACACCTCTACCGGCATGCCGAGCAAATGCCTGCAAATCGCTCCCCATT TCACCCAATTGTAGATATGCTAACTCCAGCAATGAGTTGATGAATCTCGGTGTGTATTTT ATGTCCTCAGAGGACAATACCTGTTGTAATCGTTCTTCCACACGGATCCGCATCAGGCGA AATTGTAAACGTTAATATTTTGTTAAAATTCGCGTTAAATATTTGTTAAATCAGCTCATT TTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGAT AGGGTTGAGTGTTGCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAA CGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTA ATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCC GAAAGGAGCGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCAC ACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCATTCACTGCA

FIGURE 95D

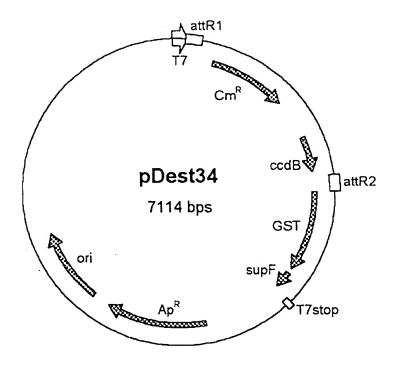


FIGURE 96A

#### pDEST34 7114 bp

Location (Base Nos.)	Gene Encoded
19571	attRl
304963	CmR
13051610	ccdB
16511775	. attR2
17802472	GST .
26752720	T7stop
33344194	ampR
43434982	ori

ATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTC CCTCTAGATCACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATAT CAATATATTAAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACA TATCCAGTCACTATGGCGGCCGCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGC TCGTATAATGTGTGGATTTTGAGTTAGGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCT AAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAA GAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTG GATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTT ATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGAC GGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACT GAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATA TATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATT GAGAATATGTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAAC GTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAA GGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTC CATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGG TAAACGCGTGGATCCGGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGAT TTTTGCGGTATAAGAATATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTGTG CTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCAT ATATGATGTCAATATCTCCGGTCTGGTAAGCACCATGCAGAATGAAGCCCGTCGTCT GCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTAT TGAAATGAACGGCTCTTTTGCTGACGAGAACAGGGACTGGTGAAATGCAGTTTAAGGTTT ACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTG ACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAG TCTCCCGTGAACTTTACCCGGTGGTGCATATCGGGGATGAAAGCTGGCGCATGATGACCA CCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGATCTCAGCCACC GCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCT CCCTTATACACAGCCAGTCTGCAGGTCGACCATAGTGACTGGATATGTTGTGTTTTACAG TATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTATATCATTT TACGTTTCTCGTTCAGCTTTCTTGTACAAAGTGGTGATTATGTCCCCTATACTAGGTTAT TGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTTTTGGAATATCTTGAAGAAAAA TATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAA TTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACAG TCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAA GAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTTCG AGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCT GAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCAT GTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCCA ATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCA CAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAA GCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGTCCATGGGGA TCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCCACCGCTGAGCGCTT CCCGATAAGGGAGCAGGCCAGTAAAAGCATTACCCGTGGTGGGGTTCCCGAGCGGCCAAA GGGAGCAGACTCTAAATCTGCCGTCATCGACTTCGAAGGTTCGAATCCTTCCCCCACCAC CATCACTTTCAAAAGTGAATTCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAA- ACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCGGATATCCACAGGACGG GTGTGGTCGCCATGATCGCGTAGTCGATAGTGGCTCCAAGTAGCGAAGCGAGCAGGACTG GGCGGCGGCCAAAGCGGTCGGACAGTGCTCCGAGAACGGGTGCGCATAGAAATTGCATCA ACGCATATAGCGCTAGCAGCACGCCATAGTGACTGGCGATGCTGTCGGAATGGACGATAT CCCGCAAGAGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTACAGCATCCAGGGTGA CGGTGCCGAGGATGACGATGAGCGCATTGTTAGATTTCATACACGGTGCCTGACTGCGTT AGCAATTTAACTGTGATAAACTACCGCATTAAAGCTTATCGATGATAAGCTGTCAAACAT GAGAATTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATG ATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCT ATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGA TAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCC CTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTG AAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTC AACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACT TTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTGTTGACGCCGGGCAAGAGCAACTC GGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAG CATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGAT AACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTT GCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAACAACGTTGCGC AAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATG GCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCA GATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGAT GAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCA GACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGG ATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCG TTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT CCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATA CCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCA CCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAG TCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGC TGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGA TACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGG TATCCGGTAAGCGGCAGGGTCGGAACAGGAGGGGCGCACGAGGGAGCTTCCAGGGGGAAAC GCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTG TGATGCTCGTCAGGGGGGGGGGGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGG TTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCT GTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACC GAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCTGATGCGGTATTTTCTCCTT ACGCATCTGTGCGGTATTTCACACCGCATATATGGTGCACTCTCAGTACAATCTGCTCTG ATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACGTGACTGGGTCATGGCTGC GCCCCGACACCCGCCAACACCCGCTGACGCCCTGACGGGCTTGTCTGCTCCCGGCATC CGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTC ATCACCGAAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCGTGGTCGTGAAGCGATTC ACAGATGTCTGCCTGTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAGAAGCGTTAATGT CTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTTCCTGTTTGGTCACTGATGC GCTCACGATACGGGTTACTGATGATGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAA ACAACTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGGTCAATGCCAGCG CTTCGTTÄATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGATGCAGAT CCGGAACATAATGGTGCAGGGCGCTGACTTCCGCGTTTCCAGACTTTACGAAACACGGAA ACCGAAGACCATTCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCA CGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGCCAGCCTAG CCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGACCCAACGCTGCC CGAGATGCGCCGCGTGCGGCTGCTGGAGATGGCGGACGCGATGGATATGTTCTGCCAAGG 

FIGURE 96C

GAATCCGTTAGCGAGGTGCCGCCGGCTTCCATTCAGGTCGAGGTGGCCCGGCTCCATGCA CCGCGACGCAACGCGGGGAGGCAGACAAGGTATAGGGCGGCGCCTACAATCCATGCCAAC CCGTTCCATGTGCTCGCCGAGGCGGCATAAATCGCCGTGACGATCAGCGGTCCAGTGATC GAAGTTAGGCTGGTAAGAGCCGCGAGCGATCCTTGAAGCTGTCCCTGATGGTCGTCATCT ACCTGCCTGGACAGCATGGCCTGCAACGCGGGCATCCCGATGCCGCCGGAAGCGAGAAGA ATCATAATGGGGAAGGCCATCCAGCCTCGCGTCGCGAACGCCAGCAAGACGTAGCCCAGC GCGTCGGCCGCCATGCCGGCGATAATGGCCTGCTTCTCGCCGAAACGTTTGGTGGCGGGA CCAGTGACGAAGGCTTGAGCGAGGGCGTGCAAGATTCCGAATACCGCAAGCGACAGGCCG ATCATCGTCGCGCTCCAGCGAAAGCGGTCCTCGCCGAAAATGACCCAGAGCGCTGCCGGC ACCTGTCCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGCGACGATAGTCATG CCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCGATCG ACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCCAGTAGTAGGTTGAGGCCGTT GAGCACCGCCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCCCCGGC CACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGCCCGAAGTGGCGAGC CCGATCTTCCCCATCGGTGATGTCGGCGATATAGGCGCCAGCAACCGCACCTGTGGCGCC GGTGATGCCGGCCACGATGCGTCCGGCGTAGAGG

FIGURE 960

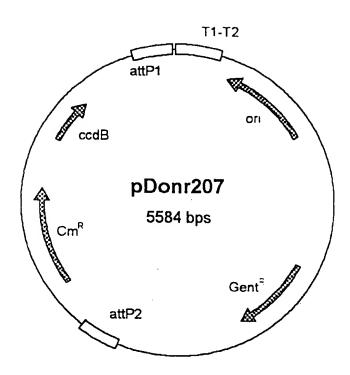


FIGURE 97A

pDONR207

5584 bp

GCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGGAAGACTGGGC CTTTCGTTTTATCTGTTGTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGGG AACTGCCAGGCATCAAACTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGTTTCT ACAAACTCTTCCTGGCTAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGA AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG GCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT CGCTCCAAGCTGGGCTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCC GGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCACCC ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG TGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATT TTGGTCATGAGCTTGCGCCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTACAACC AATTAACCAATTCTGATTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCA TATCAGGATTATCAATACCATATTTTTĞAAAAAGCCGTTTCTGTAATGAAGGAGAAAACT CACCGAGGCAGTTCCATAGGATGCCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTC CAACATCAATACAACCTATTAGTAGCCAACCACTAGAACTATAGCTAGAGTCCTGGGCGA ACAAACGATGCTCGCCTTCCAGAAAACCGAGGATGCGAACCACTTCATCCGGGGTCAGCA CCACCGGCAAGCGCCGCGACGCCGAGGTCTTCCGATCTCCTGAAGCCAGGGCAGATCCG TGCACAGCACCTTGCCGTAGAAGAACAGCAAGGCCGCCAATGCCTGACGATGCGTGGAGA CCGAAACCTTGCGCTCGTTCGCCAGCCAGGACAGAAATGCCTCGACTTCGCTGCCCCA AGGTTGCCGGGTGACGCACACCGTGGAAACGGATGAAGGCACGAACCCAGTTGACATAAG CCTGTTCGGTTCGTAAACTGTAATGCAAGTAGCGTATGCGCTCACGCAACTGGTCCAGAA CCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGGTTTTCATGGCTTGTTATGACT GTTTTTTTGTACAGTCTATGCCTCGGGCATCCAAGCAGCAAGCGCGTTACGCCGTGGGTC GATGTTTGATGTTATGGAGCAGCAACGATGTTACGCAGCAGCAACGATGTTACGCAGCAG GGCAGTCGCCCTAAAACAAAGTTAGGTGGCTCAAGTATGGGCATCATTCGCACATGTAGG CTCGGCCCTGACCAAGTCAAATCCATGCGGGCTGCTCTTGATCTTTTCGGTCGTGAGTTC GGAGACGTAGCCACCTACTCCCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGCTC CGTAGTAAGACATTCATCGCGCTTGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTC GCGGCTTACGTTCTGCCCAGGTTTGAGCAGCCGCGTAGTGAGATCTATATCTATGATCTC GCAGTCTCCGGCGAGCACCGGAGGCAGGGCATTGCCACCGCGCTCATCAATCTCCTCAAG CATGAGGCCAACGCGCTTGGTGCTTATGTGATCTACGTGCAAGCAGATTACGGTGACGAT CCCGCAGTGGCTCTCTATACAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATC GACCCAAGTACCGCCACCTAACAATTCGTTCAAGCCGAGATCGGCTTCCCGGCCTAATTT CCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGG GAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCG GCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAA TACCTGGAATGCTGTTTTTCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGAC CATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGG CGCATCGGGCTTCCCATACAAGCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCG AGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTCGACGT TTCCCGTTGAATATGGCTCATAACACCCCCTGTATTACTGTTATGTAAGCAGACAGTTT TATTGTTCATGATGATATTTTTTATCTTGTGCAATGTAACATCAGAGATTTTGAGACAC GGGCCAGAGCTGCAGCTGGATGGCAAATAATGATTTTATTTTGACTGATAGTGACCTGTT CGTTGCAACAATTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTG AACGAGAAACGTAAAATGATATAAATATCAATATATAAATTAGATTTTGCATAAAAAAC AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATG-

FIGURE 97B

GTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAAT CCGGGAAGCCCTGGGCCAACTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTC CAACTTTCACCATAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTATCGAGATT TTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATAT TAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCA CAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATT CCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACAC CGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTT CCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTA TTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTT CACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCAT GGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCA TGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGA TGAGTGGCAGGGCGGGGCGTAATCGCGTGGATCCGGCTTACTAAAAGCCAGATAACAGTA TGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTATACCCGAAG TATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACAGC TATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCATGC AGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGATGG  $\tt CTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGGACTGGT$ GAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGAT GTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGCA CGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATCGGGGATGAA AGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAA GTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCTGG GGAATATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGATACAGTAGAAAT TACAGAAACTTTATCACGTTTAGTAAGTATAGAGGCTGAAAATCCAGATGAAGCCGAACG ACTTGTAAGAGAAAAGTATAAGAGTTGTGAAATTGTTCTTGATGCAGATGATTTTCAGGA CTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTCACACAAAAAAGAGGC TCGCACCTCTTTTTCTTATTTCTTTTTTATGATTTAATACGGCATTGAGGACAATAGCGAG CATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCT GTTTTTTTTTGCAAAATCTAATTTAATATTGATATTTATATCATTTTACGTTTCTCGTT CAGCTTTTTTGTACAAAGTTGGCATTATAAAAAAGCATTGCTCATCAATTTGTTGCAACG AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGGGGCCCGAGATCCATGCTAGCGT TAAC

FIGURE 97C

#### pMAB85

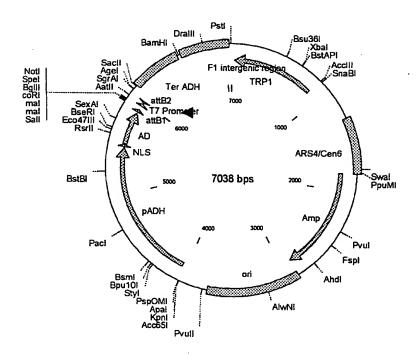


FIGURE 98A

234/240

pMAB85 7038 bp

AATACTACTCAGTAATAACCTATTTCTTAGCATTTTTGACGAAATTTGCTATTTTGTTAG AGTCTTTTACACCATTTGTCTCCACACCTCCGCTTACATCAACACCAATAACGCCATTTA ATCTAAGCGCATCACCAACATTTTCTGGCGTCAGTCCACCAGCTAACATAAAATGTAAGC TTTCGGGGCTCTCTTGCCTTCCAACCCAGTCAGAAATCGAGTTCCAATCCAAAAGTTCAC CTGTCCCACCTGCTTCTGAATCAAACAAGGGAATAAACGAATGAGGTTTCTGTGAAGCTG CACTGAGTAGTATGTTGCAGTCTTTTGGAAATACGAGTCTTTTAATAACTGGCAAACCGA GGAACTCTTGGTATTCTTGCCACGACTCATCTCCATGCAGTTGGACGATATCAATGCCGT ATTTCGGAGTGCCTGAACTATTTTATATGCTTTTACAAGACTTGAAATTTTCCTTGCAA TAACCGGGTCAATTGTTCTCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCAT CGGAATCTAGAGCACATTCTGCGGCCTCTGTGCTCTGCAAGCCGCAAACTTTCACCAATG GACCAGAACTACCTGTGAAATTAATAACAGACATACTCCAAGCTGCCTTTGTGTGCTTAA TTTTTTCGACCGAATTAATTCTTAATCGGCAAAAAAAGAAAAGCTCCGGATCAAGATTGT ACGTAAGGTGACAAGCTATTTTTCAATAAAGAATATCTTCCACTACTGCCATCTGGCGTC ATAACTGCAAAGTACACATATATTACGATGCTGTCTATTAAATGCTTCCTATATTATATA TATAGTAATGTCGTTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAA GCCAGCCCGACACCCGCCAACACCCGCTGACGCCCTGACGGGCTTGTCTGCTCCCGG CATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCAC CGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTA ATGTCATGATAATAATGGTTTCTTAGGACGGATCGCTTGCCTGTAACTTACACGCGCCTC ACAAGAAAAGCAGATTAAATAGATATACATTCGATTAACGATAAGTAAAATGTAAAATCA CAGGATTTTCGTGTGTGGTCTTCTACACAGACAAGATGAAACAATTCGGCATTAATACCT GAGAGCAGGAAGACAAGATAAAAGGTAGTATTTGTTGGCGATCCCCCTAGAGTCTTTTA CATCTTCGGAAAACAAAACTATTTTTTCTTTAATTTCTTTTTTTACTTTCTATTTTAA GACCCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAA ATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT TGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCG GCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAA GATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTT GAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGT GGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTAT TCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATG ACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTA CTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTTCACAACATGGGGGAT CGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAA GGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCC GGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGT ATCGTAGTTATCTACACGACGGCAGTCAGGCAACTATGGATGAACGAAATAGACAGATC GCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATAT ATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTT TTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGAC CCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGC ACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTA GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT CTGCTAATCCTGTTACCAGTGGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC- ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG GTCGGAACAGGAGGCGCACGAGGGAGCTTCCAGGGGGAACGCCTGGTATCTTTATAGT CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG CCGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGG CCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACC GCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTG AGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATT CATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCA ATTAATGTGAGTTACCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCT CCTATGTTGTGGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCAT GATTACGCCAAGCTCGGAATTAACCCTCACTAAAGGGAACAAAAGCTGGGTACCGGGCCC CCCCTCGAGATCCGGGATCGAAGAAATGATGGTAAATGAAATAGGAAATCAAGGAGCATG AAGGCAAAAGACAAATATAAGGGTCGAACGAAAAATAAAGTGAAAAAGTGTTGATATGATG TATTTGGCTTTGCGGCGCCGAAAAAACGAGTTTACGCAATTGCACAATCATGCTGACTCT GTGGCGGACCCGCGCTCTTGCCGGCCCGGCGATAACGCTGGGCGTGAGGCTGTGCCCGGC GGAGTTTTTTGCGCCTGCATTTTCCAAGGTTTACCCTGCGCTAAGGGGCGAGATTGGAGA AGCAATAAGAATGCCGGTTGGGGTTGCGATGATGACGACCACGACAACTGGTGTCATTAT TTAAGTTGCCGAAAGAACCTGAGTGCATTTGCAACATGAGTATACTAGAAGAATGAGCCA AGACTTGCGAGACGCGAGTTTGCCGGTGGTGCGAACAATAGAGCGACCATGACCTTGAAG GTGAGACGCGCATAACCGCTAGAGTACTTTGAAGAGGAAACAGCAATAGGGTTGCTACCA GTATAAATAGACAGGTACATACAACACTGGAAATGGTTGTCTGTTTGAGTACGCTTTCAA TTCATTTGGGTGTGCACTTTATTATGTTACAATATGGAAGGGAACTTTACACTTCTCCTA TGCACATATATTAATTAAAGTCCAATGCTAGTAGAGAAGGGGGGTAACACCCCTCCGCGC TCTTTTCCGATTTTTTTCTAAACCGTGGAATATTTCGGATATCCTTTTGTTGTTTCCGGG TGTACAATATGGACTTCCTCTTTTCTGGCAACCAAACCCATACATCGGGATTCCTATAAT ACCTTCGTTGGTCTCCCTAACATGTAGGTGGCGGAGGGGAGATATACAATAGAACAGATA CCAGACAAGACATAATGGGCTAAACAAGACTACACCAATTACACTGCCTCATTGATGGTG GTACATAACGAACTAATACTGTAGCCCTAGACTTGATAGCCATCATCATATCGAAGTTTC ACTACCCTTTTTCCATTTGCCATCTATTGAAGTAATAATAGGCGCATGCAACTTCTTTTC TTTTTTTTTTTTTCTCTCTCCCCCGTTGTTGTCTCACCATATCCGCAATGACAAAAAAA ATGATGGAAGACACTAAAGGAAAAATTAACGACAAAGACAGCACCAACAGATGTCGTTG TAAAAAAGTTTGCCGCTTTGCTATCAAGTATAAATAGACCTGCAATTATTAATCTTTTG TTTCCTCGTCATTGTTCTCGTTCCCTTTCTTCCTTGTTTCTTTTTCTGCACAATATTTCA AGCTATACCAAGCATACAATCAACTCCAAGCTTATGCCCAAGAAGAAGCGGAAGGTCTCG  ${\tt AGCGGCGCCAATTTTAATCAAAGTGGGAATATTGCTGATAGCTCATTGTCCTTCACTTTC}$ CAACCAATTGCCTCCTCTAACGTTCATGATAACTTCATGAATAATGAAATCACGGCTAGT TATAACGCGTTTGGAATCACTACAGGGATGTTTAATACCACTACAATGGATGATGTATAT ACAAGTTTGTACAAAAAAGCAGGCTTGTCGACCCCGGGAATTCAGATCTACTAGTGCGGC CGCACGCGTACCCAGCTTTCTTGTACAAAGTGGTGACGTCGAGCTCCCTATAGTGAGTCG TATTACACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACACCGGTGAGCTCTAAGT AAGTAACGGCCGCCACCGCGGTGGAGCTTTGGACTTCTTCGCCAGAGGTTTGGTCAAGTC TCCAATCAAGGTTGTCGGCTTGTCTACCTTGCCAGAAATTTACGAAAAGATGGAAAAGGG TCAAATCGTTGGTAGATACGTTGTTGACACTTCTAAATAAGCGAATTTCTTATGATTTAT GATTTTTATTATTAAATAAGTTATAAAAAAAATAAGTGTATACAAATTTTAAAGTGACTC TTAGGTTTTAAAACGAAAATTCTTGTTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCT TTCTCAGGTATAGCATGAGGTCGCTCTTATTGACCACACCTCTACCGGCATGCCGAGCAA ATGCCTGCAAATCGCTCCCCATTTCACCCAATTGTAGATATGCTAACTCCAGCAATGAGT TGATGAATCTCGGTGTGTATTTTATGTCCTCAGAGGACAATACCTGTTGTAATCGTTCTT CCACACGGATCCGCATCAGGCGAAATTGTAAACGTTAATATTTTGTTAAAATTCGCGTTA AATATTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTAT AAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCA CTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGC-

FIGURE 98C

FIGURE 98D

#### pMAB86

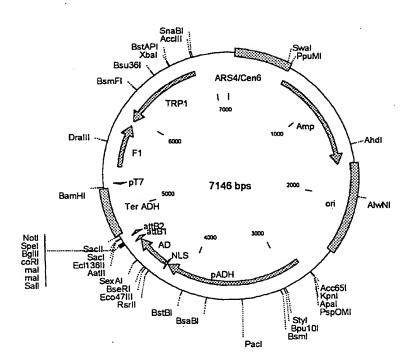


FIGURE 99A

pMAB86 7146 bp

GACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTT CTTAGGACGGATCGCTTGCCTGTAACTTACACGCGCCTCGTATCTTTTAATGATGGAATA ATTTCAACAAAAGCGTACTTTACATATATTTTATTAGACAAGAAAAGCAGATTAAATA TCTACACAGACAAGATGAAACAATTCGGCATTAATACCTGAGAGCAGGAAGAGCAAGATA AAAGGTAGTATTTGTTGGCGATCCCCCTAGAGTCTTTTACATCTTCGGAAAACAAAACT ATTTTTTCTTTAATTTCTTTTTTTACTTTCTATTTTTAATTTAATATATATATATATAAAAA ATTTAAATTATATTTTTTATAGCACGTGATGAAAAGGACCCAGGTGGCACTTTTCGG GGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCG CTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGT ATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCCTTCCTGTTTTT GCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTG GGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAA CGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATT GACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAG TACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGT CCGAAGGAGCTAACCGCTTTTTTTCACAACATGGGGGATCATGTAACTCGCCTTGATCGT TGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTA CAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCC CTTCCGGCTGGCTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGT GGCAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTG CTTCATTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAA ATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA CTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACT GGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCAC CACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTG GCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG GATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGA ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCC GAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACG AGGGAGCTTCCAGGGGGGAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTC TGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCCGAGCCTATGGAAAAACGCC AGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTT GCTCGCCGCAGCCGAACGACCGAGCGAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGC CCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGAC AGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTACCTCACT CATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCCTATGTTGTGTGGAATTGTG AGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCGGAATT AACCCTCACTAAAGGGAACAAAAGCTGGGTACCGGGCCCCCCTCGAGATCCGGGATCGA AGAAATGATGGTAAATGAAATAGGAAATCAAGGAGCCATGAAGGCAAAAGACAAATATAAG GGTCGAACGAAAAATAAAGTGAAAAGTGTTGATATGATGTATTTGGCTTTGCGGCGCCGA AAAAACGAGTTTACGCAATTGCACAATCATGCTGACTCTGTGGCGGACCCGCGCTCTTGC CGGCCCGGCGATAACGCTGGGCGTGAGGCTGTGCCCGGCGGAGTTTTTTGCGCCTGCATT TTCCAAGGTTTACCCTGCGCTAAGGGGCGAGATTGGAGAAGCAATAAGAATGCCGGTTGG GGTTGCGATGACGACCACGACAACTGGTGTCATTATTTAAGTTGCCGAAAGAACCTG AGTGCATTTGCAACATGAGTATACTAGAAGAATGAGCCAAGACTTGCGAGACGCGAGTTT GCCGGTGGTGCGAACAATAGAGCGACCATGACCTTGAAGGTGAGACGCGCATAACCGCTA- GAGTACTTTGAAGAGGAAACAGCAATAGGGTTGCTACCAGTATAAATAGACAGGTACATA CAACACTGGAAATGGTTGTCTGTTTGAGTACGCTTTCAATTCATTTGGGTGTGCACTTTA CCAATGCTAGTAGAGAGGGGGGTAACACCCCTCCGCGCTCTTTTCCGATTTTTTCTAA ACCGTGGAATATTTCGGATATCCTTTTGTTGTTTCCGGGTGTACAATATGGACTTCCTCT TTTCTGGCAACCAAACCCATACATCGGGATTCCTATAATACCTTCGTTGGTCTCCCTAAC ATGTAGGTGGCGGAGGGGAGATATACAATAGAACAGATACCAGACAAGACATAATGGGCT AAACAAGACTACACCAATTACACTGCCTCATTGATGGTGGTACATAACGAACTAATACTG TAGCCCTAGACTTGATAGCCATCATCATATCGAAGTTTCACTACCCTTTTTCCATTTGCC CCCCGTTGTTGTCTCACCATATCCGCAATGACAAAAAAATGATGGAAGACACTAAAGGA AAAAATTAACGACAAGACAGCACCAACAGATGTCGTTGTTCCAGAGCTGATGAGGGGGTA TCTTCGAACACGAAACTTTTTCCTTCCTTCATTCACGCACACTACTCTCTAATGAGCA ACGGTATACGGCCTTCCTTCCAGTTACTTGAATTTGAAATAAAAAAAGTTTGCCGCTTTG CTATCAAGTATAAATAGACCTGCAATTATTAATCTTTTGTTTCCTCGTCATTGTTCTCGT TCCCTTTCTTCCTTGTTTCTTTTTCTGCACAATATTTCAAGCTATACCAAGCATACAATC AACTCCAAGCTTATGCCCAAGAAGAAGCGGAAGGTCTCGAGCGGCGCCAATTTTAATCAA AACCTCATAACAACTCAAACAAATTCTCAAGCGCTTTCACAACCAATTGCCTCCTCTAAC GTTCATGATAACTTCATGAATAATGAAATCACGGCTAGTAAAATTGATGATGGTAATAAT TCAAAACCACTGTCACCTGGTTGGACGGACCAAACTGCGTATAACGCGTTTGGAATCACT GATACCCCACCAAACCCAAAAAAAAGGGGTGGGTCGATCACAAGTTTGTACAAAAAAGCA GGCTTGTCGACCCCGGGAATTCAGATCTACTAGTGCGGCCGCACGCGTACCCAGCTTTCT TGTACAAAGTGGTGACGTCGAGCTCTAAGTAAGTAACGGCCGCCACCGCGGTGGAGCTTT GGACTTCTTCGCCAGAGGTTTGGTCAAGTCTCCAATCAAGGTTGTCGGCTTGTCTACCTT GCCAGAAATTTACGAAAAGATGGAAAAGGGTCAAATCGTTGGTAGATACGTTGTTGACAC AATAAGTGTATACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCTTGTTCTT GAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTCTCAGGTATAGCATGAGGTCGCTCTTAT TGACCACACCTCTACCGGCATGCCGAGCAAATGCCTGCAAATCGCTCCCCATTTCACCCA ATTGTAGATATGCTAACTCCAGCAATGAGTTGATGAATCTCGGTGTATTTTATGTCCT CAGAGGACAATACCTGTTGTAATCGTTCTTCCACACGGATCCCAATTCGCCCTATAGTGA GTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGT TACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGA GGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGACGCCCC TGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTT GCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTTCTCGCCACGTTCGCC GGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA CGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCC TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTG TTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATT TTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAAT TTTAACAAAATATTAACGTTTACAATTTCCTGATGCGGTATTTTCTCCTTACGCATCTGT TAACCTATTTCTTAGCATTTTTGACGAAATTTGCTATTTTGTTAGAGTCTTTTACACCAT TTGTCTCCACACCTCCGCTTACATCAACACCAATAACGCCATTTAATCTAAGCGCATCAC CAACATTTTCTGGCGTCAGTCCACCAGCTAACATAAAATGTAAGCTTTCGGGGCTCTCTT GCCTTCCAACCCAGTCAGAAATCGAGTTCCAATCCAAAAGTTCACCTGTCCCACCTGCTT CTGAATCAAACAAGGGAATAAACGAATGAGGTTTCTGTGAAGCTGCACTGAGTAGTATGT TGCAGTCTTTTGGAAATACGAGTCTTTTAATAACTGGCAAACCGAGGAACTCTTGGTATT CTTGCCACGACTCATCTCCATGCAGTTGGACGATATCAATGCCGTAATCATTGACCAGAG AACTATTTTATATGCTTTTACAAGACTTGAAATTTTCCTTGCAATAACCGGGTCAATTG TTCTCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCATCGGAATCTAGAGCAC ATTCTGCGGCCTCTGTGCTCTGCAAGCCGCAAACTTTCACCAATGGACCAGAACTACCTG TGAAATTAATAACAGACATACTCCAAGCTGCCTTTGTGTGCTTAATCACGTATACTCACG 

FIGURE 99C

TAATTCTTAATCGGCAAAAAAAGAAAAGCTCCGGATCAAGATTGTACGTAAGGTGACAAG CTATTTTCAATAAGAATATCTTCCACTACTGCCATCTGGCGTCATAACTGCAAAGTAC CGCCAACACCCGCTGACGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGAC AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAC GCGCGA

FIGURE 99D

## INDICATIONS RELATING TO A DEPOSITED MICROORGAN SHEC'D (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 54, line	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	•
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and coun	ury)
1815 N. University Street Peoria, Illinois 61604 United States of America	
Date of deposit February 27, 1999	Accession Number NRRL B-30103
C. ADDITIONAL INDICATIONS (leave blank if not appropriate to the state of the state	licable) This information is continued on an additional sheet
Escherichia coli DB3.1(pEZC15101)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATION	ONS ARE MADE (if the indications are not for all designated States)
E. SEPARATE FURNISHING OF INDICATIONS (leave	e blank if not applicable)
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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Authorized officer B. Fullie	Authorized officer

#### INDICATIONS RELATING TO A DEPOSITED MICROORGANISM (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	•
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and coun	try)
1815 N. University Street Peoria, Illinois 61604 United States of America	÷
Date of deposit February 27, 1999	Accession Number NRRL B-30100
C. ADDITIONAL INDICATIONS (leave blank if not appr	licable) This information is continued on an additional sheet
Escherichia coli DB3.1(pENTR-1A)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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Authorized officer Bulliu	Authorized officer

# INDICATIONS RELATING TO A DEPOSITED MICROORGANISM. (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet 🛭
Name of depositary institution	
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and coun	try)
1815 N. University Street Peoria, Illinois 61604 United States of America	
Date of deposit February 27, 1999	Accession Number NRRL B-30102
C. ADDITIONAL INDICATIONS (leave blank if not appl	(icable) This information is continued on an additional sheet
Escherichia coli DB3.1(pENTR-3C)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave	e blank if not applicable)
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROOR GANISM (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page55, line16	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	•
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and count	(רצו)
1815 N. University Street Peoria, Illinois 61604 United States of America	·
Date of deposit February 27, 1999	Accession Number NRRL B-30101
C. ADDITIONAL INDICATIONS (leave blank if not appl	icable) This information is continued on an additional sheet
Escherichia coli DB3.1(pENTR-2B)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave	e blank if not applicable)
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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Authorized officer  D Ludiu	Authorized officer

### INDICATIONS RELATING TO A DEPOSITED MICROORGANISM (PCT Rule 13bis)

A. The indications made below relate to the microorganism 20-21	n referred to in the description on page WIPQ1 IMCT
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	
Agricultural Research Culture Collection (NRRL) International Depository Authority	·
Address of depositary institution (including postal code and coun	try)
1815 N. University Street Peoria, Illinois 61604 United States of America	·
Date of deposit February 27, 1999	Accession Number NRRL B-30108
C. ADDITIONAL INDICATIONS (leave blank if not appl	licable) This information is continued on an additional sheet
Escherichia coli DB10B(pCMVSport6)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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#### INDICATIONS RELATING TO A DEPOSITED MICROOR <u>ANISM</u> (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page, line	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and coun	ntry)
1815 N. University Street Peoria, Illinois 61604 United States of America	·
Date of deposit February 27, 1999	Accession Number NRRL B-30105
C. ADDITIONAL INDICATIONS (leave blank if not app	licable) This information is continued on an additional sheet
Escherichia coli DB3.1(pEZC15103)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (learn	ve blank if not applicable)
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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#### INDICATIONS RELATING TO A DEPOSITED MICROPH (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page	
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	·
Agricultural Research Culture Collection (NRRL) International Depository Authority	
Address of depositary institution (including postal code and coun	(ער)
1815 N. University Street Peoria, Illinois 61604 United States of America	
Date of deposit February 27, 1999	Accession Number NRRL B-30104
C. ADDITIONAL INDICATIONS (leave blank if not appl	icable) This information is continued on an additional sheet $\Box$
Escherichia coli DB3.1(pEZC15102)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leav	e blank if not applicable)
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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Authorized officer Bludie	Authorized officer

### INDICATIONS RELATING TO A DEPOSITED MICROORGARESM (PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page, line31		
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet	
Name of depositary institution		
Agricultural Research Culture Collection (NRRL) International Depository Authority	O P E VOOT	
Address of depositary institution (including postal code and country)		
1815 N. University Street Peoria, Illinois 61604	CATENT & TONOGRAP	
United States of America		
Du. 61		
Date of deposit February 27, 1999	Accession Number NRRL B-30099	
C. ADDITIONAL INDICATIONS-fleave blank if not app	olicable) This information is continued on an additional sheet	
Escherichia coli DB3.1(pAHPKan) or Escherichi	a coli DB3.1(pAttPKan)	
In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)		
E. SEPARATE FURNISHING OF INDICATIONS (lear		
The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")		
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Authorized officer Barbara Fridie POT Operations - ICFD Team 1 7031 305-3230 (FA):	Authorized officer	

Escherichia coli DB3.1(pENTR-3C)

#### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

### **NORWAY**

₹``

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent office or any person approved by the applicant in the individual case.

### **SINGAPORE**

Escherichia coli DB3.1(pENTR-3C)

### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

### UNITED KINGDOM

Escherichia coli DB3.1(pENTR-2B)

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

### **CANADA**

The applicant hereby requests that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

### **DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent office or any person approved by the applicant in the individual case.

### **FINLAND**

Escherichia coli DB3.1(pENTR-2B)

#### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

### **NORWAY**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent office or any person approved by the applicant in the individual case.

### **SINGAPORE**

Escherichia coli DB3.1(pENTR-2B)

### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

### UNITED KINGDOM

Escherichia coli DB3.1(pENTR-1A)

### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

### **CANADA**

The applicant hereby requests that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

#### **DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent office or any person approved by the applicant in the individual case.

#### **FINLAND**

Escherichia coli DB3.1(pENTR-1A)

#### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

#### **NORWAY**

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### **SINGAPORE**

Escherichia coli DB3.1(pENTR-1A)

### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

### **UNITED KINGDOM**

### Escherichia coli DB10B(pCMVSport6)

### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

### **CANADA**

The applicant hereby requests that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

### **DENMARK**

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#### **FINLAND**

Escherichia coli DB3.1(pAHPKan) or Escherichia coli DB3.1(pAttPKan)

### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **CANADA**

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### **DENMARK**

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### **FINLAND**

Escherichia coli DB3.1(pAHPKan) or Escherichia coli DB3.1(pAttPKan)

#### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### **NETHERLANDS**

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### **NORWAY**

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#### **SINGAPORE**

Escherichia coli DB3.1(pAHPKan) or Escherichia coli DB3.1(pAttPKan)

### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

### **UNITED KINGDOM**

### Escherichia coli DB10B(pCMVSport6)

### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **NETHERLANDS**

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### **NORWAY**

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### **SINGAPORE**

### Escherichia coli DB10B(pCMVSport6)

#### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

#### UNITED KINGDOM

Escherichia coli DB3.1(pEZC15103)

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

### **CANADA**

The applicant hereby requests that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

### **DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent office or any person approved by the applicant in the individual case.

### **FINLAND**

Escherichia coli DB3.1(pEZC15103)

#### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

#### NORWAY

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### **SINGAPORE**

Escherichia coli DB3.1(pEZC15103)

### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

### **UNITED KINGDOM**

Escherichia coli DB3.1(pEZC15102)

#### **AUSTRALIA**

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### **CANADA**

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#### DENMARK

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### **FINLAND**

Escherichia coli DB3.1(pEZC15102)

### **ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### **NETHERLANDS**

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### **NORWAY**

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#### **SINGAPORE**

Escherichia coli DB3.1(pEZC15102)

### **SWEDEN**

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### UNITED KINGDOM

Escherichia coli DB3.1(pEZC15101)

### **AUSTRALIA**

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### **FINLAND**

Escherichia coli DB3.1(pEZC15101)

#### **ICELAND**

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#### **SINGAPORE**

Escherichia coli DB3.1(pEZC15101)

#### **SWEDEN**

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### UNITED KINGDOM

Escherichia coli DB3.1(pENTR-3C)

# **AUSTRALIA**

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### **FINLAND**

# INTERNATIONAL SEARCH REPORT

In mational application No. PCT/US00/05432

A. CLAS	A. CLASSIFICATION OF SUBJECT MATTER				
IPC(7) :Please See Extra Sheet.					
US CL :435/91.2, 252.3, 320.1; 530/350; 536/ 23.1, 24.1					
According to International Patent Classification (IPC) or to both national classification and IPC					
B. FIELDS SEARCHED					
Minimum documentation searched (classification system followed by classification symbols)					
U.S. : 435/91.2, 252.3, 320.1; 530/350; 536/ 23.1, 24.1					
Documentation	on searched other than minimum documentation to the	extent that such documents are included	in the fields searched		
NONE					
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)					
Please See Extra Sheet.					
C. DOCUMENTS CONSIDERED TO BE RELEVANT					
Category*	Citation of document, with indication, where ap	propriate, of the relevant passages	Relevant to claim No.		
X,P	US 5,888,732 A (HARTLEY et al.)	30 March 1999, see entire	1-21, 25-30 36-38		
l	document.		22.04.21.25		
Y,P			22-24, 31-35		
x	HASAN et al. Escherichia coli genome targeting, I. Cre-lox- 1-5, 10, 11, 19-21				
-	mediated in vitro generation of ori-				
Y	chromosomal integration and retrieva	l. Gene. 1994, Vol. 150,	15-18, 22-38		
	pages 51-56, see entire document.				
X	KAT7 et al. Site-specific recombinati	on in Esherichia coli hetween	1-11, 19-21		
-	KATZ et al. Site-specific recombination in Esherichia coli between 1-11, 19-21 the att sites of plasmid pSE211 from Saccharopolyspora erythraea.				
Y	Mol. Gen. Genet. 1991, Vol. 227, pages 155-159, see entire 15-18, 22-38				
-	document.				
X Further documents are listed in the continuation of Box C. See patent family annex.					
* Special categories of cited documents:  "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the private or theory underlying the international filing date or priority date and not in conflict with the application but cited to understand the private or theory underlying the international filing date or priority date and not in conflict with the application but cited to understand					
	be of particular relevance	the principle or theory underlying the			
ļ	lier document published on or after the international filing date	"X" document of particular relevance; the considered novel or cannot be conside when the document is taken alone			
cite	cument which may throw doubts on priority claim(s) or which is d to establish the publication date of another citation or other		e claimed invention cannot be		
special reason (as specified)  *O* document referring to an oral disclosure, use, exhibition or other		considered to involve an inventive step when the document is combined with one or more other such documents, such combination			
	nument published prior to the international filing date but later than	being obvious to a person skilled in to  document member of the same patent			
Date of the actual completion of the international search  Date of mailing of the international search report			irch report		
·					
08 MAY 2000 <b>23</b> MAY 2000					
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT  Authorized officer  Authorized officer  For PCT  FOR					
Washington, D.C. 20231  Facsimile No. (703) 305-3230  Telephone No. (703) 308-0196					

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/05432

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
<b>(</b>	ASTUMIAN et al. Site-specific recombination between cloned attP and attB sites from the Haemophilus influenzae bacteriophage HP1 propagated in recombination deficient Escherichia coli. J of Bacteriology. March 1989, Vol. 171, No. 3, pages 1747-1750, see entire document.	1-11, 19-21  15-18, 22-38
		·
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### INTERNATIONAL SEARCH REPORT

n...mational application No. PCT/US00/05432

A. CLASSIFICATION OF SUBJECT MATTER: IPC (7):

C07H 21/04; C07K 1/00, 14/00; C12N 1/21, 15/00, 15/09, 15/63, 15/70; C12P 19/34

**B. FIELDS SEARCHED** 

Electronic data bases consulted (Name of data base and where practicable terms used):

WEST, STN (CAPLUS); DIALOG (MEDLINE, BIOSIS, SCISEARCH, PASCAL)

Terms: att (B?, P?, R?, L?), MCS, POLYLINKER, PLASMID, VECTOR, LOCALIZATION, SIGNAL, TRANSCRIPTION, TERMIN?, TRANSLATION?, ORI, REPLICON, GST, HEXHIST?, THIOREDOX?, CLEAVAGE, SITE?, SPECIF?, DIRECT?, RECOMBIN?, CLON?, INSERT?

Form PCT/ISA/210 (extra sheet) (July 1998)\*